

GenCore version 5.1.3  
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# OM profile - multiple search, using frame-plus.p2n model

Run on: January 31, 2003, 07:12:56 ; Search time 6558 Seconds  
(without alignments)  
4544.262 Million cell updates/sec

Title: US-09-697-089-2  
Perfect score: 5459  
Sequence: 1 MNFKDNRALQRMGMVTI.....MQPDDDLVITGAFKLYTA 1024

Scoring table:  
PAM120  
Xgapop 4.0 , Xgapext 12.0  
Ygapop 4.0 , Ygapext 12.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

## Command line parameters:

-MODEL=frame-plus.model -DEV=xlh  
-O=/cgn2.1/USPTO\_spool/US09697089/tunat\_29012003\_092504\_19158/app-query.fasta.1.1223  
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=pam120 -TRANS=human40.cdi -LIST=45  
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -HEAPSIZE=500 -MTLEN=0 -MAXLEN=200000000  
-USER=US09697089/ecgn\_1.1.4449/etunat\_29012003\_092504\_19158 -NCPU=6 -ICPU=3  
-NO\_XLPHY -NO\_MMAP -LARGEOQUERY -NEG\_SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120  
-WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=4 -XGAPEXT=12 -FGAPOP=6 -FGAPEXT=7  
-XGAPOP=4 -XGAPEXT=12 -DELOP=6 -DELEXT=7

## Database :

1: gb\_ba:\*  
2: gb\_hcg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*

29: em\_vl:\*  
30: em\_hcg\_hum:\*  
31: em\_hcg\_inv:\*  
32: em\_hcg\_other:\*  
33: em\_hcg\_mus:\*  
34: em\_hcg\_pln:\*  
35: em\_hcg\_rod:\*  
36: em\_hcg\_mam:\*  
37: em\_hcg\_vrt:\*  
38: em\_sy:\*  
39: em\_hlgo\_hum:\*  
40: em\_hlgo\_mus:\*  
41: em\_hlgo\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5459	100.0	3133	9	AY032589 Homo sapi
2	5453	99.9	3219	9	AY035391 Homo sapi
3	5453	99.9	3360	9	BC031555 Homo sapi
4	5448	99.8	3581	9	AE376061 Homo sapi
5	5447	99.8	3355	9	AK095467 Homo sapi
6	5438	99.6	3396	6	AX318091 Homo sapi
7	5438	99.6	3396	6	AY027787 Homo sapi
8	3543	64.9	160583	2	AC010968 Homo sapi
9	3539	64.8	138909	2	CNS01DS3
10	2740	50.2	183469	2	AC101793
11	2300	42.1	1355	9	IR2005417
12	1398	29.3	891	6	AX318174
13	1424	26.1	1395	6	AX318093
14	1424	26.1	1395	6	AY027788 Homo sapi
15	1084	19.9	618	6	AX318176
16	853	15.6	768	6	AX318097
17	853	15.6	768	6	AY027789 Homo sapi
18	516	9.5	162982	2	CNS01DS8
19	516	9.5	152881	2	AC011232
20	493	9.0	578	6	AX318095
21	493	9.0	578	6	AY027790 Homo sapi
22	485	8.9	261	6	AX318172
23	363	6.6	107885	2	AC107111
24	358	6.6	83866	2	AC131423
25	307	5.6	553	11	G55568
26	300	5.5	117791	10	AF242431S1
27	297	5.4	41613	10	AF242433S1
28	296	5.4	206808	2	AC093971
29	292	5.3	6829	10	AF135494
30	289	5.3	5269	10	AF135492
31	289	5.3	179252	10	AF131205
32	287	5.3	165	6	AX318178
33	281	5.1	5362	10	AF135491
34	281	5.1	5497	10	AF007769
35	281	5.1	196486	2	AC116741
36	279	5.1	4013	9	AB048534
37	279	5.1	5366	6	E23944
38	279	5.1	5366	6	E24990
39	279	5.1	5502	6	A64509
40	279	5.1	5984	6	E23943
41	279	5.1	5984	6	E24989
42	279	5.1	5984	6	E38321
43	279	5.1	6124	6	A64529
44	279	5.1	6124	6	AX335820
45	279	5.1	6124	9	HS019251

RESULT 1

## ALIGNMENTS

AY032589 Homo sapi  
AY035391 Homo sapi  
BC031555 Homo sapi  
AE376061 Homo sapi  
AK095467 Homo sapi  
AX318091 Homo sapi  
AY027787 Homo sapi  
AC010968 Homo sapi  
AL121653 BAC seque  
AC101793 Mus muscu  
AL189934 Homo sapi  
AX318174 Sequence  
AX318093 Sequence  
AY027788 Homo sapi  
AX318176 Sequence  
AX318097 Sequence  
AY027789 Homo sapi  
AL121658 BAC seque  
AC011232 Homo sapi  
AX318095 Sequence  
AY027790 Homo sapi  
AX318172 Sequence  
AC107111 Rattus no  
AC131423 Rattus no  
G55568 SHGC-100923  
AF242431 Mus muscu  
AF242433 Mus muscu  
AC093971 Rattus no  
AF135494 Mus muscu  
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AF131205 Mus muscu  
AX318178 Sequence  
AF135491 Mus muscu  
AF007769 Mus muscu  
AC116741 Mus muscu  
AB048534 Homo sapi  
E23944 Excessive o  
E24990 Apoptosis-1  
A64509 Sequence 1  
E23943 Excessive o  
E24989 Apoptosis-1  
E38321 Monoclonal  
A64529 Sequence 21  
AX335820 Sequence  
U19251 Homo sapien





Db 1116 ACGCTGTCACATCTTATGATCTGTGATACAGAAAAACAAACATATAAGT 1175  
 QY 381 ValAlaIaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGly 400  
 Db 1176 GTGGCTGCAAGTACTTATTCGGAGCCCTGGACCACTGTGGACACTGCTCTGGAGGGT 1235  
 QY 401 ValIlePheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAspGluAspVal 420  
 Db 1236 GTGTTCTCCCAAGATTGATTGCAACTGCAGATGTCTCAGCGTAAATGAGCATGTC 1295  
 QY 421 LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys 440  
 Db 1296 CTGGCAACACTGGGCTCTCTGTAAATATACAGCTCAAAAGTTCAACCCAAAGATATAA 1355  
 QY 441 PhePheHisLysSerPheGlnGluTyrThrAlaGlnArgPheLysProLysTyrLys 460  
 Db 1356 TTCTTTCACAAAGTATTCAGAGATGACACAGACAGACAAACATCAGAGATTATTCAGC 1415  
 QY 461 SerHisGluProGlnGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle 480  
 Db 1416 TCTCATGACCAAGAGAGAGTACCAAGGGAATGTTACTTCAGAAATGTTCCATT 1475  
 QY 481 SerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu 500  
 Db 1476 TCGGACATTACATCCACTTATAGCAGCCCTCGCGGTACACCTGTGGTCACTGTGGAA 1535  
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 Db 1596 CTTTCACATCGGCAAGAGCCCTCTCGAGACAGGAATCTTGGCAAAAGTGAAAAACACC 1655  
 QY 541 ThrGlnGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGlyCysGlyIleHis 560  
 Db 1656 ACTAGCAAGAAATTCGAAAGCCATTAACATCAATTCCTTGTAGAGTGTGGCATCCAT 1715  
 QY 561 LeuTyrGlnGlnSerThrSerLysSerAlaLeuSerGlnGlnPheGlnAlaPhePheGln 580  
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 Db 1896 ATGGCTTCATAGGAAAAAGCTCGAGAAACACAGTGGATCCACATGGAGAAGGCCCA 1955  
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 Db 2076 GGGAAAAATATTCAGCTCTCCACAAAGCCCTCAGGCTGCAATATAAGATGTCTGTGG 2135  
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 LOCUS AY035391 3219 bp mRNA linear PRI 24-JUL-2001  
 DEFINITION Homo sapiens ICE-protease activating factor mRNA, complete cds.  
 ACCESSION AY035391  
 VERSION AY035391.1 GI:14334214  
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 SOURCE Homo sapiens.  
 ORGANISM Homo sapiens.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 3219)

AUTHORS Poeyt,J.L., Srinivasula,S.M., Tnani,M., Razmzare,M.,  
 TITLE Fernandes-Alnemri,T. and Alnemri,E.S. 1-activating protein  
 related to Apaf-1  
 JOURNAL J. Biol. Chem. 276 (30), 28309-28313 (2001)  
 MEDLINE 21359454  
 PUBMED 11390368  
 REFERENCE 2 (bases 1 to 3219)  
 AUTHORS Poeyt,J.-L., Srinivasula,S.M., Fernandes-Alnemri,T. and  
 Alnemri,E.S.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-MAY-2001) Microbiology and Immunology, Thomas  
 Jefferson University, 233 S. 10th Street, Philadelphia, PA 19107,  
 USA

FEATURES  
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BASE COUNT 934 a 696 c 748 g 841 t

ORIGIN

Alignment Scores:  
 Pred. No.: 0 Length: 3219  
 Score: 5453.00 Matches: 1023  
 Percent Similarity: 99.90% Conservative: 0  
 Best local Similarity: 99.90% Mismatches: 1  
 Query Match: 99.89% Indels: 0  
 DB: Gaps: 0

US-09-697-089-2 (1-1024) x AY035391 (1-3219)

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 QY 21 LysGlnIlethrAspAspLeuPheValTTPasNValLeuAsnArgJugluValAsnIle 40  
 Db 205 AAGCAATTCACAGATGACCTATTGTATGGAATGTCTCGAATCCGAAAGATTAACATC 264  
 QY 41 IlecyScygluLySValgluGlnAspAlaAlaArgglYlleleHsmelleuLyS 60  
 Db 265 ATTTGCTCGGAGAGGTGGACAGAGATGCTGTAGAGGAGCATTCACATGATTTTAAA 324  
 QY 61 LysGlnSerGluSerCysAsnLeuPheLeuLySserLeuLySgluTPasNtyrProleu 80  
 Db 325 AAGGCTTACAGAGTCTCTTCTTAATCCCTTAAGAGAGTGAACATATCTCTTA 384

QY 81 PheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGlnAspLeuAsp 100  
 Db 385 TTTCAGAGCTTGATGATGACAAAGCTTTTTCATCAGACATCAGAGAGAGCTGGACAGT 444  
 QY 101 LeuAlaGlnAspLeuLySAspLeuTyrHisThrProSerPheLeuAsnPheTyrProleu 120  
 Db 445 TTGGCTCGAGATTTAAAGAGCTTGATACCATACCCCATCTTTTGAACTTTATCCCTT 504  
 QY 121 GlyGlnAspIleAspIleIlePheAsnLeuLySserThrPheTrgUpValIleTTP 140  
 Db 505 GGTGAAGATATGACATTAATTTTAAGTGAAGAAAGCACTTCACAGAACTGTCTGTGG 564  
 QY 141 ArgLySAspGlnHisHisHisArgValgluGlnLeuThrLeuAsnGlyLeuGlnAla 160  
 Db 565 AGGAAGACCAACACATCACCCTGTGAGACAGCTGACCTGATGGCTCTGTGACAGCT 624  
 QY 161 LeuGlnSerProCysIleIleIleGluGluGluSerGlyLySgluLySserThrLeuGln 180  
 Db 625 CTTCAGAGCCCTGATCATGATGAAGGGGAATCTGGCAAGGCAAGTCCACTCTCTGAC 684  
 QY 181 ArgIleAlaMetLeuThrTrpGlySerGlyLyScysAlaLeuThrLySAspGlnVal 200  
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 Db 805 CTGGATATACCTGGACATCAGGAAGACACATTCATGCGCATGCTGTAACCTGGG 864  
 QY 241 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLySProGlnAsnCysProGlu 260  
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 QY 261 IleGlnAlaLeuIleLySglnAsnHisArgPheLySAsnMetValIleValThrThr 280  
 Db 925 ATCGAAGCCCTGATGAAGAAACCAACCGCTTCAAGAACATGCTATGTCACCACTCC 984  
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 Db 985 ACTGATGCTCTAAGGACATACGAGATGTTGGTGGCTGACTGCTGAGAGTGGGATATG 1044  
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QY 441 PhePheHisLysSerPheGlnGluTrpThrAlaGlyArgGluSerSerLeuThr 460  
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 Db 1705 CTTTCCATCGCCAGAGGCTCTGTGAGACAGGAATCTTTCGAAAGTGTGAAAAACACC 1764  
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 AUTHORS Strausberg, R.  
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 JOURNAL Submitted (06-JUN-2002) National Institutes of Health, Mammalian  
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 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA  
 CONTACT NIH-MGC Project URL: http://mgc.ncl.nih.gov  
 COMMENT  
 Email: cgabs-remail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 CDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Baylor College of Medicine Human Genome

Sequencing Center  
 Center code: BCM-HGSC  
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
 Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)  
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 Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found  
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AUTHORS Gingras, M.-C., Qiu, J. and Margolin, J.F.  
TITLE Differential expression of the caspase recruitment domain protein 12 (CARD12) during monocytic differentiation  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 3581)  
AUTHORS Gingras, M.-C., Qiu, J. and Margolin, J.F.  
TITLE Direct Submission  
JOURNAL Submitted (03-MAY-2001) Pediatric/Texas Children's Cancer Center, Baylor College of Medicine, 6621 Fannin St. MC3-3320, Houston, TX 77030, USA  
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Location/Qualifiers

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ORGANISM  
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
 AUTHORS  
 Kodaira,H., Furuya,T., Takahashi,M., Kikkawa,E., Omura,Y., Abe,K.,  
 Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M.,  
 Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S.,  
 Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T.,  
 Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M.,  
 Kikuchi,H., Murakawa,K., Kanehori,K., Takahashi-Fujii,A.,  
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 NEDO human cDNA sequencing project  
 Unpublished  
 2 (bases 1 to 3355)  
 REFERENCE  
 Isogai,T. and Yamamoto,J.  
 Direct Submission  
 Submitted (04-JUL-2002) Takeo Isogai, FII Project(HRI Team); 2-6-7

## COMMENT

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 (E-mail: genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)  
 NEDO human cDNA sequencing project supported by Ministry of  
 Economy, Trade and Industry of Japan; cDNA full insert sequencing:  
 Research Association for Biotechnology (RAB); cDNA library  
 construction: Heli Research Institute (HRI) (supported by Japan  
 Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,  
 HRI, and Biotechnology Center, National Institute of Technology and  
 Evaluation; clone selection for full insert sequencing: HRI and

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QY	681	GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaIylVal	700
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QY	701	AlaGlySerLeuSerLeuValIleuSerThrCysLysAsnIleTyrSerLeuMetValGlu	720
Db	2362	GCTGGAAAGCCCACTGGTGGTCCACACCTGTAAACATTAATTCCTCATGTGTGCA	2421
QY	721	AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuysThr	740
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QY	741	LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyIleuThrAspSerLeuGly	760
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QY	761	AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluAspAla	780
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QY	781	IleLysLeuAlaGluGlyLeuLysAsnLeuLysMetCysLeuPheHisLeuThrHis	800
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QY	801	LeuSerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCys	820
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QY	841	AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeu	860
Db	2782	GCTCAGATTCACAAATTTGGTCAAACTGACACTTCATTTATCGAAAAATATACCTG	2841
QY	861	GluLysAspGlyAsnGlnAlaLeuHisGluLeuIleAspArgMetAsnValLeuGlnGln	880
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QY	881	LeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeu	900
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Db	3082	CAGTTGAATTTGGCGGGAATCTGTGACACACTGATGATGCTTCCTCATGGGTGA	3141
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Qy	1001	ArgLeuValGlyTyrGlnPheAspAspAspAspLeuSerValIleIleThrGlyAlaPheLys	1020
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ACCESSION	AX318091		
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KEYWORDS	GI:17900820		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	Reed,J.C., Plo,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H.,		
JOURNAL	Oliveira,V.A., Hayashi,H. and Pawlowski,K.		
FEATURES	Card domain containing polypeptides, encoding nucleic acids, and		
source	Methods of use		
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QY	701	AlaGlySerLeuSerLeuValIleSerThrCysLysAsnIleTyrSerLeuMetValGlu	720
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JOEURL	Genomics 75 (1-3), 77-83 (2001)
MEDLINE	21365712
PUBMED	11472070
REFERENCE	2 (bases 1 to 3396)
AUTHORS	Stehlik, C., Damiano, J.S., Plo, F., Godzik, A. and Reed, J.C.
TITLE	Direct Submission
JOEURL	Submitted (21-FEB-2001) Program on Apoptosis and Cell Death Research, The Burnham Institute, 10901 North Torrey Pines Road, La Jolla, CA 92037, USA
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ACCESSION AC010968
VERSION AC010968.5 GI:9845170
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SOURCE Homo sapiens.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1 (bases 1 to 160583)
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 160583)
REFERENCE Direct Submission
AUTHORS Waterston,R.H.
TITLE 2 (bases 1 to 160583)
JOURNAL Submitted (28-SEP-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT On Aug 18, 2000 this sequence version replaced gi:8439959.

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----- Genome Center -----  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: <http://genome.wustl.edu/gsc/index.shtml>

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----- Project Information -----
Center project name: H.NH0093002
----- Summary Statistics -----
Sequencing vector: M13; 598
Sequencing vector: plasmid; 418
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Chemistry: Dye-terminator Big Dye; 53% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: bases at least Q40
Consensus quality: bases at least Q30
Consensus quality: bases at least Q20
Insert size: 147000; agarose-ff
Insert size: 159583; sum-of-contigs
Quality coverage: 6.64 in Q20 bases; agarose-ff
Quality coverage: 6.38 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 11 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
1 1080: contig of 1080 bp in length
1 1081 1180: gap of unknown length
1 1181 2476: contig of 1296 bp in length
1 2477 2576: gap of unknown length
1 2577 5035: contig of 2459 bp in length
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1 45138 45237: gap of unknown length
1 45238 65522: contig of 20285 bp in length
1 65523 65623: gap of unknown length
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DG:	2	Gaps:	0

US-09-697-089-2 (1-1024) x AC010968 (1-160583)

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VERSION	AL121653		
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SOURCE	human.		
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AUTHORS	1 (bases 1 to 138909)		
	Hazan, J., Fonknechten, N., Mavel, D., Paternotte, C., Samson, D., Arigenaue, F., Davoine, C. S., Ciraud, C., Durr, A., Winkler, P., Brodier, P., Catolico, L., Barbe, V., Burgunder, J. M., Prud'Homme, J. F., Brice, A., Fontaine, B., Heilig, R. and Weissenbach, J.		
TITLE	Spstin, a novel AAA protein, is altered in the most frequent form of autosomal dominant spastic paraplegia		
JOURNML	Nat. Genet. (1999) In press		
REFERENCE	2 (bases 1 to 138909)		
AUTHORS	Genoscope.		
TITLE	Direct Submission		
JOURNAL	Submitted (18-APR-2002) Genoscope - Centre National de Sequenace : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr		
COMMENT	- Web : www.genoscope.cns.fr		
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 AC101793  
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 KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_FULLTOP.  
 SOURCE house mouse.  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 185469)  
 Birren,B., Nusbaum,C. and Lander,E.  
 Mus musculus, clone RP24-178L2  
 JOURNAL  
 TITLE Unpublished  
 2 (bases 1 to 185469)  
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,  
 Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B.,  
 Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,  
 Choepel,Y., Collangelo,M., Collins,S., Collamore,A., Cook,A.,  
 Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Fato,S.,  
 Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,  
 Gande,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,  
 Hagos,B., Hearford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,  
 Jones,C., Kamat,A., Karatas,A., Kells,C., Lacroque,K.,  
 Lamazares,R., Landers,T., Lehoczeky,J., Levine,R., Liu,G.,  
 Maclean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,

McCarthy,M., McEwan,P., McKernan,K., McPeeters,R., Meldrum,J.,  
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 Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,  
 Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,  
 Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,  
 Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupack,R.,  
 Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,  
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 Topham,K., Travers,M., Travis,N., Trillio,J., Vassiliev,H.,  
 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,  
 Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.  
 Direct Submission  
 Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 3 (bases 1 to 185469)  
 Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,  
 Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhgalter,B.,  
 Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collamore,A.,  
 Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,  
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 Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,  
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 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,  
 Zembek,L., Zimmer,A. and Zody,M.  
 Direct Submission  
 Submitted (21-AUG-2002) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Aug 21, 2002 this sequence version replaced g1:17060568.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996, 1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html  
 Genome Center  
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 Center code: WIBR  
 Web site: http://www-seq.wi.mit.edu  
 Contact: sequence\_submissions@genome.wi.mit.edu  
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 Center clone name: 178L2  
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 Chemistry: Dye-terminator Big Dye; 100% of reads  
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 Insert size: 181269; sum-of-contin  
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 Quality coverage: 6.6 in Q20 bases; sum-of-contin  
 NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 43 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.  
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 61 160: gap of 100 bp in length  
 161 824: contig of 664 bp in length  
 825 924: gap of 100 bp in length  
 925 1843: contig of 919 bp in length



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3319	3418:	gap of	100	bp
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4525	4624:	gap of	100	bp
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 REFERENCE 1 (bases 1 to 1355)  
 AUTHORS Aufiray,C., Anserge,M., Ballabio,A., Estivill,X., Gibson,K.,  
 Lehnach,H., Pouska,A. and Lundeberg,J.  
 TITLE The European IMAGE consortium for integrated Molecular analysis of  
 human gene transcripts  
 JOURNAL unpublished  
 REFERENCE 2 (bases 1 to 1355)  
 AUTHORS Pluvinet,R., Estivill,X., Escarceller,M. and Sumoy,L.  
 TITLE Direct Submission  
 JOURNAL Submitted (15-JUL-2000) Dept. Genetica Molecular, Institut de  
 Recerca Oncologica (IRO), Hospital Duran i Reynals, Av. Gran Via  
 s/n Km 2,7 L'Hospitalet de Llobregat, 08907 Barcelona, Catalunya,  
 SPAIN. Tel: ++34-93-260-7775 Fax: ++34-93-260-7776 WWW site:  
 http://www.iro.es e-mail enquiries: lsunoy@iro.es  
 COMMENT EURO-IMAGE Consortium Contact: Aufiray C  
 CNRS UPR 420 - Genetique Moleculaire et Biologie du Developpement  
 IFR 1221 - Rue Guy Moquet 19, Batiment G - BP 8  
 94801 Villejuif Cedex, FRANCE  
 Tel: ++33-1-49 58 34 98  
 Fax: ++33-1-49 58 35 09  
 e-mail: aufiray@infobiogen.fr  
 This clone is available royalty-free through IMAGE Consortium  
 Distributors.  
 IMPORTANT: This sequence represents the full insert of this IMAGE  
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 corresponds to the full-length of the original mRNA from which it  
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KGVASDFIRSLRDLALBGVFSHFDELODVSSVEDVLLTFLTLCKYTAQRK  
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BASE COUNT 237 a 228 c 217 g 209 t  
ORIGIN

Alignment Scores:  
Pred. NO.: 3.77e-234 Length: 891  
Score: 1598.00 Matches: 296  
Percent Similarity: 99.66% Conservative: 0  
Best Local Similarity: 99.66% Mismatches: 1  
Query Match: 29.27% Indels: 0  
DB: Gaps: 0

US-09-697-089-2 (1-1024) x AX318174 (1-891)

QY 161 LeuGlnSerProCysIleIleGlnGlyLeuSerGlyLysGlySerThrLeuGln 180  
DB 1 CTTGAGAGCCCTGCATCATTTGAAGGGAACTGGCAAGCAAGTCCACTCTGTCAG 60  
QY 181 ArgIleAlaMetLeuThrGlySerGlyLysAlaLeuThrLysPheLysPheVal 200  
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QY 201 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuCysAspGlnLeu 220  
DB 121 TTTCTTCCCTGCTCAGAGAGGCCAGGGTGACTTTTGAACCCCTGTGATCAACTC 180  
QY 221 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLysLeuArg 240  
DB 181 CTGGATATACCTGGCAATCAGCAAGACATTCATGGCATGCTGTAAGCTGCGG 240  
QY 241 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnGlyProGlu 260  
DB 241 CAGAGGGTCTTTTCTTCTTGATGGCTACAAATGAAATTCAGCCCAAGCTGCCAGAA 300  
QY 261 IleGlnAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThrThr 280  
DB 301 ATCGAAGCCCGATTAAGAAAGAACACCGCTTCAAGAACATGTCATGTCACCACTAAC 360  
QY 281 ThrGlnCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 300  
DB 361 ACTGAGTCCCTGAGGACATCAGGAGATTGTCCTGACCTGAGAGTGGGGATATG 420  
QY 301 ThrGlnAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGlnGly 320  
DB 421 ACAGAAAGACAGGCCAGGCTCTCATCCGAGAAAGTGTGATCAAGAGGCTGCTGAAGGC 480  
QY 321 LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe 340  
DB 481 TTGTTGTCCTCAAAATTCACAAATCCAGTGCTTGAGAGATTCATCAAGCCCTCTCTTT 540  
QY 341 ValValIleThrCysAlaIleGlnMetGlyLysGluPheHisSerHisThrGlnThr 360  
DB 541 GTGGTCATCAGCTTGTGCATCCAGATGGGTGAAGTGAATTCACCTCACACACAACA 600  
QY 361 ThrLeuPheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysHisLysGly 380  
DB 601 ACGGTGTTCCATCTTATGATCTGTGATACAGAAACAAACAAACAAATTAAGGT 660  
QY 381 ValAlaIleAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGlnGly 400  
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QY 401 ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal 420  
DB 721 GTGTTTCCCAAGATTGATTTCGAAGTGCAGATGTGTCAGAGGTGAATGAGATGTC 780  
QY 421 LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys 440  
DB 781 CTGCTGACAACTGGGCTCTCTGTAAATATACAGCTCAAAAGTTCAAGCCAAAGTATAAA 840

QY 441 PhePheHisLysSerPheGlnGluTyrThrAlaGlyArgArgLeuSer 457  
DB 841 TTTCTTCAAAAGTCAATTCAGAGATACACAGCAGCAAGACTCAGAGT 891

RESULT 13  
AX318093  
LOCUS AX318093 1395 bp DNA Linear PAT 14-DEC-2001  
DEFINITION Sequence 98 from Patent WO0190156.  
ACCESSION AX318093  
VERSION AX318093.1 GI:17900822  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Reed,J.C., Pto,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H.,  
Oliveira,V.A., Hayashi,H. and Pawlowski,K.  
TITLE Card domain containing polypeptides, encoding nucleic acids, and  
methods of use  
JOURNAL Patent: WO 0190156-A 98 29-NOV-2001;  
The Burnham Institute (US)  
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source Location/Qualifiers  
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BASE COUNT 436 a 248 c 327 g 384 t  
ORIGIN

Alignment Scores:  
Pred. NO.: 2.88e-207 Length: 1395  
Score: 1424.00 Matches: 271  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.63% Mismatches: 0  
Query Match: 26.09% Indels: 0  
DB: Gaps: 0

US-09-697-089-2 (1-1024) x AX318093 (1-1395)

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QY 773 IleLysMetAsnGlnGluAspAlaIleLysLeuAlaGlnGlyLysAsnLeuLysLys 792  
DB 598 ATAAAGATGATGAAGAAGATGCTTAAACTAGCTGAAGGCTGAATAAAGCTGAAGAG 657  
QY 793 MetCysLeuPheHisLeuThrHisLeuSerAspIleGlyGlnGlyMetAspTyrIleVal 812  
DB 658 ATGTGTTATTTCATTTGACCCACTTGTCTGACATTTGAGAAGGGAATGATTAATAGTTC 717  
QY 813 LysSerLeuSerSerGlnProCysAspLeuGlnGluIleGlnLeuValSerCysGlyLeu 832  
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QY 833 SerAlaAsnAlaValLysIleLeuAlaGlnAsnLeuHisAsnLeuValLysLeuSerIle 852  
DB 778 TCTGCAAAATGCAAGTAAATCTAGCTCAGAAATCTTCAATTTGGTCAAAAGTGAAGCAT 837  
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Db 838 CTTGATTATTCAGAAATATCTCGAAGAAAGATGAGAAATGAGAACTCTTCATGACATGCATC 897  
Oy 873 ASPATGmetAsnValLeuGlnGlnLeuThrAlaLeuMetLeuProTyrGlyAspVal 892  
Db 896 GACAGAGATGAAAGCTCTGAGAACAGCTACCGACGATGATCTCTCCCTGGGGCTGTGACGTG 957  
Oy 893 GlnGlySerLeuSerSerLeuLeuYshsLeuGlnGluValProGlnLeuValLysLeu 912  
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Db 1318 AGTGTTATTACAGGTCTTTTAACTAGTAAGTACTGCT 1353

RESULT 14  
AY027788 1395 bp mRNA linear PRI 20-JUL-2001

LOCUS Homo sapiens CLANB (CLAN1) mRNA, complete cds.  
DEFINITION AY027788  
ACCESSION AY027788.1 GI:14324114  
VERSION AY027788.1 GI:14324114  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1395)  
AUTHORS Damiano,J.S., Stehlik,C., Plo,F., Godzik,A. and Reed,J.C.  
TITLE Clan, a novel human ced-4-like gene  
JOURNAL Genomics 75 (1-3), 77-83 (2001)  
MEDLINE 21365712  
PUBMED 11472070

REFERENCE 2 (bases 1 to 1395)  
AUTHORS Stehlik,C., Damiano,J.S., Plo,F., Godzik,A. and Reed,J.C.  
TITLE Direct Submission  
JOURNAL Submitted (21-FEB-2001) Program on Apoptosis and Cell Death  
Research, The Burnham Institute, 10901 North Torrey Pines Road, La  
Jolla, CA 92037, USA

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BASE COUNT 436 a 248 c 327 g 384 t  
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Alignment Scores:  
Pred. No.: 2,88e-207 Length: 1395  
Score: 1424.00 Matches: 271  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.63% Mismatches: 0  
Query Match: 26.09% Indels: 0  
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US-09-697-089-2 (1-1024) x AY027788 (1-1395)

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Db 598 ATAAAGATGAATGAAGAAGATCTTAAACAGCTGAAGGCTGAAAAAAGCTGAAGAAG 657  
Oy 793 MetCysLeuPheHisLeuThrHisLeuSerAspIleGlyGlyMetAspTyrIleVal 812  
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LOCUS AX318176 618 bp DNA linear PAT 14-DEC-2001  
DEFINITION Sequence 181 from Patent WO0190156.  
ACCESSION AX318176  
VERSION AX318176.1 GI:17900867  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS 1  
TITLE Reed, J.C., Plo, F.F., Godzik, A., Stehlik, C., Damiano, J.S., Lee, S.H.,  
Oliveira, V.A., Haysahl, H. and Pawlowski, K.  
Card domain containing polypeptides, encoding nucleic acids, and  
methods of use  
JOURNAL Patent: WO 0190156-A 181 29-NOV-2001;  
The Burnham Institute (US)  
FEATURES  
source location/Qualifiers  
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Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 19.86% Indels: 0  
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QY 800 HisleuseraspiileglylmetaspyrillevallysserleuserSerGluasp 819  
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Db 121 CACTTGTCTGACATGAGAGGAGATGATTAAGTCAAGTCTCTCTCAAGTCAACCC 180  
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Job time : 6830 secs

GenCore version 5.1.3  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 31, 2003, 07:11:06 ; Search time 487 Seconds

(without alignments)  
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Title: US-09-697-089-2

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Searched: 2185239 segs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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-YGAPOP=4 -YGAPEXT=12 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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5	5188	95.0	3615	22	AAS03946	Human caspase recr
6	3950	72.4	2215	22	AAH78218	Nucleotide sequenc
7	3346	61.3	2950	22	AAH9581	Human protein enco
8	1598	29.3	891	24	ABK22766	Human cDNA encodin
9	1424	26.1	1395	24	ABK22732	Human cDNA encodin
10	1084	19.9	618	24	ABK22767	Human cDNA encodin
11	1005	18.4	608	22	AAS26160	Human cDNA encodin
12	954	17.5	2735	22	AAH34171	Human colon cancer
13	853	15.6	768	24	ABK22734	Human cDNA encodin
14	725	13.3	522	22	AAS26575	Human cDNA encodin
15	493	9.0	578	24	ABK22735	Human cDNA encodin
16	485	8.9	261	24	ABK22765	Human cDNA encodin
17	435	8.0	421	22	ABA5612	Human breast cell
18	435	8.0	421	22	ABA56119	Human foetal liver
19	435	8.0	421	22	ABA25770	Probe #4236 for ge
20	435	8.0	421	22	AAK04305	Human brain expres
21	435	8.0	421	22	AAK29801	Human bone marrow
22	435	8.0	421	22	AAI14389	Probe #4322 for ge
23	435	8.0	421	22	AAI35764	Probe #4450 used t
24	435	8.0	421	22	AAI04213	Probe #4204 used t
25	435	8.0	421	24	ABS04362	Human genome-deriv
26	391	7.2	220	22	ABA50734	Human breast cell
27	391	7.2	220	22	ABA68704	Human foetal liver
28	391	7.2	220	22	ABA55668	Probe #4134 for g
29	391	7.2	220	22	AAK17044	Human brain expres
30	391	7.2	220	22	AAK42828	Human bone marrow
31	391	7.2	220	22	AAI23590	Probe #13523 for g
32	391	7.2	220	22	AAI48904	Probe #17590 used t
33	391	7.2	220	22	AAI09206	Probe #1979 used t
34	391	7.2	220	24	ABS16884	Human genome-deriv
35	287	5.3	165	24	ABK22768	Human cDNA encodin
36	279	5.1	5366	20	AAK58001	Gonadotrophic hormo
37	279	5.1	5502	17	AAK56273	Human apoptosis in
38	279	5.1	5502	17	AAK30092	Neuronal apoptosis
39	279	5.1	5502	18	AAI71263	Neuronal apoptosis
40	279	5.1	5984	20	AAK58000	Gonadotrophic hormo
41	279	5.1	5984	20	AAK56272	Human apoptosis in
42	279	5.1	5984	21	AAA39808	Human NAIP cDNA.
43	279	5.1	6124	18	AAAT71265	Neuronal apoptosis
44	279	5.1	6124	24	ABL67992	Ovary cancer relat
45	279	5.1	6133	18	AAAT71264	Neuronal apoptosis

## ALIGNMENTS

RESULT 1	
AAS03945	standard; cDNA: 3133 BP.
AC	AAS03945;
XX	
XX	
DE	Human caspase recruitment domain 12 (CARD-12) cDNA.
XX	
XX	Caspase recruitment domain; CARD-12; apoptosis; stress-related pathway;
KW	cancer; viral infection; poxvirus; adenovirus; autoimmune disorder; stroke;
KW	systemic lupus erythematosus; arthritis; neurological disorder; stroke;
KW	Alzheimer's disease; amyotrophic lateral sclerosis; haematologic disease;
KW	aplastic anaemia; myocardial infarction; inflammatory disorder;
KW	Crohn's disease; insulin-dependent diabetes; contact dermatitis;
KW	psoriasis; graft rejection; bacterial infection; lepromatous leprosy;
KW	tuberculosis; ischaemic brain injury; hypoxic brain injury; ss;



kidney ischaemia; reperfusion injury; acute bacterial meningitis;  
excitotoxic brain damage; liver disease.

XX Homo sapiens.

OS  
FH Key Location/Qualifiers  
FM 35..3110  
FT CDS /\*tag= a  
TT /product= "Human CARD-12"

PN MO200130971-A2.

XX  
PD 03-MAY-2001.

XX  
PF 26-OCT-2000; 2000MO-US29643.

XX  
PR 27-OCT-1999; 99US-0161822.

XX  
PA (MILL-) MILLENNium PHARM INC.

XX  
PI Bertin J, Robison KE;

XX  
PI WPI: 2001-308628/32.

DR P-PSDB: MAU02860.

XX  
XX Isolated caspase recruitment domain-12 polypeptide and nucleic acids  
PT encoding them, useful for treating and diagnosing disorders associated  
PT with abnormal apoptosis such as cancer, arthritis and Alzheimer's  
PT disease -  
XX  
XX  
PS Claim 2; Fig 1; 93pp; English.

XX  
XX The sequence represents a cDNA which encodes the human caspase  
CC recruitment domain 12 (CARD-12) polypeptide. CARD domains are found in a  
CC number of proteins that transmit signals that activate apoptosis and  
CC inflammatory pathways in response to stress and other stimuli. Therefore  
CC CARD-12 and its corresponding nucleic acid may be used in treatment and  
CC diagnosis of patients suffering from disorders associated with an  
CC abnormal level (an increase or a decrease) of apoptotic cell death or  
CC abnormal activity of stress-related pathways. The disorders include  
CC cancer, viral infections (e.g. caused by poxviruses, adenoviruses),  
CC autoimmune disorders (e.g. systemic lupus erythematosus, arthritis),  
CC neurological disorders (e.g. Alzheimer's disease, amyotrophic lateral  
CC sclerosis), haematologic diseases (e.g. aplastic anaemia, myocardial  
CC infarction, stroke), inflammatory and immune system disorders (e.g.  
CC Crohn's disease, insulin-dependent diabetes, contact dermatitis,  
CC psoriasis, graft rejection), bacterial infections (e.g. tuberculosis,  
CC lepromatous leprosy), ischaemic and hypoxic brain injury, kidney  
CC ischaemia/reperfusion injury, excitotoxic brain damage, acute bacterial  
CC meningitis and liver disease.

XX  
XX  
SQ Sequence 3133 BP; 903 A; 691 C; 729 G; 810 T; 0 other;

Alignment Scores:

Align. No.:	0	Length:	3133
Score:	5459.00	Matches:	1024
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	22	Gaps:	0

US-09-697-089-2 (1-1024) x AAS03945 (1-3133)

QY 1 MetAsnPhelIeLYsAsPAsnSeRfARgAlaLeuIllegInARgMetGlyMetHrrAlIle 20

Db 36 ATGAATTTTCATAAAGAGCAATAGCCGAGCCCTTATTTCATTAAGCAATGGCAATGACTGTATA 95

QY 21 LysGInIleHrrAsPAsPleuPhEvaIjTRPAsnVaIleuAsnARgIugIuVaIaSnIle 40

Db 96 AAGCAAAATCACAGATGACCTATTGTATGGAATGTTCTGAATGGCGAAGAAGTAACATC 155

QY 41 ILeCySGyGluLySvaIgluGInAsPaIaAlaARgIlyIleIleHIsMetIleuLyS 60

|||||

Db	156	ATTGCTGCGAGAAAGTGCGAGCAGAGATGCGTACGAGGGCATATTCACATGATTTTGAA	215
Oy	61	LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTrpProLeu	80
Db	216	AAGGCTTACAGAGTCCTGCTAACCTCTTCTTAAATCCCTTAAAGAGTGGAACTACATCTCTA	275
Oy	81	PheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAspAsp	100
Db	276	TTTTCAGGACTTGGAATGGACAAGCTCTTTTTCATCAACATCAAGAAAGAGACTTGAGCAT	335
Oy	101	LeuAlaGlnAspLeuLysAspLeuTrpHisThrProSerPheLeuAsnPheTrpProLeu	120
Db	336	TTGGCTCAGGATTTAAAGACCTGTACACATACCCCATCTTTCTGACTTTATCCCTT	395
Oy	121	GlyGluAspIleAspIleIlePheAsnLeuLysSerThrPheThrGluProValLeuTrp	140
Db	396	GGTGAGATATATGACATTATTTTAACTTGAAAGACCTTCACAGAACCTGTCTCGTGG	455
Oy	141	ArgLysAspGlnHisHisSarGValGluGlnLeuThrLeuAsnGlyLeuGlnAla	160
Db	456	AGGAAAGACCAACCCATCAACCCGCGAGACAGCTGACCCCTAAAGGCTCTCGAGCT	515
Oy	161	LeuGlnSerProCysIleIleGlyGlyGlnSerGlyLysGlyLysSerThrLeuLeuGln	180
Db	516	CTTGAGACCCCTGTCATCATTTGAAGGGGAACTCTGGCAAAAGCAAGTCCACTGTGCGAG	575
Oy	181	ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal	200
Db	576	CGCATTTGCCAATGCTCTGGGGCTCCGGAAAGTGCAGAGCTGTGCCAAGTCAAAATTCCTC	635
Oy	201	PhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGluThrLeuCysAspGlnLeu	220
Db	636	TTTCTTCCTCCGCTCACACAGGGCCGAGGGGTGACTTTTGAACCCCTGTGTATCAATCTC	695
Oy	221	LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg	240
Db	696	CTGATATTACTGGCAATTCAGAAAGACAGACATTTATGGCCATGTGTGAAGCTGGGG	755
Oy	241	GlnArgValLeuPheLeuLeuAspGlyTrpAsnGluPheLysProGlnAsnCysProGlu	260
Db	756	CAGAGGGTCTTTTCCCTTTGATGGGTACAATGATTCAGCCCAAGACTGCCACAGA	815
Oy	261	IleGluAlaLeuIleLysGluAsnHisSarGlyPheLysAsnMetValIleValThrThrThr	280
Db	816	ATCCAAAGCCCTGATAAAGAAACCAACCCGTTCAAGAACATGTCATGTCAACCCCTACC	875
Oy	281	ThrGluCysLeuArgHisIleArgGlnPheGlyValaLeuThrAlaGluValaGlyAspMet	300
Db	876	ACTGAGTGCCTGAGGCAATACGGCAAGTTTGATGGCTTACTGCTGAGGTGGGGATATG	935
Oy	301	ThrGluAspSerAlaGlnAlaLeuIleArgGluValaLeuIleLysGluLeuAlaGluGly	320
Db	936	ACAGAGACAGAGCCGCCAGGGCTCTCATCCGAGAAAGTGTGATCAAGAGAGTTGTGTAAGCC	995
Oy	321	LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe	340
Db	996	TTTGTGCTCCAAATTCAGAAATCCAGATGCTTGAGAAATCATATAGACCCCTCTCTTT	1055
Oy	341	ValValIleThrCysAlaIleGlnMetGlyGlnSerGluPheHisSerHisThrGlnThr	360
Db	1056	GTGGTCATCACTTGTGCATTCAGATGGAGTGGGAAGTGAATTCACCTCTCACACACAAACA	1115
Oy	361	ThrLeuPheHisThrPheTrpAspLeuLeuIleGlnLysAsnLysHisLysHisLysGly	380
Db	1116	ACGCTGTTCCATACCTCTTATGATCTGTGTGATACAAATAAACACACAAACATATAAGT	1175
Oy	381	ValAlaAlaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGly	400
Db	1176	GTGGCTGCAAGTACTTCATTTCCGAGGCTGTGACCACTGTGGAGACCTTACTGTGAGAGGT	1235
Oy	401	ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspAla	420
Db	1236	GTGTTCCTCCCAAGTTTGATTTTCGAATCTCAGAGATGTGTCCAGCGTGATATAGGATATCT	1295



QY 421 LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys 440  
 |||||  
 Db 1296 CTGTGCAAACTGGGCTCCCTCTGTAATATACACTCAAGGTTCAAGCCCAAGTATATAA 1335  
 QY 441 PhePheHisLysSerPheGlnGluTyrThrAlaGlyArgArgLysSerSerLeuLeuThr 460  
 |||||  
 Db 1356 TTCTTTCACAAGTCATTCACAGAGATACACAGACAGAGAGACTCAGACAGTTTATGACG 1415  
 QY 461 SerHisGlnProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle 480  
 |||||  
 Db 1416 TCTCATAGCCAGAGAGGAGGACCAAGGAAATGTTACTTGCAAAATGTTTCCATT 1475  
 QY 481 SerAspIleHisSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu 500  
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 Db 1476 TCGGACATTACATCCACTTATAGACGCTCTCCGATACACTTGCGGTATCTGTGGAA 1535  
 QY 501 AlaThrArgAlaValMetLysHisLeuAlaValTyrGlnHisGlyCysLeuLeuGly 520  
 |||||  
 Db 1536 GCCACCGGGCTGTATGAAGACACCTCGACAGCTGTATCAACACGGGCTGCTTCGGA 1595  
 QY 521 LeuSerIleAlaLysArgProLeuThrArgGlnGlnSerLeuGlnSerValLysAsnThr 540  
 |||||  
 Db 1596 CTTTCCATCGCCAAAGAGGCTCTCTGGAGACAGGAATCTTGGCAAACTGTGAAAACACC 1655  
 QY 541 ThrGlnGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGlyCysGlyIleHis 560  
 |||||  
 Db 1656 ACTGACGAGAAATTCGAAAGCCATTAACATCAATTCCTTGTAGAGTGGGATCATCAT 1715  
 QY 561 LeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGlnAlaPheGln 580  
 |||||  
 Db 1716 TTAATATACAGAGATACATCCAAATCAGCCCTGAGCCACAGATTTGGAAGCTTTCTTCAA 1775  
 QY 581 GlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPheGln 600  
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 Db 1776 GGTAAAGCTTATATATCACTCAGGAAACATCCCGATTTACTTATTTGACTTTTGGAA 1835  
 QY 601 HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyAla 620  
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 Db 1836 CATTTGCCCAATGTGCAAGTCTCTGACTTCATTAACGTGAGCTTTTGGGGAGCT 1895  
 QY 621 MetAlaSerTrpGlyLysAlaIleGluAspThrGlyIleHisMetGlnGluAlaPro 640  
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 Db 1896 ATGGCTTCATGAGGAAAGGCTGCAAGAGACACAGGTGAATCCACATGGAAGAGGCCCA 1955  
 QY 641 GlnThrTyrIleProSerArgAlaValSerLeuPhePheAsnTyrLysGlnLysPheArg 660  
 |||||  
 Db 1956 GAAACCTACATCCACACAGGCTGTATCTTTGTTCTTCAACTGGAAGAGGAATTCAGG 2015  
 QY 661 ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeu 680  
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 Db 2016 ACTGTGAGGTGACACATCCGGGATTCAGCAAGTTGAATGAAGCAAGATACACATATCTG 2075  
 QY 681 GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVal 700  
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 Db 2076 GGGAAATATTCAGCTCTGCCACAAAGCTCAGGCTCAAAATAAAGAAATGTGGTGTG 2135  
 QY 701 AlaglySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGlu 720  
 |||||  
 Db 2136 GCTGGAAGCTCAGTTGGTCTTCAGACCTGTAAAGAACTTTATTTCTCATAGTGTGAA 2195  
 QY 721 AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr 740  
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 Db 2196 GCCAGTCCCTCAACATAGAAAGATGAGAGACATCATCTGTGAACAAACCTCAAAACC 2255  
 QY 741 LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyLysLeuThrAspSerLeuGly 760  
 |||||  
 Db 2256 TTGAGTTCATGACTACAGAAATCAACGCGCTGCCGGGTGCTGATGACACCTGGGT 2315  
 QY 761 AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGlnGluAspAla 780  
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 Db 2316 AACTTGAAGAACTTACAAAGGCTCATATATGATTAAGATGAAGATGAAGAGATGCT 2375

QY 781 IleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis 800  
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 Db 2376 ATAAAACTAGCTGAAGGCTGCAAAACCTGAAGAGATGTGTTTATTTTCATTGTACCCAC 2435  
 QY 801 LeuSerAspIleGlyGlnGlyMetAspTyrIleValLysSerLeuSerSerGluProCys 820  
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 Db 2436 TTGCTGACATTGGAGAGGAAATGATTAATGATGATGATGATGATGATGATGATGATGAT 2495  
 QY 821 AspLeuGlnGluIleGlnLeuValSerCysLeuSerSerAlaAsnAlaValLysIleLeu 840  
 |||||  
 Db 2496 GACCTGAAGAAATTCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2555  
 QY 841 AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeu 860  
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 Db 2556 GCTGAGATCTTCACATTTGGTGTCAAACTGACGATTTGTGATTATACAGAAATTTACTG 2615  
 QY 861 GluLysAspGlyAsnGlnAlaLeuHisGluLeuIleAspArgMetAsnValLeuGln 880  
 |||||  
 Db 2616 GAAAAAGATGGAAATGAAAGCTCTTCATGAACTGATCAGACAGAGATGAACGTGCTGAAACAG 2675  
 QY 881 LeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeu 900  
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 Db 2676 CTCACCGACTGATGCTGCCCTGGGCTGTGACGTGCAAGGACACCTGACACAGCTGTGTG 2735  
 QY 901 LysHisLeuGlnGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThr 920  
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 Db 2736 AAACATTTGGAGAGAGGTCCCAAACTGCTCAGCTTGCGTTGGAAGAACTGAGAGCTCACA 2795  
 QY 921 AspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln 940  
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 Db 2796 GATACAGAGATTTGAATTTTGAAGTGTGCAATTTTGGAAAGAACCTCTGAAAAACCTTCAG 2855  
 QY 941 GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyThrLeuAlaPheMetGlyVal 960  
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 Db 2856 CAGTTGAATTTGGCGGGAATTCGTGTGACAGATGATGATGATGATGATGATGATGATGATGAT 2915  
 QY 961 PheGlnAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGlnPheLeuProAsp 980  
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 Db 2916 TTTCAGATCTTAAGCAATTAAGTGTGTTTGTGACTTGTGATCACTTAAGAAATTTCTACGAT 2975  
 QY 981 ProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGluAla 1000  
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 Db 2976 CCAGCATTAAGTCAGAAACCTTAAGCAAGTGTATATCAAGATTAATCTTTCGCAAGAGCT 3035  
 QY 1001 ArgLeuValGlyTrpGlnPheAspAspAspLeuSerValIleThrGlyAlaPheLys 1020  
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 Db 3036 AGGCTTGTGGTGGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3095  
 QY 1021 LeuValThrAla 1024  
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 Db 3096 CTAGTACTGCT 3107  
 RESULT 2  
 ID AAH78219 standard; DNA: 3213 BP.  
 XX AAH78219:  
 DE 26-NOV-2001 (first entry)  
 XX  
 Nucleotide sequence of a human secreted polypeptide.  
 DE Human: secreted polypeptide; nervous disease; muscular disease; tumour;  
 KW gastrointestinal ulceration; spinal cord disease; trachea disease;  
 KW thyroid gland disease; ovary disease; prostate disease; heart disease;  
 KW renal gland disease; small intestine disease; thymus disease;  
 KW lymph node disease; muscular system disease; colon disease;  
 KW lipase deficiency; cystic fibrosis; pancreatitis; clot formation;  
 KW myocardial infarction; angioplasty; liver disease; coagulation disorder;  
 KW microbial disease; immune disorder; inflammation; transplant rejection;  
 KW bone thickness; bone density; ferroxidase loss; apoptosis;  
 KW vascular smooth cell proliferation; vaccine; ss.  
 XX

OS Homo sapiens.  
 XX Key Location/Qualifiers  
 FH 1..3213  
 FT CDS /\*tag- a  
 FT /product= "secreted polypeptide"  
 XX  
 PN W020016690-A2.  
 XX  
 XX 13-SEP-2001.  
 XX  
 XX 05-MAR-2001: 2001MO-US07143.  
 XX  
 XX 06-MAR-2000: 2000US-0187107.  
 PR 13-MAR-2000: 2000US-0188916.  
 PR 03-OCT-2000: 2000US-0236874.  
 PR 03-OCT-2000: 2000US-0237846.  
 XX  
 PA (SMK ) SMITHKLINE BEECHAM CORP.  
 PA (SMK ) SMITHKLINE BEECHAM PLC.  
 XX  
 PI Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z:  
 DR WPI: 2001-570768/64.  
 DR P-PDB: AAG67527.  
 XX  
 PT Novel isolated secreted polypeptide useful for treating nervous and  
 PT muscular diseases, gastrointestinal ulceration, coagulation and immune  
 PT disorders, microbial diseases, inflammation and transplant rejection -  
 XX  
 PS Claim 2: Page 53-54; 102pp; English.  
 XX  
 CC The present sequence encodes a human secreted polypeptide. The  
 CC secreted polypeptides and polynucleotides are useful for treating  
 CC nervous and muscular diseases, for inhibiting tumour formation and  
 CC metastasis, for treating gastrointestinal ulceration, for preventing  
 CC and treating diseases in spinal cord, thyroid gland, ovary, prostate,  
 CC renal gland, small intestine, heart, trachea, thymus, lymph node,  
 CC muscular system and colon, for treating lipase deficiency in cystic  
 CC fibrosis and pancreatitis, for treating undesirable clot formation  
 CC such as myocardial infarction, during angioplasty and all surgical  
 CC procedures that require decreased blood clot formation, for treating  
 CC liver diseases, coagulation disorders and microbial diseases, for  
 CC treating immune disorders, for treating inflammation and transplant  
 CC rejection, for enhancing bone thickness and increasing bone density,  
 CC for reducing the loss of essential ferroxidases, for suppressing  
 CC apoptosis, and for regulating vascular smooth cell proliferation. They  
 CC may also be used as vaccines.  
 CC  
 XX  
 SO Sequence 3213 BP; 916 A; 704 C; 756 G; 837 T; 0 other;  
 XX  
 Alignment Scores:  
 Pred. No.: 0 Length: 3213  
 Score: 5448.00 Matches: 1022  
 Percent Similarity: 99.90% Conservative: 1  
 Best Local Similarity: 99.80% Mismatches: 1  
 Query Match: 99.80% Indels: 0  
 DB: 22 Gaps: 0  
 US-09-697-089-2 (1-1024) x AAH78219 (1-3213)  
 QY 1 MetAsnPhlelleysAspsnsrArgAlaIleuIleGlnIArgMetGlyMetThrValIle 20  
 Db 139 TTGAATTTATTAAGACATAGCCGAGCCCTTATTCAAAGATGGGAATGACTGTATA 198  
 QY 21 LysGlnIleThrAspAspleuPheValITrPAsnValIleuAsnArgGluIuValAsnIle 40  
 Db 199 AAGCAATACAGATACCTATTGATGATGATGCTTAAATGCCAAGAGTAAACATC 258  
 QY 41 IleCysCysGluLysValGluGlnAspAlaIleArgGlyIleIleHisMetIleuLys 60  
 Db 259 ATTGCTGCGAGAGGTGAGCAGGATGCTGTAGAGGATCATTCACATGATTTTGAAA 318

QY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluITrPAsnITrProLeu 80  
 Db 319 AAGGTTACAGAGTCTCTTAACCTCTTAAATCCCTTAAGAGGTGGAACATACCTCTA 378  
 QY 81 PheGlnAspleuAsnGlyGlnSerLeuPheHisGlnIThrSerGluGlyAspLeuAsp 100  
 Db 379 TTTCAGACTTGAATGACAAAGCTTTTCATCAGACATCAGAGGAGACTTGAGCAT 438  
 QY 101 LeuAlaGlnAspleuLysAspLeuITrHisIThrProSerPheLeuAsnITrProLeu 120  
 Db 439 TTGGCTCAGATTTAAAGAGCTTGTACCATACCATCTTTCTGAACTTTATCCCTT 498  
 QY 121 GlyGluAspIleAspIleIlePheAsnLeuLysSerIThrPheITrGluITrProVal 140  
 Db 499 GTTGAAGATATTTGACATATTTTAACTGAAAGACCTTCAAGACCTGCTGCTGG 558  
 QY 141 ArgLysAspGlnHisITrHisITrArgValGluGlnLeuIThrLeuAsnGlyLeuGlnAla 160  
 Db 559 AGGAAGGACCAACACCATCAACCCGTGGAGCAGCTGACCTGAAATGGCTCTGAGGCT 618  
 QY 161 LeuGlnSerProCysITrIleIleGluGluSerGlyLysGlySerITrLeuLeuGln 180  
 Db 619 CTTCAGAGCCCTGACATCATTTGAAGGAAITGGCAAGCAAGTCCACTGTGTGAG 678  
 QY 181 ArgIleAlaMetLeuITrPrgLysGlyLysCysLysAlaLeuIThrLysPheLysPheVal 200  
 Db 679 CGAATGCCATGCTCTGCGGCTCCGGAAGTGCMAAGGCTGTGACCAAGTTCAATTCGTC 728  
 QY 201 PhePheLeuArgLeuSerITrArgAlaGlnGlyGlyLeuPheGluIThrLeuCysAspGlnLeu 220  
 Db 739 TTCTTCCTCGTCCACAGAGGCCAGGGTGAGCTTTTAAACCCCTGTGTATCAATC 798  
 QY 221 LeuAspIleProGlyIThrITrLeuArgLysGlnIThrPheMetAlaMetLeuLysLeuArg 240  
 Db 799 CTGATATTCCTGACCAATCAGAAACAGACATTCAGTCCCTGCTGAAAGCTGGG 858  
 QY 241 GlnArgValLeuPheLeuLeuAspGlyITrAsnGluPheLysProGlnAsnCysProGlu 260  
 Db 859 CAGAGGTTCTTTCTTCTTGTATGGCTCAATGAATTCAGGCCCAAGAACTCCAGAA 918  
 QY 261 IleGlnAlaLeuIleLysGluAsnHisITrPheLysAsnMetValIleValIThrIThr 280  
 Db 919 ATCGAAGCCCTGATTAAGAAACACCCCTTAAACATGGTCAATCTCAGCACTATCC 978  
 QY 281 ThrGluCysLeuArgHisITrArgGlnPheGlyAlaLeuIThrAlaGluValGlyAspMet 300  
 Db 979 ACTGAGTGGCTGAGCAATACGCGAGTTTGGTCCCTGACTGCTGAGGTGGGATATG 1038  
 QY 301 ThrGluAspSerITrAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 320  
 Db 1039 ACAGAGACAGGCCCCAGGCTCTCATCCGAGATGCTGATCAAGAGCTTGTGAAAGGC 1098  
 QY 321 LeuLeuLeuGlnIleGlnLysSerITrGlySerITrAsnLeuIThrIThrProLeuPhe 340  
 Db 1099 TTGTTCTCTCAATTTAGAAATCCAGGTGCTTGAGAAATCTCATGAAAGCCCTCTTT 1158  
 QY 341 ValValIleIThrCysAlaIleGlnMetGlyGluSerGluPheHisITrHisIThrIThr 360  
 Db 1159 GTGGTCATCATTTGTCATATCCAGATGGGTGAAGTGAATTCACCTGCACACACAAACA 1218  
 QY 361 ThrLeuPheHisIThrPheITrAspLeuLeuIleGlnLysAsnLysHisITrHisITr 380  
 Db 1219 AGCCTCTTCCATACCTTCTATGATCTGTGATACGAAACAAACACAAACATATAAGCT 1278  
 QY 381 ValAlaAlaSerITrPheIleITrArgSerITrLeuAspHisITrCysGlyITrAspLeuITr 400  
 Db 1279 GTGGCTGCAAGTACTTCAATTCGAGCTGGAGCCACTGTGGAGACTTCTGAGAGGT 1338  
 QY 401 ValPheSerHisITrLysPheAspPheGluGlnITrAspValITrSerITrValITrAsnITr 420  
 Db 1339 GTGTTCTCCACAAAGTTTATTTGACATCGCAGATGTTCTCAGCTGAAATAGAGATGTC 1398  
 QY 421 LeuLeuIThrIThrGlyLeuLeuCysLysITrIThrAlaGlnIThrPheLysITrLysITr 440

|||||  
Db 1399 CTGCTGACAACTGGGCTCTGTAAATATACAGCTCAAGGTTCAAGCCAAAGTATAAA 1458  
OY 441 PhePheHisLysSerPheGlnGluTyrThrAlaGlyArgLeuSerSerLeuThr 460  
Db 1459 TTCTTTCACAACTGATTCAGAGATCACAGACGAGACGAACTGACGAGTTTATTTGAG 1518  
OY 461 SerHisGluProGlnGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle 480  
Db 1519 TCTCATGAGCCGAGAGAGAGTGACCAAGGGAAATGGTTACTTCCAAAAATGGTTTCCATT 1578  
OY 481 SerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu 500  
Db 1579 TCGGACATTACATCCATTATAGCAGCTGCTCCGGTACACCTGGGACATCTGTGGA 1638  
OY 501 AlaThrArgAlaValMetLysHisLeuValAlaValTyrGlnHisGlyCysLeuLeuGly 520  
Db 1639 GCCACCAAGGGCTGTATGAGACCTCCGACAGATGTATCAACACAGCGGCTTCTCGGA 1698  
OY 521 LeuSerIleAlaLysArgProLeuThrArgGlnGlnSerLeuGlnSerValLysAsnThr 540  
Db 1699 CTTTCCATCGCCCAAGAGGCTCTCTGAGACAGAGATCTTTCACAAAGTGTGAAAAACAC 1758  
OY 541 ThrGlnGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHis 560  
Db 1759 ACTGAGCAAGAAATCTGAAAGCCATAAATCAATTCCTTGTAGAGTGGCATCCAT 1818  
OY 561 LeuTyrGlnGlnSerThrSerLysSerAlaLeuSerGlnGlnPheGlnAlaPheGln 580  
Db 1819 TTAATATCAAGAGATACATCCAAATACGCCCTGACCAAGAAATTTGAACCTTTCTTCAA 1878  
OY 581 GlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPheGlu 600  
Db 1879 GGTAAACGTTATATATATCACTACAGGAACATCCCGATTACTTATTGACTTCTTTGAA 1938  
OY 601 HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyAla 620  
Db 1939 CATTTGCCCAATTTGCAAGTCCCTGGACTTCAATTAACCTGGACTTTATGGGGAGCT 1998  
OY 621 MetAlaSerTrpGlnLysAlaAlaGlnAspThrGlyGlyIleHisMetGlnLysLysPro 640  
Db 1999 AGCGTTTCATGGGAAAGCGTCCAGACAGACAGATGAGATCCACATGGAAAGGCCCA 2058  
OY 641 GluThrTyrIleProSerArgAlaValSerLeuPheAsnTrpLysGlnLysPheArg 660  
Db 2059 GAAACCTACATTCCACAGAGGCTATCTTTGTTCTTCACTGGAAGCAGGAATTCAGG 2118  
OY 661 ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeu 680  
Db 2119 ACTCTGAGGTCACACTCCGGGATTTACAGCAAGTTGAATTAACAGATATTCAGATATCG 2178  
OY 681 GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVal 700  
Db 2179 GGGAAAAATATTCAGCTGTCCACAAAGCTCAGGCTCAAAATTAAGATGTCTGTGTG 2238  
OY 701 AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGlu 720  
Db 2239 GCTGGAAGCCTCAGTTTGTCTCTCAGACCTGTAAAGACATTATCTCTCTCATGGTGGAA 2298  
OY 721 AlaSerProLeuThrIleGlnAspGlnArgHisIleThrSerValThrAsnLeuLysThr 740  
Db 2299 GCGAATCCCTCAGCATAGAGATGAGAGGCACATCATCTGTATCAAAACCTGAAACCC 2358  
OY 741 LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly 760  
Db 2359 TTGATATATTCATGACCTTCAGATCAACGGCTCGGGGTGTGCTGACAGCAGCTTGGGT 2418  
OY 761 AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAspGlnGlnAspAla 780  
Db 2419 AACTTGAAGAACCTTACAAAGCTCAATATGATTAACATTAAGATAAATGAAGAAATGCT 2478  
OY 781 IleLysLeuAlaGlnGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis 800  
|||||

Db 2479 ATMAAACTAGCTGAAGCCCTGAAAAACCTGAAGAGATGTGTTATTTCAATTGACCCAC 2538  
OY 801 LeuSerAspIleGlyGlnGlyMetAspTyrIleValLysSerLeuSerSerGluProCys 820  
Db 2539 TTGTCTGACATTGGAGAGGAAATGATTAACATAGTCAAGATCTCTGTCAAGTGAACCTGT 2598  
OY 821 AspLeuGlnGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu 840  
Db 2599 GACCTTGAAGAAATTCATTATGATCTCCGCTGCTGTGTGCAAAATGCAAGTGAATCTTA 2658  
OY 841 AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeu 860  
Db 2659 GCTCAGAAATCTTCACAAATTTGGTCAACTGACATCTTGATTTATCAGAAAAATTAACCTG 2718  
OY 861 GlyLysAspGlyAsnGlnAlaLeuHisGlnGluLeuIleAspArgMetAsnValLeuGlnGln 880  
Db 2719 GAAAAAGATGAAATGAAGCTTTTATGATGACTGATCGACAGAGATACGCTGCTAAGACG 2778  
OY 881 LeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeu 900  
Db 2779 CTCACCGCACATGATGCTGCTGGGGCTGTGACGTGCAAGCAGCGCTGACGACCTGTGTTG 2838  
OY 901 LysHisLeuGlnGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThr 920  
Db 2839 AAACATTTGGAGAGAGTCCACACACTCGTCAAGCTTGGGTTGAAAAACTGGAGACTCACA 2898  
OY 921 AspThrGluIleArgIleLeuGlnAlaPhePheGlyLysAsnProLeuLysAsnPheGln 940  
Db 2899 GATACAGAGATTAGAAATTTAGTGCATTTTGGAAAAAACCCCTGAAAAAACTTCAG 2958  
OY 941 GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGlyVal 960  
Db 2959 CAGTTGAATTTGGCGGGAATGCTGTGACACTGATGATGATGCTTCCCTTCAATGGCTGTA 3018  
OY 961 PheGluAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuProAsp 980  
Db 3019 TTTGAGAAATCTTAAACAAATTTAGTGTTTTGTGACTTATTAAGAAATTTCTTACCTGAT 3078  
OY 981 ProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGlnLys 1000  
Db 3079 CCAGATTAGTCAGAAATTAAGCCAGAGTGTATCAAGTTAACTTTCTGCAAAACCT 3138  
OY 1001 ArgLeuValGlyTrpGlnPheAspAspAspAspLeuSerValIleThrGlyAlaPheLys 1020  
Db 3139 AGCGTTGTGGTGGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3198  
OY 1021 LeuValThrAla 1024  
Db 3199 CTAGTAACTGCT 3210  
RESULT 3  
ABK22731  
ID ABK22731 standard; cDNA: 3396 BP.  
XX ABK22731;  
AC 26-MAR-2002 (first entry)  
XX  
DE Human cDNA encoding CLAN A.  
XX  
KW Caspase recruitment domain; CARD; ss: NB-ARC; ANGIO-R; LRR; SAM;  
KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;  
KW autoimmune disease; inflammation; keratinocyte hyperplasia;  
KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;  
KW leukoemia; allergy; arthritis; lupus; Schrodgen's syndrome;  
KW Crohn's disease; graft-versus-host disease; stroke;  
KW myocardial infarction; heart failure; neurodegenerative disease;  
KW Parkinson's disease; Alzheimer's disease; HIV;  
KW human immunodeficiency virus infection.  
XX Homo sapiens.  
XX

PN WO200190156-A2.  
XX  
PD 29-NOV-2001.  
XX  
PF 24-MAY-2001; 2001WO-US17158.  
XX  
PR 24-MAY-2000; 2000US-0579240.  
PR 10-OCT-2000; 2000US-0686347.  
PR 14-MAR-2001; 2001US-275980P.  
PR 23-MAY-2001; 2001US-0864921.  
XX  
PA (BURN-) BURNHAM INST.  
PI Reed JC, Plo FF, Godzik A, Stehlik C, Damiano JS, Lee SH;  
PI Oliveira VAM, Hayashi H, Pawlowski K;  
XX  
XX WPI: 2002-083086/11.  
DR P-PSDB; AAU80861.  
DR  
XX New caspase recruitment domain (CARD)-containing polypeptides and  
PT encoding nucleic acids, useful for treating abnormal cell proliferation  
PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,  
PT arthritis or stroke  
PS  
PS Claim 1; Page 166-171; 216pp; English.  
XX  
XX The invention relates to an isolated caspase recruitment domain (CARD)  
CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain  
CC from it, and the polynucleotides encoding them. Also included are a  
CC recombinant vector comprising the polynucleotide, recombinant cells  
CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian  
CC and insect cells) and an anti-CARD antibody. The CARD-containing  
CC polypeptide and CARD-encoding nucleic acid are useful for treating a  
CC pathology characterised by abnormal cell proliferation (e.g. cancer),  
CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In  
CC particular, the polypeptide and nucleic acid are useful for treating  
CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth  
CC muscle cell proliferation in arteries following balloon angioplasty  
CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,  
CC arthritis, arthritis, lupus, Crohn's syndrome, Crohn's disease,  
CC graft-versus-host disease, stroke, myocardial infarction, heart failure,  
CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's  
CC disease) or immunodeficiency associated disease (e.g. human  
CC immunodeficiency virus (HIV) infection). The nucleic acids are useful  
CC in a variety of diagnostic applications. The present sequence is a  
CC cDNA encoding a CARD domain containing protein.  
XX  
XX Sequence 3396 BP; 992 A; 737 C; 793 G; 874 T; 0 other;  
SQ  
Alignment Scores:  
Pred. No.: 0 Length: 3396  
Score: 5438.00 Matches: 1021  
Percent Similarity: 99.80% Conservative: 1  
Best Local Similarity: 99.71% Mismatches: 2  
Query Match: 99.62% Indels: 0  
Gaps: 24  
US-09-697-089-2 (1-1024) x ABR22731 (1-3396)  
QY 1 Metasphellielysaspasnserrargalaleuileglnargmetglymethrvaltle 20  
DB 277 ATGAATTTCAATAAAGGACAAATGCGAGCCCTTATTCAAAAGTGGGAATGACTGTTATA 336  
QY 21 Lysglnlthrspaspaleuphevaltrpaspnvalleuasnargslglvalasnlle 40  
DB 337 AAGCAAAATCACAGATGACCTTTTGTATGCAATGTTCCGAATCCGAAAGAACTAAACATC 396  
QY 41 IleCysCysglulysValgluglnaspalaalaarglylleleHsmetlleuulys 60  
DB 397 ATTGCTCGCGAAGGTGGAGCAGAGTGCCTGTAAGAGGATCATTCACATATTTTGA 456  
QY 61 LysgllysergluserCysasnleupheleulysserleulysgluttrpansrtyrproleu 80  
|||||

DB 457 AAGGTTCCAGAGTCCTGTAACTCTTTCTTAATCCCTTAAAGAGTGGAACTATCTCTA 516  
QY 81 pheglnaspheuasnglylnserleuphehsglntrhserrgluylaspheuasasp 100  
DB 517 TTTCAGACCTTGAATGGACAAAGTCTTTTTCATGACATCAGAGGAGCTTGAGCAT 576  
QY 101 LeuAlaGlnaspheulysaspheulysrhrhsrproserpheleuasnphetyrproleu 120  
DB 577 TTGGCTCAGGATTTAAAGGACTTGTACCATCCCATCTTTTGAACCTTTATCCCTT 636  
QY 121 Glylunspilleaspillelepheasnleulyserrhrphetrgluprovaleutr 140  
DB 637 GGTACAGATATTGACATTTATTTTAACTGAAAGCACTTCACAGAACCATCTCTGG 696  
QY 141 ArglyaspghlnhshshsargValgluglnleuphrleuasnglyleuGlnAla 160  
DB 697 AGGAAGGACAAACCATCACCGGCTGGAGCACTGACCTCGAATGGCTCTCCAGGCT 756  
QY 161 LeuGlnserProCysillelelglygluSerGlylysglylserrhrleuGln 180  
DB 757 CTTGAGAGCCCTGCATCATGTAAGGGGAAATCTGCAAGCAAGTCACACTCTGTCAG 816  
QY 181 ArgyleaMetleutrpglyserglylyscyslysAlaLeuthrlysrphelyrphelal 200  
DB 817 CCATTCGCATGCTCTGGGGCTCCGGAAGGTGCAAGGCTTGACCAAGTTCAAAATTCGTC 876  
QY 201 PhepheleuarlyleuSerargAlaGlnlygluLeuphegluttrhrleuCyaspGlnleu 220  
DB 877 TTCTTCCTCCGCTCCAGCAGAGGCCAGGCTGACTTTTGAACCTCTGTGATCAACCTC 936  
QY 221 LeuaspilleProGlythrIlearglyslglntrhrPheMetAlaMetleuulysleuarg 240  
DB 937 CTGATATATACCTGGCACAAATCAGAGAGCAGACATTCAGCCATGCGCTTAACCTCGG 996  
QY 241 GlntrValleupheleuLeuaspGlylytrsnglupheleuProGlnasnCyProGln 260  
DB 997 CAGAGGGTCTTTCTCTCTGATGAGCTACATGAATTAAGCCCGAAGTCCCGAA 1056  
QY 261 lleglualaleuilelyslglnasnhsarPheylsasnmetVallevalthrThrThr 280  
DB 1057 ATCGAAGCCCTGATTAAGGAACACCGCTTCANAGAAATGTCATCGTCCACCTAC 1116  
QY 281 ThrGlyCysleuArghisIleargGlnPheGlyAlaLeuthralaGluvalGlyaspmet 300  
DB 1117 ACTGATGCTCCGAGGACATCGGACAGTTTGTGCTCCCTGACTGCTGGAGTGGGATATG 1176  
QY 301 ThrGlnspseralaglnAlaLeuIleargsluvalleuilelyslglnleuAlaGlnly 320  
DB 1177 ACAGAGACAGCCGCCAGGCTCTCATCCGAGAACTGCTGATCAAGACCTTGCTGAAGGC 1236  
QY 321 LeuLeuLeuGlnIleGlnlySerArgCysleuArghasnleuMetlysrhrProleuphe 340  
DB 1237 TTGTTGCTCCCAATTCAGAAATCCAGGTCGTGAAGATTCATGAAGACCCCTCTCTT 1296  
QY 341 ValValIlethrCysAlaIleGlnmetGlygluSerGluPhehshserrhrshglnthr 360  
DB 1297 GTGTCATCACTTGTGCATCCAGATCGGTGAAGTGAAGTGCCTCCATCCACCAACA 1356  
QY 361 ThrleuphehshsrhrphetyrAspleuileglnlysnasnlyshshslyslg 380  
DB 1357 AGCGTGTTCATACCTTGTATGATCTGTGATACAGAAACAAACAAACATTAAGGT 1416  
QY 381 ValAlaIleAspPheIleargSerLeuaspHiscysgllyaspheAlaIleGlnly 400  
DB 1417 GTGGCTGCAATGACTTCATTCGAGAGCTGAGCACCCGTGAGACCTAGCTTGAGAGGT 1476  
QY 401 ValPheSerHslysrPheaspPheGlnleuGlnaspValSerSerValasnGluaspVal 420  
DB 1477 GTGTTCTCCCAAGATTGATTCGAACCTGAGATGTCACAGGAATGAGAGATGTC 1536  
QY 421 LeuLeuthrThrGlyleuLeuCylysetyrThrAlaGlnarPheulysProlysetylyls 440  
DB 1537 CTGCTGACAACTGGGCTCTCTGTAAATATACAGCTCAAAAGTTCAGCCAAAGTATAAA 1596  
|||||

QY 441 PhePheHisLysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerSerLeuLeuThr 460  
|||||  
Db 1597 TTCCTTCACAGATCATTCACAGAGTACACAGCAGACGAAAGACTCATTCATTATTCAGC 1656  
QY 461 SerHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle 480  
|||||  
Db 1657 TCTCAAGAGCCAGAGGAGGAGGACCAAGGGAAATGGTTACTTGCAGAAAATGGTTCCATT 1716  
QY 481 SerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu 500  
|||||  
Db 1717 TCGGACATTCACATCCACTATACACGCTCCGGTACACCTGGTGCATCTGTGGAA 1776  
QY 501 AlaThrArgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuLeuGly 520  
|||||  
Db 1777 GCCACAGGGCTGTATTGAAAGCCTCGCAGCAGCATATCAACAGCGCTCCCTTCGGA 1836  
QY 521 LeuSerIleAlaLysArgProLeuTyrParGlnGluSerLeuGlnSerValLysAsnThr 540  
|||||  
Db 1837 CTTTCATCGCCCAAGAGGCTCTCTGAGACAGAAATCTTTGCCAAGTGTGAAAACACC 1896  
QY 541 ThrGlnGlnGlnIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHis 560  
|||||  
Db 1897 ACTGACCAAGAAATTCGAAAGCCATTAACATCAATTCCTTTGTAGAGTGTGGCATCCAT 1956  
QY 561 LeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePheGln 580  
|||||  
Db 1957 TTATATCAAGAGAGTACATCCAAATCAGCCCTGAGCCAAAGAAATTTAGCTTTCTTCAA 2016  
QY 581 GlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPhePheGlu 600  
|||||  
Db 2017 GGTAAAGCTTATATATCAACTCAGGGAACATCCCGATTACTTATTTGACTCTTTGAA 2076  
QY 601 HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyGlyAla 620  
|||||  
Db 2077 CATTTGCCCAATTTGTCCAAGTGCCTGGACTTCATTAACCTGCACTTTATGGGGAGCT 2136  
QY 621 MetaLaserTrpGluLysAlaIleGluAspThrGlyGlyIleHisMetGlnGluAlaPro 640  
|||||  
Db 2137 ATGGCTTCATGGGAAAGGCTCGCAAGACACAGCTGCAATCCACATCGAAGAGGCCCA 2196  
QY 641 GluThrTyrIleProSerArgAlaValSerLeuPhePheAsnTrpLysGlnGluPheArg 660  
|||||  
Db 2197 GAAACCTACATTCGCCAGAGGCTGTATCTTGTCTTCACTGGAAGCAGGAATTCAG 2256  
QY 661 ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeu 680  
|||||  
Db 2257 ACTCTGGAGGTCAACCTCGGGATTTCAAGATTGAATGAAGCAAGATATCAGATATCTG 2316  
QY 681 GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVal 700  
|||||  
Db 2317 GGGAAATATTCAGCTCTCCACAAAGCTCAGGCTCAAAATTAAGATGTGCTGGTGTG 2376  
QY 701 AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGlu 720  
|||||  
Db 2377 GCTGGAAAGCTCAGTTGGTCTCCACAGCCTGTAAAGAAATTAATCTCTCAATGGTGA 2436  
QY 721 AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr 740  
|||||  
Db 2437 GCGAGTCCCTCACCATTAAAGATGAGAGGACCATACATCTGTAAACCAACCTGAAACCC 2496  
QY 741 LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly 760  
|||||  
Db 2497 TTGAGATTCATGACTACAGAAATCAAGGCTGCCGGGTCTGTGACTACAGCTTGGGT 2556  
QY 761 AsnLeuLysAsnLeuThrTyrLeuIleMetAspAsnIleLysMetAsnGluGluAspAla 780  
|||||  
Db 2557 AACTTGAAGAAACCTTCAAAAGCTCATTAATGATTAACATAAAGATGAATGAAGAGATGCT 2616  
QY 781 IleLysLeuAlaGlnGlyLeuLysAsnLeuLysMetCysLeuPheHisLeuThrHis 800  
|||||  
Db 2617 ATAAACTAGCTGAAAGGCTGAAAAACCTGAAGAAAGATGTGTTTATTTGATTTGACCCAC 2676

QY 801 LeuSerAspIleGlyGlnGlyMetAspTyrIleValLysSerLeuSerGluProCys 820  
|||||  
Db 2677 TTGTCTGACTTTGGAGGGAAATGATTTACATGTCAAGTCTCTGTCAAGTGAACCTGT 2736  
QY 821 AspLeuGlnGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu 840  
|||||  
Db 2737 GACCTTGAAGAAATTCATTAATAGTCTCTGCTCTTCTTCAAAATCAGTGAAGAAATCTTA 2796  
QY 841 AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeu 860  
|||||  
Db 2797 GCTCAGAAATCTTCAATTTGGTCAAACTGAGCATTCCTGATTTATCAGAAAATTAACCTG 2856  
QY 861 GluLysAspGlyAsnGlnLualLeuHisGluLeuIleAspArgMetAsnValLeuGlnGln 880  
|||||  
Db 2857 GAAAGATGGAATGAATAGCTTTCATGAACATATGACAGATGAAGTGAACCTGCTAGAACG 2916  
QY 881 LeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeu 900  
|||||  
Db 2917 CTCACGCACTGATGTGCTGCCCTGGGCTGTGACGTGCAGAGGACGCTGAGCAGCTGTG 2976  
QY 901 LysHisLeuGlnGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThr 920  
|||||  
Db 2977 AAACATTTGGAGGAGGTCCACAACTGTCAAAGCTTGGGTGAAAACCTGAGACATCACA 3036  
QY 921 AspThrGluIleArgIleLeuGlnGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln 940  
|||||  
Db 3037 GATACAGACTTATGAATTTAGTGCATTTTGGAAAGAACCTCTGAAAACCTTCCAG 3096  
QY 941 GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrLeuAlaPheMetGlyVal 960  
|||||  
Db 3097 CAGTTGAATTTGGCGGGAATCTGTGACAGCAGATGAGATGGCTTCCTTCATAGGCTGTA 3156  
QY 961 PheGluAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuProAsp 980  
|||||  
Db 3157 TTTGAAATCTTAAGCAATTAAGTGTGTTTGTGACTTAAGAAATTTCACTGAT 3216  
QY 981 ProAlaLeuValArgLysLeuSerGlnValIleSerLysLeuThrPheLeuGlnGluAla 1000  
|||||  
Db 3217 CCAGCTTATGTCGAAAACTTACCCAAAGTATTCCAAGTTAACTTTTGTGCAAGAGCT 3276  
QY 1001 ArgLeuValGlyTrpGlnPheAspAspAspLeuSerValIleThrGlyAlaPheLys 1020  
|||||  
Db 3277 AGGCTTGTGGGGCGCAATTTGATGATGATGATCAGTGTATACAGTGTCTTTAA 3336  
QY 1021 LeuValThrAla 1024  
|||||  
Db 3337 CTAGTAAGTGTCT 3348  
RESULT 4  
AAH98254  
ID AAH98254 standard; cDNA: 3545 BP.  
XX  
AC AAH98254;  
XX  
DT 12-OCT-2001 (first entry)  
XX  
DE Murine EST-derived coding sequence SEQ ID NO: 111.  
XX  
KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;  
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;  
KW diagnostics; forensic test; gene mapping; genetic disorder;  
KW biodiversity; gene therapy; nutrition; ss.  
OS Mus musculus.  
XX  
XX WO200154477-A2.  
PN 02-AUG-2001.  
XX  
PD 25-JAN-2001; 2001WO-US02687.  
PF 25-JAN-2000; 2000US-0491404.  
XX  
XX 17-JUL-2000; 2000US-0617746.  
PR

PR 03-AUG-2000; 2000US-0631451.  
PR 15-SEP-2000; 2000US-0663870.  
XX  
PA (HXSE-) HXSEQ INC.  
PI Tang XT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;  
PI Cao Y, Dmanac RA, Zhang J, Wehrman T;  
XX WPI: 2001-476164/51.  
DR P-PSDB: AAM23595.  
XX  
PT Isolated polypeptide for treatment of diseases, diagnostics, raising  
PT antibodies and research use -  
XX  
PS Claim 1; Page 250-251; 1275pp; English.  
XX  
CC The present invention provides the protein and coding sequences of novel  
CC proteins from a variety of organisms, including human, dog, cat, horse,  
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea  
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)  
CC from the organism of interest. They can be used in diagnostics,  
CC forensics, gene mapping, identification of mutations, to assess  
CC biodiversity and for nutritional purposes. The present sequence is a cDNA  
CC of the invention.  
XX  
SQ Sequence 3545 BP; 1038 A; 755 C; 816 G; 936 T; 0 other;

Alignment Scores:  
Pred. No.: 0 Length: 3545  
Score: 5438.00 Matches: 1021  
Percent Similarity: 99.71% Conservative: 3  
Best Local Similarity: 99.71% Mismatches: 0  
Query Match: 99.62% Indels: 0  
DB: Gaps: 0

US-09-697-089-2 (1-1024) x AAH98254 (1-3545)

QY 1 MetAspHeiLeuLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20  
Db 232 ATGATTTTCATAAAGAACAAATAGCCGAGCCCTTATTCAAGAAATGGAGATGACTGTATA 291  
QY 21 LysGlnIleThrAspAspLeuPheValITrpaSnValLeuAsnArgGluValAsnIle 40  
Db 292 AAGCAAAATCACAGATGACCTATTGTATGAAATGTTCTGAATCGCGAAGAACTAAACATC 351  
QY 41 IleCysCysGluLysValGlnGlnAspAlaIleArgGlyIleIleHisMetIleLeuLys 60  
Db 352 ATTTCCTCGAGAAAGGTGGAGAGATGCTGCTAGAGGATATTCACATGATTTTGAAGA 411  
QY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluITrpaSnITrProLeu 80  
Db 412 AAGGTCAGAGTCTCTGTAACCTTTCTTAATCCCTTAAGAGAGGAACTATCCTCTGA 471  
QY 81 PheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnITrSerGlnGlyAspLeuAsp 100  
Db 472 TTTTCGGACITGAAATGGAAGAGCTTTTTCATCAGACATCGAAGAGGAGACTTGGACGAT 531  
QY 101 LeuAlaGlnAspLeuLysAspLeuITrHisITrProSerPheLeuAsnPheITrProLeu 120  
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QY 121 GlyIleAspIleAspIleIlePheAsnLeuLysSerITrPheITrGluITrValIleITr 140  
Db 592 GGTGAAGATATTGACATATTATTTTAACITTGAAAAGCACCCTTCACGAACCTCTCTGTGG 651  
QY 141 ArgLysAspGlnHisHisArgValGlnGlnLeuITrLeuAsnGlyLeuLeuGlnAla 160  
Db 652 AGGAAGGACCAACACCATCACCGCGTGGAGCAGCTGACCTGAATGGCCTCTGACGGCT 711  
QY 161 LeuGlnSerITrCysIleIleGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 180  
Db 712 CTTGAGAGCCCTGCATCATTTGAAGGGAAATCTGGCAAAAGGCAATGCCACTCTGCTGGAG 771

QY 161 ArgIleAlaMetLeuITrPglYSerGlyLysCysLysAlaLeuITrLysPheLysPheVal 200  
Db 772 CGCATTTGCCATGCTCTGGGGGCTCCGAAAGTCAAGGCTCTGACCAAGTTCAATTCCTGCTC 831  
QY 201 PhePheLeuArgLeuSerArgAlaGlnGlnGlyLeuPheGlnITrLheuCysAspIleLeu 220  
Db 832 TTTCTTCCTCCGCTCAGAGAGGGCCAGGGTGAGCTTTTGAAGCCCTGTGATCACTGCT 891  
QY 221 LeuAspIleITrGlnITrHisITrArgLysGlnITrPheMetAlaMetLeuLysLeuArg 240  
Db 892 CTGATATACCTGGACACATCGAAGCAGACACATTCATGCGCATGCTGTAAGCTGGGG 951  
QY 241 GlnArgValLeuPheLeuLeuAspGlyITrHisGlnITrPheLysITrGlnAsnITrProL 260  
Db 952 CAGAGGGTCTTTTCTTCTTGATGCTACATGAATTCAGGCCCAAGACCTGCCAGAA 1011  
QY 261 IleGlnAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValITrThrITr 280  
Db 1012 ATCGAAGCCCTGATAAAGAAACCAACCGCTTCAAGAACATGTCATGTCACCACTACC 1071  
QY 281 ThrGluCysLeuArgHisIleArgGlnPheGlnAlaLeuITrAlaGluValGlyAspMet 300  
Db 1072 ACTGAGTGCCTGAGGCACATACGAGATTTGCTGCCCTGACCTCGAGGTGGGGATATG 1131  
QY 301 ThrGluAspSerAlaGlnAlaLeuITrLeuITrValIleLysGluLeuAlaGluGly 320  
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QY 341 ValValIleITrCysAlaIleGlnMetGlyGlnSerGluPheHisSerHisITrGlnITr 360  
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QY 361 ThrLeuPheHisITrPheITrAspLeuLeuIleGlnLysAsnLysHisITrLysGly 380  
Db 1312 ACGCTGTTCCAACTCTTATGATCTGTGAATACAGAAACCAACCAACATGTAAGGT 1371  
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Db 1432 GTGTTCTCCCAACAATGTTGATTTCGAACTGCAGATGtGTCCAGGGTGAATGAGGATGTC 1491  
QY 421 LeuLeuITrThrGlyLeuLeuCysLysITrThrAlaGlnArgPheLysITrLysITrLys 440  
Db 1492 CTGCTGACAACTGGGCTCCTGTGAATATACAGCTCAAGGTTCAAGCCAAAGTATGAA 1551  
QY 441 PhePheHisLysSerPheGlnGlnITrThrAlaGlyArgLeuSerSerLeuLeuITr 460  
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QY 461 SerHisGluITrGlnGlnValITrLysGlyAsnGlyITrLysGlnITrLysMetValSerIle 480  
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QY 481 SerAspIleITrSerITrLysSerSerLeuLeuArgITrThrCysGlySerSerValGlu 500  
Db 1672 TCGGACATATACATCCACTATATGACGCTGCTCGGCTACACTGTGGGTCACTGTGGAA 1731  
QY 501 AlaITrArgAlaValMetLysHisLeuAlaValITrGlnHisGlyCysLeuLeuGly 520  
Db 1732 GCCACCAAGGGGTATATGAAGCACCTCCAGCAGAGTGTATCAACAGCGCTGCTTCGGA 1791  
QY 521 LeuSerITrAlaLysArgITrProLeuITrParGlnGlnGlnGlnGlnGlnGlnGlnGln 540  
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QY 541 ThrGlnGlnIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHis 560



|||||  
Db 1852 ACTGAGCAAGAAATTCGTAAGACCATAAACATCAATTCCTTTGTAGAGTGGCATCCAT 1911  
QY 561 LeuTYrGInGluSerThrSerLysSerAlaLeuSerGInGluPheGluAlaPheGln 580  
Db 1912 TTATTTTCAGAGAGATACATCCAAATCAGCCCTGAGCCCAAGAAATTTGAACCTTTCTTCAA 1971  
QY 581 GLYSerSerLeuTYrIleAsnSerGlyAsnIleProAspTYrLeuPheAspPheGlu 600  
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QY 621 MetAlaSerTrpGluLysAlaAlaGluAspThrGlyGlyIleHisMetGluLysPro 640  
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Db 2152 GAAACCTACATTCCTCAGCAGGAGCTGATCTTTGTTCTTCACTGGAGAGCAATTCAGG 2211  
QY 661 ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGInAspIleThrTYrLeu 680  
Db 2212 ACTGTGAGAGTCACACCTCGGATTTCAAGCAAGTTGAATAGACAGATATCATATCTG 2271  
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QY 701 AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTYrSerLeuMetValGlu 720  
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QY 721 AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr 740  
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QY 801 LeuSerAspIleGlyGluGlyMetAspTYrIleValLysSerLeuSerSerLysProCys 820  
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QY 821 AspLeuGluGluIleGlnLeuValSerCysLysSerAlaAsnAlaValLysIleLeu 840  
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QY 841 AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTYrLeu 860  
Db 2752 GCTCAGAAATCTTCACAAATTTGGTCAAACTGAGACATTTCTGATTATTCAGAAATTAACCTG 2811  
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Db 2812 GAAAAAGATGAATGAAGCTCTTCATGAATCATGATGACAGGATTAACGCTGTAAACAG 2871  
QY 881 LeuThrAlaLeuMetLeuProTrpGlyCysAspValGInGlySerLeuSerSerLeuLeu 900  
Db 2872 CTCACCGCAGCATATGCTGCGCTGGGGCTGTGACGTGCAGAGGAGGCTGAGCGCTGTGG 2931  
QY 901 LysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThr 920  
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Db 2932 AAACATTTGGAGAGAGTCCACCAACTGCTCAAGCTTGGGTTGAAAAACGTGAGACTCACA 2991  
QY 921 AspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln 940  
Db 2992 GATACAGACATTAAGAAATTTTACGTCAATTTTGGAAAAAGAACCTCTGAAAAACCTCCAG 3051  
QY 941 GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGlyVal 960  
Db 3052 CAGTTGCAATTTGGCGGAAATGCTGTGAGCAGATGATGATGCTTGCCTTCATGGGTGTA 3111  
QY 961 PheGluAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuProAsp 980  
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QY 981 ProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGluAla 1000  
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QY 1001 ArgLeuValGlyTrpGlnPheAspAspAspLeuSerValIleThrGlyAlaPheLys 1020  
Db 3232 AGCTTTGTTGGGTGGCAATTTGATGATGATGATCTCAGTGTTATTTACAGGTCTTTTAA 3291  
QY 1021 LeuValThrAla 1024  
Db 3292 CTAGTAAGTGT 3303  
RESULT 5  
AAS03946  
ID AAS03946 standard; DNA; 3615 BP.  
XX  
AC AAS03946;  
XX  
DT 12-SEP-2001 (first entry)  
XX  
DE Human caspase recruitment domain 12 (CARD-12) genomic DNA.  
XX  
KW Caspase recruitment domain; CARD-12; apoptosis; stress-related pathway;  
KW cancer; viral infection; poxvirus; adenovirus; autoimmune disorder;  
KW systemic lupus erythematosus; arthritis; neurological disorder; stroke;  
KW Alzheimer's disease; amyotrophic lateral sclerosis; hematologic disease;  
KW aplastic anaemia; myocardial infarction; inflammatory disorder;  
KW Crohn's disease; insulin-dependent diabetes; contact dermatitis;  
KW psoriasis; graft rejection; bacterial infection; lepromatous leprosy;  
KW tuberculosis; ischaemic brain injury; hypoxic brain injury; ds;  
KW kidney ischaemia; reperfusion injury; acute bacterial meningitis;  
KW excitotoxic brain damage; liver disease.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..3615  
FT /tag= a  
FT /product= "Human CARD-12"  
XX  
PN WO200130971-A2.  
XX  
PD 03-MAY-2001.  
XX  
PF 26-OCT-2000; 2000WO-US29643.  
XX  
PR 27-OCT-1999; 99US-0161822.  
XX  
PA (MILL-) MILLENNIUM PHARM INC.  
XX  
PI Bertin J, Robison KE;  
XX  
DR WPI; 2001-308628/32.  
XX  
P-PSDB; AAU02881.  
XX  
PT Isolated caspase recruitment domain-12 polypeptide and nucleic acids  
PT encoding them, useful for treating and diagnosing disorders associated  
PT with abnormal apoptosis such as cancer, arthritis and Alzheimer's  
PT disease -

XX Disclosure; Fig 2; 93pp; English.

CC The sequence represents a genomic DNA which encodes the human caspase  
CC recruitment domain 12 (CARD-12) polypeptide. CARD domains are found in a  
CC number of proteins that transmit signals that activate apoptosis and  
CC inflammatory pathways in response to stress and other stimuli. Therefore  
CC CARD-12 and its corresponding nucleic acid may be used in treatment and  
CC diagnosis of patients suffering from disorders associated with an  
CC abnormal level (an increase or a decrease) of apoptotic cell death or  
CC abnormal activity of stress-related pathways. The disorders include  
CC cancer, viral infections (e.g. caused by poxviruses, adenoviruses),  
CC autoimmune disorders (e.g. systemic lupus erythematosus, arthritis),  
CC neurological disorders (e.g. Alzheimer's disease, amyotrophic lateral  
CC sclerosis), haematologic diseases (e.g. aplastic anaemia, myocardial  
CC infarction, stroke), inflammatory and immune system disorders (e.g.  
CC Crohn's disease, insulin-dependent diabetes, contact dermatitis,  
CC psoriasis, graft rejection), bacterial infections (e.g. tuberculosis,  
CC lepromatous leprosy), ischaemic and hypoxic brain injury, kidney  
CC ischaemia/reperfusion injury, excitotoxic brain damage, acute bacterial  
CC meningitis and liver disease.

Sequence 3615 BP; 1041 A; 811 C; 845 G; 918 T; 0 other;

Alignment Scores:

Pred. No.:	0	Length:	3615
Score:	5188.00	Matches:	1014
Percent Similarity:	98.16%	Conservative:	1
Best Local Similarity:	98.07%	Mismatches:	1
Query Match:	95.04%	Indels:	18
DB:	22	Gaps:	1

US-09-697-089-2 (1-1024) x AAS03946 (1-3615)

OY	1	Melc	nsPhe	lle	lys	asp	asn	ser	trg	ala	leu	ile	gln	arg	met	g	ly	met	trp	val	lle	20							
		::::																											
Db	418	GTG	AT	TTC	AT	TCA	AAA	GGC	CA	AT	A	TAC	CGC	G	AGC	CTT	AT	TCA	AAA	GAT	GGG	AT	GC	TCT	TAT	A	477		
OY	21	Lys	gln	ile	trp	asp	leu	phe	val	trp	asp	val	leu	asn	arg	g	lu	val	asn	lle		40							
Db	478	AAG	CA	AT	C	AC	AG	TG	AC	CT	TAT	T	GT	AT	G	AT	T	G	AT	T	G	AT	T	G	AT	T	G	AT	537
OY	41	Ile	cys	cys	g	lu	ys	val	g	lu	g	ln	asp	ala	ala	arg	g	ly	ile	ile	his	met	lle	leu	ys		60		
Db	538	ATT	TG	CT	CG	G	AA	G	AG	G	GT	G	AG	CA	G	AG	AT	CG	T	AG	AG	G	AT	C	AT	T	CA	AT	597
OY	61	Lys	g	lu	ys	g	lu	ys	cys	asn	leu	phe	leu	ys	ser	leu	g	lu	trp	asn	trp	leu		80					
Db	598	AAG	GT	T	CA	G	AT	C	AG	T	C	CT	CT	TA	AC	CT	T	T	CT	T	TA	A	T	C	CT	T	T	TA	657
OY	81	Phe	g	ln	asp	leu	asn	g	ly	g	ln	ser																	88
Db	658	TTT	CA	G	AC	T	T	G	AA	T	T	G	CA	AA	G	T	T	T	T	T	T	T	T	T	T	T	T	T	717
OY	89	-----																											102
Db	718	ACC	T	T	CT	T	CA	T	AA	T	AG	G	CT	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	777
OY	103	Gln	asp	leu	lys	asp	leu	trp	his	thr	pro	ser	phe	leu	asn	phe	trp	leu	g	lu		122							
Db	778	CAG	CT	T	T	T	AAA	GG	AT	C	GT	G	T	CA	AT	CC	CA	CT	T	T	T	T	T	T	T	T	T	T	837
OY	123	Asp	ile	asp	ile	ile	phe	asn	leu	ys	ser	thr	phe	thr	g	ln	pro	val	leu	trp	arg	lys		142					
Db	838	GAT	AT	T	G	CA	T	AT	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	897
OY	143	Asp	gln	his	his	his	arg	val	g	lu	g	ln	leu	thr	leu	asn	g	ly	leu	deu	gln	ala	leu	ln		162			
Db	898	GAC	CA	CA	C	CA	T	CA	CC	G	G	T	G	AG	CA	CT	CA	CC	T	CA	CC	T	TA	A	CT	CT	CT	CT	957
OY	163	Ser	pro	cys	ile	ile	g	lu	g	ly	g	lu	ys	g	ly	ys	ser	thr	leu	deu	gln	arg	ile		182				
Db	958	AGC	CC	T	TC	AT	CA	T	AT	T	G	AA	G	GA	AT	T	CG	CA	AA	G	CA	CT	CA	CT	CT	CT	CT	CT	1017

QY	183	AlaMetLeuThrProGlySerGlyIysCysLysAlaLeuThrLysProLysPheValPhePhe	202
Db	1018	GCAATGCTCTGGGGCTCCGGAAAGGTCAAGGCTCTGCACCAATTTCAAAATTCGTCTTCTC	1077
QY	203	LeuArgLeuSerArgAlaGlnGlnGlyLeuPheGlnThrLeuCysAspGlnLeuLeuAsp	222
Db	1078	CTCCGCTCTCAGCAGGCCCCAGGGTGGACCTTTTGAACCCCTGTGTGATCAACTCTCTGAT	1137
QY	223	IleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArgGlnArg	242
Db	1138	ATACCTGGCAACAATCAGGAGCAGACATTCATGGCCATGCTGCTGAACCTCGCAGAGG	1197
QY	243	ValLeuPheLeuLeuAspGlyTyrAsnGlnPheLysProGlnAsnCysProGlnIleGln	262
Db	1198	GTCTCTTCTCTTGTGATGGCTCAATGAAATTCACGCCCAAGACTGCCAGAAATGCAA	1257
QY	263	AlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValThrThrThrGln	282
Db	1258	GCCCTGATAAAGGAAACCAACCCCTTCAGAACATGTGTCATGCCACTACCACTAG	1317
QY	283	CysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMetHisGln	302
Db	1318	TGCCGAGGCGCAATACGCGAGTTGGTCCCTGCATCGCTGAGAGTGGGGAATATGACAAA	1377
QY	303	AspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGlnLeuAlaGlnLeuLeu	322
Db	1378	GACACGCCCGCCAGGCTCTCATCCCGAAGATCTGATACAGAGACTTGCTGAAGCTTGTG	1437
QY	323	LeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPheValVal	342
Db	1438	CTCCAAATTCAGAAATCCAGGTGCTTGAGAAATCTCATGAACCCCTCTCTTGTGGTC	1497
QY	343	IleThrCysAlaIleGlnMetGlyGlnSerGlnPheHisSerHisThrGlnThrThrLeu	362
Db	1498	ATCACTTGTGCATTCAGATGGGGTGAAGATGAATTCACCTCTCACACACCAACACGCTG	1557
QY	363	PheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysGlnValAla	382
Db	1558	TTCGATACCTCTATGATCTGTGGATGCACAGAAACCAACACCAACATTAAGGTGTGCT	1617
QY	383	AlaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGlnGlyAlaPhe	402
Db	1618	GCAATGTGCTTCATTCGAGACTGTGCACACTGTGGAGACTGTGAGGGGTGTGTC	1677
QY	403	SerHisLysPheAspPheGlnLeuGlnAspValSerSerValAsnGlnAspValLeuLeu	422
Db	1678	TGCCCAAGTTTGATTTTCGAACTGCAGAGATGTCTCAGCGTGAATGAGAGATCTCTGTG	1737
QY	423	ThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLysPhePhe	442
Db	1738	ACAACTGGGCTCCCTGTAAATATACAGCTCAAAAGGTTCAACCCAAAGATATAATCTTCT	1797
QY	443	HisLysSerPheGlnGlnGlyTyrThrAlaGlyArgArgLeuSerSerLeuLeuThrSerHis	462
Db	1798	CACAGATATTCGAGGAGTACACACGACGAGACGAAAGTACAGACGTTTATGACGTCTAT	1857
QY	463	GlnProGlnGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerLieserAsp	482
Db	1858	GAGCGACGAGGAGTGACCAAGGGAATGGTTACTTCACAAATAATGGTTTCCATTTCCGAC	1917
QY	483	IleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlnValThr	502
Db	1918	ATTACATCCACTTATACAGCTGTCTCCGTTACACTGTGGGTCACTGTGGAAACCCACC	1977
QY	503	ArgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuLeuGlyLeuSer	522
Db	1978	AGGGTGTATTAGGAACACTGCAGCAGTGATCAACACAGGCGCTTCTCGAATTTC	2037
QY	523	IleAlaLysArgProLeuThrProGlnGlnSerLeuGlnSerValLysAsnThrThrGln	542
Db	2038	ATCCGCAAGAGCGCTCTCTGGAGCACGGAATCTTTCGAAAGTGTGAACCAACCACTAG	2097



QY 543 GINGLIIleLeuLysAlaIleasnIleasnSerPheValGluCysGlyIleHisIleuTy 562  
 DB 2098 CAGAGAAATTCGAAAGCCATAACATCAATTCCTTGTGAGAGTGGCATTCATTTATAT 2157  
 QY 563 GINGIuSerThrSerLysSerAlaLeuSerGInguIleuAlaPhePheGInguLys 582  
 DB 2158 CAGAGAGACATCCCAATTCACCCCTGAGGCCAAGAAATTTGAAGCTTTCTTCAAGTAA 2217  
 QY 583 SerLeuTyrlIleasnSerGlyasnIleProAspTyrlIleuPheAspPheHeuHisIleu 602  
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 DB 2398 TACATTCCTCAGAGGGGTGTATCTTTGTTCTTCACTGGAAACAGGAATTCAGACTCTG 2457  
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 DB 2458 GAGGTCAACCTCCGGGATTTCCAGCAAGTTGAATTAAGCAAGATATCAGATATCTGGGGAAA 2517  
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 DB 2518 AATATCAGCTCGCCACAAGCCTCAGGCTGCAAAATAAAGATGATGCTGTGCTGGTGA 2577  
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 DB 2638 CCCCTCACCATGAAAGATGAGAGCACATCAGATCTGTATACAACTGAAACCTTGAT 2697  
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 DB 2698 AATTCATGACCTACAAATCAACAGGCTGCCGTGCTGACAGACGCTTGGTAACTTG 2757  
 QY 763 LysAsnIleuThrLysIleuIleMetAspAsnIleLysMetAsnGluGlnAspAlaIleLys 782  
 DB 2758 AAGAACCTTACAAAGCTCTAATATGATACATTAAGATGAATGAAGAAATGCTATAAA 2817  
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 DB 2818 CTAGCTGAAGGCTGAAAAACCTGAAGAAGATGTGTTATTTTCATTTTGACCCACTTGCT 2877  
 QY 803 AspIleGlyGluGlyMetAspTyrlIleValLysSerLeuSerSerGluProCysAspLeu 822  
 DB 2878 GACATTTGGAGAGGATGATATACATGACATGCTCTGTCAAGTGAACCTGTGACTTT 2937  
 QY 823 GluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAlaGln 842  
 DB 2938 GAGAGAAATTCATTAAGTCTCTGCTGCTGCTGTGCAAAAGCAGTGAATAATCTAGCTCAG 2997  
 QY 843 AsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrlLeuGluLys 862  
 DB 2998 AATCTTCACAAATTTGGTCAAACTGAGCATTTTGATTTATCAGAAATTAATCTGAAAAA 3057  
 QY 863 AspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeuThr 882  
 DB 3058 GATGGAATTAAGAGCTTCATGATGATGACAGATGACAGATGACGCTGATGAACAGCTCACC 3117  
 QY 883 AlaLeuMetLeuProTrpGlyCysAspValGInguLysSerLeuSerSerLeuLeuLysHis 902  
 DB 3118 GCACGTGATGCTGCTCCCTGGGGCTGTGACGTGCAAGGACAGCTGTGTTGAAACAT 3177  
 QY 903 LeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThrAspThr 922

DB 3178 TTGGAGAGAGTCCCAACACTGCTCAAGCTTGGGTTGAAAAAACTGGAGACTCAATAC 3237  
 QY 923 GIuIIeArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGInguLeu 942  
 DB 3238 GAGATTAGAAATTTAGTGTGATCTATTTTGGAAAGAACCCCTGAAAAAACTTCCAGCAGTTG 3297  
 QY 943 AsnLeuAlaGlyAsnArgAlaSerSerAspGlyTrpLeuAlaPheMetGlyAlaPheGlu 962  
 DB 3298 AATTTGGCGGGAATGCTGTGAGCAGTGAATGGATGGCTTGCTCAATGGGTATTTTGAG 3357  
 QY 963 AsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuProAspProAla 982  
 DB 3358 AATCTTAAGCAATTTAGTGTTTTGTGACTTATGACTTAAGAAATTTCTACTGATCCAGCA 3417  
 QY 983 LeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGluAlaArgLeu 1002  
 DB 3418 TTAGTCAGAAAACTTAGCCCAAGTGTATCCCAAGTTTCTGCAAGAAACCTAGGCTT 3477  
 QY 1003 ValGlyTrpGlnPheAspAspAspAspLeuSerValIleThr 1016  
 DB 3478 GTTGGGTGGCAATTTGATGATGATGATGATCTCAGTGTATTACA 3519  
 RESULT 6  
 AAH78218  
 ID AAH78218 standard; DNA; 2215 BP.  
 AC AAH78218;  
 XX  
 DT 26-NOV-2001 (first entry)  
 DE Nucleotide sequence of a human secreted polypeptide.  
 XX  
 KW Human; secreted polypeptide; nervous disease; muscular disease; tumour;  
 KW gastrointestinal ulceration; spinal cord disease; trachea disease;  
 KW thyroid gland disease; ovary disease; prostate disease; heart disease;  
 KW renal gland disease; small intestine disease; thymus disease;  
 KW lymph node disease; muscular system disease; colon disease;  
 KW lipase deficiency; cystic fibrosis; pancreatitis; clot formation;  
 KW myocardial infarction; angioplasty; liver disease; coagulation disorder;  
 KW microbial disease; immune disorder; inflammation; transplant rejection;  
 KW bone thickness; bone density; ferrooxidase loss; apoptosis;  
 KW vascular smooth cell proliferation; vaccine; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT 1..2214  
 FT /\*tag= a  
 FT /product= "secreted polypeptide"  
 FT /note= "no termination codon given"  
 XX  
 PN WO200166690-A2.  
 PD 13-SEP-2001.  
 XX  
 PE 05-MAR-2001; 2001WO-US07143.  
 XX  
 PR 06-MAR-2000; 2000US-0187107.  
 PR 13-MAR-2000; 2000US-0188916.  
 PR 03-OCT-2000; 2000US-0236874.  
 PR 03-OCT-2000; 2000US-0237846.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX  
 PI Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;  
 DR WPT: 2001-570768/64.  
 DR P-PSDB: AAG67526.  
 XX  
 PT Novel isolated secreted polypeptide useful for treating nervous and  
 PT muscular diseases, gastrointestinal ulceration, coagulation and immune

PT disorders, microbial diseases, inflammation and transplant rejection -  
XX  
PS Claim 2; Page 52-53; 102pp; English.  
XX  
CC The present sequence encodes a human secreted polypeptide. The  
CC secreted polypeptides and polynucleotides are useful for treating  
CC nervous and muscular diseases, for inhibiting tumour formation and  
CC metastasis, for treating gastrointestinal ulceration, for preventing  
CC and treating diseases in spinal cord, thyroid gland, ovary, prostate,  
CC renal gland, small intestine, heart, trachea, thymus, lymph node,  
CC muscular system and colon, for treating lipase deficiency in cystic  
CC fibrosis and pancreaticitis, for treating undrizable clot formation  
CC such as myocardial infarction, during angioplasty and all surgical  
CC procedures that require decreased blood clot formation, for treating  
CC liver diseases, coagulation disorders and microbial diseases, for  
CC treating immune disorders, for treating inflammation and transplant  
CC rejection, for enhancing bone thickness and increasing bone density,  
CC for reducing the loss of essential ferroxiases, for suppressing  
CC apoptosis, and for regulating vascular smooth cell proliferation. They  
CC may also be used as vaccines.  
XX

SO Sequence 2215 BP; 621 A; 522 C; 519 G; 553 T; 0 other;

Alignment Scores:

Pred. No.:	0	Length:	2215
Score:	3950.00	Matches:	737
Percent Similarity:	99.86%	Conservative:	0
Best Local Similarity:	99.86%	Mismatches:	1
Query Match:	72.36%	Indels:	0
DB:	22	Gaps:	0

US-09-697-089-2 (1-1024) x AAH78218 (1-2215)

QY 15 MetGlyMetThrValIleIleYsGlnIleThrAspAspLeuPheValTyrPasnValLeuAsn 34  
DB 1 ATGGGAATGACTGTTATTAAGCAATACAGATGACCTATTGTAATGGAATGTTCTGAT 60  
QY 35 ArgGluGluValAsnIleIleCysCysGlnIleValGluGlnAspAlaAlaArgGlyIle 54  
DB 61 CGCAAGAGATTAACATCATTTGCTGCGAAGGTGAGCAGATGCTGTAGAGGATC 120  
QY 55 IleHisMetIleLeuIleYsGlySerGlySerCysAsnLeuPheLeuIleYsSerLeuIle 74  
DB 121 ATTACATGATTTTGAAGAGGTTCAAGTCCGTAACTCTTTTAAATVCCCTTAAG 180  
QY 75 GluTyrPasnIlePheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSer 94  
DB 181 GAGTGGAACTATCTCTATTTTCAGACTGATGACAAATCTTTTTCATCAGACATCA 240  
QY 95 GluGlyAspLeuAspAspLeuAlaGlnAspLeuIleYsAspLeuTyrHisThrProSerPhe 114  
DB 241 GAAGGAACTTGGAGATTGCTCAGGATTTAAAGCACTGTACATACCCCATCTTTT 300  
QY 115 LeuAsnPheTyrProLeuGlyGluAspIleAspIleIlePheAsnLeuIleYsSerThrPhe 134  
DB 301 CTGACATTTTATCCCTTGGAGATATTTGACATTTATTTTAACTTGAAGAACCTTC 360  
QY 135 ThrGluProValLeuTyrPargLysAspGlnHisHisAspValGluGlnLeuThrLeu 154  
DB 361 ACAGAACCTGCTCTGTGGAGAGAACACACATCCCGCTGGAGACACTGACCTG 420  
QY 155 AsnGlyLeuLeuGlnAlaLeuGlnSerProCysIleIleGlyGlyGlySerGlyIleGly 174  
DB 421 AATGGCTCTCGAGGCTCTTCAGAGCCCTGCATCATTTGAAGGGGAATCTGCAAGAGC 480  
QY 175 LysSerThrLeuLeuGlnIleAspIleAlaMetLeuTyrPargLysSerGlyIleYsValLeu 194  
DB 481 AAGTCCACTGCTGCGAGCGAATGCCATGCTGGGGCTCCGAAAGTGAAGGCTCTG 540  
QY 195 ThrIlePheIlePheValIlePheLeuArgLeuSerArgAlaGlnGlyIleGlyLeuPheGln 214  
DB 541 ACCAAGTTCAATTCGCTTCTTCTCCGCTCAGCAGGCGCCAGGGGAGACTTTTGA 600

QY 215 ThrLeuCysAspGlnLeuLeuAspIleProGlyThrIleArgIleGlnThrPheMetAla 234  
DB 601 ACCCTCTGTATCAACTCTCGATATACCTGGCAAAATCAGAGAACATTCATGCGC 660  
QY 235 MetLeuLeuIleAsnArgGlnArgValLeuPheLeuAspGlyTyrAspGlnPheIle 254  
DB 661 ATGCTGCGAAGCTCGGGCAGAGGGTCTTTCTTCTTGATGGCTCAATGAATTCAG 720  
QY 255 ProGlnAsnCysProGlnIleGlnAlaLeuIleYsGlnAsnHisAspPheIleYsAsnMet 274  
DB 721 CCCAGAACTCCCAAGAAATGAAAGCCCTGTAAAGGAAACCAACCGCTTAAAGACATG 780  
QY 275 ValIleValThrThrThrThrGlyCysLeuArgHisIleArgGlnPheGlyAlaLeuThr 294  
DB 781 GTCATCGCACACCTACACATGAGTGCCTGAGGACATACGCGAGTTGGCGCTGACT 840  
QY 295 AlaGluValGlyAspMetThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIle 314  
DB 841 GCTGAGGTGGGGATATACAGAAAGACGCGCCAGGCTCTCATCCGGAAGTCTGTATC 900  
QY 315 LysGluLeuAlaGluGlyLeuLeuLeuGlnIleGlnIleYsSerArgCysLeuArgAsnLeu 334  
DB 901 AAGGAGCTTCTGAAAGGCTTGTGCTCCAAATTCAGAAATCCAGGTGCTTGAAGATTC 960  
QY 335 MetLysThrProLeuPheValIleThrCysAlaIleGlnMetGlyGlySerGluPhe 354  
DB 961 ATGAAGAACCCCTCTCTTGTGGTCACTGTCGAATCCAGATGGGTGAAGTGAGTTC 1020  
QY 355 HisSerHisThrGlnThrThrLeuPheHisThrPheYrAspLeuIleGlnIleYsAsn 374  
DB 1021 CACTCTCACACAAACCAACGCTGTCCATACCTTATGATGTTGATACAAAAAAC 1080  
QY 375 LysHisIleYsHisIleYsGlyValAlaAlaSerAspPheIleArgSerLeuAspHisCysGly 394  
DB 1081 AAACACAAACATTAAGAGTGTGCTGCAAGTCACTTCATTCGAGCCGAGACCATGTGGA 1140  
QY 395 AspLeuAlaLeuGluGlyValIlePheSerHisIleYsPheAspPheGluLeuGlnAspValSer 414  
DB 1141 GACCTAGCTCTGAGAGGCTGTCTCCACAAAGTTTGAATTCGAAGTCCAGAGATGTGCC 1200  
QY 415 SerValAsnGluAspValLeuLeuThrThrGlyLeuLeuCysIleYsThrAlaGlnArg 434  
DB 1201 AGCGTGAATGAGATGTCCTGCTGACACATGGGCTCTGTAAATATACAGCTCAAGG 1260  
QY 435 PheIleYsProLysIleYsPhePheHisIleYsSerPheGlnGlyTyrThrAlaGlyArg 454  
DB 1261 TTCAAGCAAAAGTATTAATCTTTCAACAAGTCATTCAGAGGTACACAGCAGGAGAA 1320  
QY 455 LeuSerSerLeuLeuThrSerHisGluProGluGluValThrIleYsGlyAsnGlyTyrLeu 474  
DB 1321 CTCAGAGTTTATTTAGCTCTCAAGAGCAGAGAGGAGGACCAAGGGGAAATGTTACTTG 1380  
QY 475 GlnIleMetValSerIleSerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThr 494  
DB 1381 CAGAAATGCTTTTCATTTTCGACATTTTCATCCACTTATGACAGCTGCTCGGTACACC 1440  
QY 495 CysGlySerSerValGluAlaThrArgAlaValMetLysHisLeuAlaAlaValTyrGln 514  
DB 1441 TGTGGGTCATGTGGGAAGCACACAGGCGTGTATGAAGCACCTCGCAGAGGTATCAAA 1500  
QY 515 HisGlyCysLeuLeuGlyLeuSerIleAlaIleYsArgProLeuTyrPargGlnGlnSerLeu 534  
DB 1501 CACGGCTGCCCTTCGCGACTTTCATCGCCCAAGAGGCTCTCTGAGACAGAAATCTTGG 1560  
QY 535 GlnSerValIleYsAsnThrThrGluGlnGluIleLeuIleYsAlaIleAsnIleAsnSerPhe 554  
DB 1561 CAAGGTGTGAAGAAACACACCTGACAGCAAGAAATTTGTGAAGCCATTAATATTCCTTT 1620  
QY 555 ValGluCysGlyIleHisIleLeuTyrGlnGlySerThrSerIleYsSerAlaLeuSerGlnGlu 574  
DB 1621 GTAGAGGTGGCATCATTTATTCAGAGAGTATCATCAATCAGCCCTGAGCAGAA 1680  
QY 575 PheGluAlaPhePheGlnGlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyr 594

|||||  
Db 1681 TTGAAAGCTTCTTCAAGAGTAAAGCTTATATCAACTCAGGGAACATCCCGATTAC 1740  
QY 595 LeuphAspPhegIuHHisLeuProAsnCysAlaSerAlaLeuAspHelleuSleu 614  
Db 1741 TTATTTGACTTCTTGGACATTGTCCTCAATGTGCAGTGGCCCTGACTTCATTAAACG 1800  
QY 615 AspPheTYrGLyGLyAlaMetAlaSerTPGluYSAlaAlaGLAspThrGLyGLy 634  
Db 1801 GACTTTTATGGGGAGGAGTATGCTTCATGGGAAAAGGCTGCAGAAAGCACAGTGGAAATC 1860  
QY 635 HisMetGLuGLuAlaProGLuThrTYrIleProSerArgAlaValSerLeuPheAsn 654  
Db 1861 CACATGGAAGAGAGCCCAAAACCTACATTCACAGAGGGCTGTATCTTTGTTCTTCAAC 1920  
QY 655 TrpLYsGLInGLuPheArgThrLeuGLuValThrLeuArgAspPheSerLYsLeuAsnLYs 674  
Db 1921 TGGAAAGCAGGAATTCAGACTCTGGAGGTACACACTCCGGGATTTGACAAAGTTGAATAG 1980  
QY 675 GLuAspIleThrTYrLeuGLyLYsIlePheSerSerAlaThrSerLeuArgLeuGlnIle 694  
Db 1981 CAAAGATTCAGATATCTTGGGGAAATATTCAGCTCTGCCACAAAGCTTCAGGCTGCAATA 2040  
QY 695 LysArgCysAlaGLyValAlaGLySerLeuSerLeuValLeuSerThrCysLYsAsnIle 714  
Db 2041 AAGAGATGTGCTGTGGTGGCTGGAAGCCTCAGTTTGGTCTCAGACACCTGAAGAACAAT 2100  
QY 715 TYrSerLeuMetValGLuAlaSerProLeuThrIleGLuAspGLuArgHisIleThrSer 734  
Db 2101 TATTTCTCATGTGTGGAAGCCAGTCCCTCACATAGAAAGACAGACACTTCACATCT 2160  
QY 735 ValThrAsnLeuLYsThrLeuSerIleHisAspLeuGlnAsnGLuArgLeuPro 752  
Db 2161 GTAAACAACCTGAAACCTTGAGTATTCATGACTACAGATCAACAGGCTGCCG 2214  
RESULT 7  
AAH99581  
ID AAH99581 standard; cDNA; 2950 BP.  
XX  
AC AAH99581;  
XX  
DT 16-OCT-2001 (first entry)  
XX  
DE Human protein encoding cDNA sequence SEQ ID NO:416.  
XX  
KW Human; cancer; ulcer; HIV infection; human immunodeficiency virus;  
KW antiinflammatory; antirheumatic; antidiarrheal; immunosuppressive;  
KW antibacterial; endocrine; cardiant; central nervous system; viricide;  
KW anti-HIV; fungicide; antitumagen; cardiovascular; antianemic; anaemia;  
KW antiaggregant; haemostatic; vulnary; antilucer; osteopathic; eczema;  
KW dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;  
KW neuroprotective; antidiuretic; nootropic; antiparkinsonian; infection;  
KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;  
KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;  
KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;  
KW genetic disease; haematopoietic disorder; platelet disorder; asthma;  
KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;  
KW allergic rhinitis; diabetes; multiple sclerosis; depression;  
KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;  
KW neurological disorder; ss.  
OS Homo sapiens.  
XX  
XX WO200153455-A2.  
PM  
XX  
PD 26-JUL-2001.  
XX  
PF 22-DEC-2000; 2000WO-US35017.  
XX  
PR 23-DEC-1999; 99US-0471275.  
XX  
PR 21-JAN-2000; 2000US-0486725.  
XX  
PR 25-APR-2000; 2000US-0552317.  
XX

PA (HYSE-) HXSEQ INC.  
XX  
PI Tang YF, Liu C, Drmanac RT;  
XX  
DR WPI: 2001-457603/49.  
XX  
P-PSDB: AAM25640.  
XX  
PT Isolated human polynucleotides encoding polypeptides, useful for the  
XX treatment and diagnosis of e.g. cancer, ulcers and HIV infection -  
XX  
PS Claim 1: Page 511-512; 1217pp; English.  
XX  
XX AAH99166 to AAH99904 encode the human proteins given in AAM25225 to  
CC AAM25963. The proteins can have activities based on the tissues and  
CC cells they are expressed in, such as: antiinflammatory; antirheumatic;  
CC antidiarrheal; immunosuppressive; antibacterial; endocrine; cardiant;  
CC central nervous system; viricide; anti-HIV; fungicide; antitumagen;  
CC cardiovascular; antianemic; antiaggregant; haemostatic; vulnary;  
CC antilucer; osteopathic; dermatological; antiallergic; antiasthmatic;  
CC antidiabetic; cytostatic; neuroprotective; antidiuretic; nootropic;  
CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides  
CC encoding them can be used in gene therapy, antisense therapy and vaccine  
CC production. The proteins and polynucleotides are useful for screening for  
CC agonists or antagonists of a protein and for the treatment and diagnosis  
CC of disorders associated with the activity of a protein e.g. inflammation,  
CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,  
CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal  
CC infections, autoimmunity, genetic diseases, haematopoietic disorders,  
CC anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,  
CC osteoporosis, severe combined immunodeficiency, eczema, allergic  
CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,  
CC Alzheimer's disease, Parkinson's disease, neurodegenerative and  
CC neurological disorders.  
SQ Sequence 2950 BP; 915 A; 592 C; 628 G; 815 T; 0 other:  
Alignment Scores:  
Pred. No.: 0 Length: 2950  
Score: 3346.00 Matches: 638  
Percent Similarity: 99.53% Conservative: 1  
Best Local Similarity: 99.38% Mismatches: 3  
Query Match: 61.29% Indels: 0  
DB: 22 Gaps: 0  
US-09-697-089-2 (1-1024) x AAH99581 (1-2950)  
QY 363 AlaSerAspPheIleArgSerLeuAspHisCysGLyAspLeuAlaLeuGLuGLyValPhe 402  
Db 2 GCAAGTGAATTCATTCGGAGGCTGGACACCTGTGATACCTATCTGTGGAGGTGTTC 61  
QY 403 SerHisLYsPheAspPheGLuLeuGlnAspValSerSerValAsnGLuAspValLeuLeu 422  
Db 62 TCCCAAGATTGATTTGCAGACTGCAGATGTGTCCAGCGTAAAGAGATCTCCTGCG 121  
QY 423 ThrThrGLyLeuLeuCysLYsTYrThrAlaGlnArgPheLYsProLYsTYrLYsPhePhe 442  
Db 122 ACACTGGGCTCTGTGAATATACAGCTCAAAAGTTCCAAAGATATAATTTCTT 181  
QY 443 HisLYsSerPheGlnGLuLYrThrAlaGLyArgGLuSerSerLeuLeuThrSerHis 462  
Db 182 CACAAGTCAATTCAGAGATGACACAGCAGCAACACACAGAGTTTATGACGTCATC 241  
QY 463 GLuProGLuGLuValThrLYsGLyAsnGLyTYrLeuGlnLYsMetValSerIleSerAsp 482  
Db 242 GAGCCAGAGAGAGTACCAAGGGGATGTACTTGCAGAAATGGTTCCATTTCGGGAC 301  
QY 483 IleThrSerThrTYrSerSerLeuLeuArgTYrThrCysGLySerSerValGLuAlaThr 502  
Db 302 ATTACATCACTTATAGACAGCTGCTCCGGTACACCTTGGTGATCTGTGGAAACCCACC 361  
QY 503 ArgAlaValMetLYsHisLeuAlaAlaValTYrGlnHisGLyCysLeuLeuGLyLeuSer 522  
Db 362 AGGCTGTATAGAACACCTCGCACAGTATATCAACACAGGCTGCTCTGGAACTTTC 421



XX New caspase recruitment domain (CARD)-containing polypeptides and  
 PT encoding nucleic acids, useful for treating abnormal cell proliferation  
 PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,  
 PT arthritis or stroke

XX Claim 1: Page 200-201; 216pp; English.

CC The invention relates to an isolated caspase recruitment domain (CARD)  
 CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain  
 CC from it, and the polynucleotides encoding them. Also included are a  
 CC recombinant vector comprising the polynucleotide, recombinant cells  
 CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian  
 CC and insect cells) and an anti-CARD antibody. The CARD-containing  
 CC polypeptide and CARD-encoding nucleic acid are useful for treating a  
 CC pathology characterised by abnormal cell proliferation (e.g. cancer). In  
 CC abnormal cell death (apoptosis), autoimmune diseases or inflammation.  
 CC particular, the polypeptide and nucleic acid are useful for treating  
 CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth  
 CC muscle cell proliferation in arteries following balloon angioplasty  
 CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,  
 CC allergies, arthritis, lupus, Schogen's syndrome, Crohn's disease,  
 CC graft-versus-host disease, stroke, myocardial infarction, heart failure,  
 CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's  
 CC disease) or immunodeficiency associated disease (e.g. human  
 CC immunodeficiency virus (HIV) infection). The nucleic acids are useful  
 CC in a variety of diagnostic applications. The present sequence is a  
 CC cDNA encoding a CARD domain containing protein.

XX Sequence 891 BP; 237 A; 228 C; 217 G; 209 T; 0 other;

Alignment Scores:

Pred. No.:	3-21e-228	Length:	891
Score:	1598.00	Matches:	296
Percent Similarity:	99.66%	Conservative:	0
Best Local Similarity:	99.66%	Mismatches:	1
Query Match:	29.27%	Indels:	0
DB:	24	Gaps:	0

US-09-697-089-2 (1-1024) x ABR22766 (1-891)

QY 161 LeuGlnSerProCysIleIleGlnGlyGluSerGlyLysSerThrLeuLeuGln 180  
 DB 1 CTTGAGAGCCCTGCATCATTTGAGGGGAACTGGCAAGGAAAGCCCTGCTGCGAG 60  
 QY 181 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 200  
 DB 61 CGCATTTGCCATGCTCTGGGGCTCCGGAAGTCCAGAGGCTGTGACCAAGTTCAAAATTCGTC 120  
 QY 201 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuLysPheGlnLeu 220  
 DB 121 TTCCTCTCCGCTCGACGAGGCGCCAGGGGTGACTTTTGAAGCCCTGCTGATCAACTC 180  
 QY 221 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 240  
 DB 181 CTGGATATACCTGGGACATATCGAAGCAGACATTCATGCGCATGCTGTGAAGCTGCGG 240  
 QY 241 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 260  
 DB 241 CAGAGGGTCTTCTTCCTTCCTGATGCTACATGAATTCACCCAGAGAACGCCAGAA 300  
 QY 261 IleGlnAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValThrThrThr 280  
 DB 301 ATCGAAGCCCTATTAAGGAAACACCCCTTCAGAAACATGCTATCTCCACCTACC 360  
 QY 281 ThrGlnCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 300  
 DB 361 ACTGAGTGGCTGAGGCACATACGCGAGTTGTGGCCCTGACTGCGAGAGTGGGGATAG 420  
 QY 301 ThrGlnAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 320  
 DB 421 ACAGAGACAGGCCAGGCTCTCATCGAAGAGTGTGATCAAGAGAGCTTCTGTAAGCC 480

QY 321 LeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe 340  
 DB 481 TTGTTCTCCAAATTCAGAAATCCAGTGCTTGAGAGATCTATGAAAGACCCCTCTTT 540  
 QY 341 ValValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnThr 360  
 DB 541 GTGGTCATCATCTTGTCATTCAGATCGAGTGGTGAAGTGAAGTTCACCTCCACACACAA 600  
 QY 361 ThrLeuPheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysGly 380  
 DB 601 AGCGTTTCCATACCTCTTATATATCTGTGATGACGAAACAAACACAAACATTAAGGT 660  
 QY 381 ValAlaAlaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGly 400  
 DB 661 GTGGCTGCAGAGTACTTCTTGGAGCCCTGGACACCGTGGAGACTTGTGAGAGGT 720  
 QY 401 ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal 420  
 DB 721 GTGTTCTCCACAGATTGATTTGCAACTGCAGAGATGTGTCAGGCTGAATGAGATGTC 780  
 QY 421 LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys 440  
 DB 781 CTGCTGACAACTGGGCTCTCTGTAAATATACAGCTCAAAAGGTTCAAGCCAAAGTATAAA 840  
 QY 441 PhePheHisLysSerPheGlnGluThrThrAlaGluArgArgLeuSerSer 457  
 DB 841 TTCCTTCCAAAGTCAATTCAGAGATGACGACGAGGACGAAAGTCAAGCAGT 891

RESULT 9  
 ABR22732  
 ID ABR22732 standard; cDNA; 1395 BP.  
 AC ABR22732;  
 DT 26-MAR-2002 (first entry)  
 XX Human cDNA encoding CLAN B.  
 DE  
 XX  
 XX  
 KW Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;  
 KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;  
 KW autoimmune disease; inflammation; keratinocyte hyperplasia;  
 KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;  
 KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;  
 KW leukaemia; allergy; arthritis; lupus; Schogen's syndrome;  
 KW Crohn's disease; graft-versus-host disease; stroke;  
 KW myocardial infarction; heart failure; neurodegenerative disease;  
 KW Parkinson's disease; Alzheimer's disease; HIV;  
 KW human immunodeficiency virus infection.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200190156-A2.  
 XX  
 PD 29-NOV-2001.  
 XX  
 PE 24-MAY-2001; 2001WO-US17158.  
 XX  
 PR 24-MAY-2000; 2000US-0579240.  
 PR 10-OCT-2000; 2000US-0686347.  
 PR 14-MAR-2001; 2001US-275980P.  
 PR 23-MAY-2001; 2001US-0864921.  
 XX  
 PA (BURN-) BURNHAM INST.  
 XX  
 PI Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;  
 PI Oliveira VAM, Hayashi H, Pawlowski K;  
 DR WPI; 2002-083086/11.  
 DR P-PSDB; AAU80862.  
 XX  
 PT New caspase recruitment domain (CARD)-containing polypeptides and  
 PT encoding nucleic acids, useful for treating abnormal cell proliferation  
 PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,

PT arthritis or stroke -  
XX  
PS Claim 1; Page 174-176; 216pp; English.  
XX  
CC The invention relates to an isolated caspase recruitment domain (CARD)  
CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain  
CC from it, and the polynucleotides encoding them. Also included are a  
CC recombinant vector comprising the polynucleotide, recombinant cells  
CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian  
CC and insect cells) and an anti-CARD antibody. The CARD-containing  
CC polypeptide and CARD-encoding nucleic acid are useful for treating a  
CC pathology characterised by abnormal cell proliferation (e.g. cancer),  
CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In  
CC particular, the polypeptide and nucleic acid are useful for treating  
CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth  
CC muscle cell proliferation in arteries following balloon angioplasty  
CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukemias,  
CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,  
CC graft-versus-host disease, stroke, myocardial infarction, heart failure,  
CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's  
CC disease) or immunodeficiency associated disease (e.g. human  
CC immunodeficiency virus (HIV) infection). The nucleic acids are useful  
CC in a variety of diagnostic applications. The present sequence is a  
CC cDNA encoding a CARD domain containing protein.  
XX  
SQ Sequence 1395 BP; 436 A; 248 C; 327 G; 384 T; 0 other;

Alignment Scores:  
Pred. No.: 6,28e-202 Length: 1395  
Score: 1424.00 Matches: 271  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 99.63% Mismatches: 0  
Query Match: 26.09% Indels: 0  
DB: Gaps: 0

US-09-697-089-2 (1-1024) x ABR22732 (1-1395)

QY 753 GlycylLeuThrAspSerLeuGlyAsnLeuLysAsnLeuThrLysLeuIleMetAspAsn 772  
DB 538 AGTGGTCTGACGTGACAGCTGGTGAACCTTGAAGAACTTACATATGATGATAC 597  
QY 773 IleLysMetAsnGluGluAspAlaIleLysLeuAlaGluGluLysAsnLysLys 792  
DB 598 ATAAAGATGAATGAAGAAGATGATTAATACTGAGAGCTGAATAAACCCTGAAGAG 657  
QY 793 MetCysLeuPheHisLeuThrHisLeuSerAspIleGlyGluGlyMetAspTyrIleVal 812  
DB 658 ATGTGTTATTTCATTTCATCCACTGTCTGACATTTGAGAGGGAATGATTAATGATC 717  
QY 813 LysSerLeuSerSerGluProCysAspLeuGluGluIleGlnLeuValSerCysCysLeu 832  
DB 718 AAGTCTCTGTCAGTGAACCTGTGACCTTGAAGAAATTCATATGCTCTGCTGCTTG 777  
QY 833 SerIlaAsnAlaValLysIleLeuAlaGlnAsnLeuHisAsnLeuValLysLeuSerIle 852  
DB 778 TCTGGAAATGAGTGAATAATCCTAGCTCAGAACTTCAAAATGGTGAACCTGAGCAT 837  
QY 853 LeuAspLeuSerGluAsnTyrLeuGluLysAspGlyAsnGluAlaLeuHisGluLeuIle 872  
DB 838 CTTGATTTATCAGAAAAATTTACTCGAAAAAATGGAATGAACTCTTCAATGAACTGATC 897  
QY 873 AspArgMetAsnValLeuGluGlnLeuThrAlaLeuMetLeuProTyrPglyCysAspVal 892  
DB 898 GACAGAGATGAACGTGTGAGAACAGCTACCCGACTGATGCTGCCCTGGCGCTGAGAGCTG 957  
QY 893 GlnGlySerLeuSerSerLeuLysHisLeuGluGluValProGlnLeuValLysLeu 912  
DB 958 CAAGGAGCCCTGACAGCTCTTGAACATTTGGAGAGGCTCCCAACAACCTGCTCAAGCTT 1017  
QY 913 GlyLeuLysAsnTyrPargLeuThrAspThrGluIleArgIleLeuGluValAlaPhePheGly 932  
DB 1018 GGGTTGAAAAAAGCTGAGAGCTCAGAGATPACAGAGATTTGAATTTTGAAGTCTTTTGA 1077

QY 933 LysAsnProLeuLysAsnPheGlnGlnLeuAsnLeuAlaGlyAsnArgValSerSerAsp 952  
DB 1078 AAGAACCCTCGAAAAAATTCACACAGATTTGCGCGGAATTCGTGAGCAGCAT 1137  
QY 953 GlyThrPheAlaPheMetGlyValPheGluAsnLeuLysGlnLeuValPhePheAspPhe 972  
DB 1138 GGATGGCTGCTTCATCAGGTGGGTATTTGAGAACTTAAAGCAATTAAGTGTGTTGACTTT 1197  
QY 973 SerThrLysGluPheLeuProAspProAlaLeuValArgLysLeuSerGlnValLeuSer 992  
DB 1198 AGTACTAAGAAATTTCTACCTGATCCAGATCAGCAATAGCAGAAAACTTAGCAAGTGTATCC 1257  
QY 993 LysLeuThrPheLeuGlnGluAlaArgLeuValGlyTyrPglInPheAspAspAspLeu 1012  
DB 1258 AAGTTAACTTTTCGCAAGAGCTAGAGCTGTGTGGGTGGCAATTTGATGATGATGATCTC 1317  
QY 1013 SerValIleThrGlyAlaPheLysLeuValThrAla 1024  
DB 1318 AGTGTATTACAGGTGCTTTTAAACTAGTAACCTGCT 1353

RESULT 10

ID ABR22767 standard; cDNA; 618 BP.

AC ABR22767;

DE 26-MAR-2002 (first entry)

XX Human cDNA encoding CLAN LRR.

XX Caspase recruitment domain; CARD; SS; NB-ARC; ANGIO-R; LRR; SAM;  
XX abnormal cell proliferation; cancer; abnormal cell death; apoptosis;  
XX autoimmune disease; inflammation; keratinocyte hyperplasia;  
XX inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;  
XX balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;  
XX leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;  
XX Crohn's disease; graft-versus-host disease; stroke;  
XX myocardial infarction; heart failure; neurodegenerative disease;  
XX Parkinson's disease; Alzheimer's disease; HIV;  
XX human immunodeficiency virus infection.

OS Homo sapiens.

PN WO200190156-A2.

XX 29-NOV-2001.

PF 24-MAY-2001; 2001WO-US17158.

XX 24-MAY-2000; 2000US-0579240.

PR 10-OCT-2000; 2000US-0686347.

PR 14-MAR-2001; 2001US-275980P.

PR 23-MAY-2001; 2001US-0864921.

XX (BURN-) BURNHAM INST.

PA Reed JC, Plo FF, Godzik A, Stehlik C, Damiano JS, Lee SH;

PI Oliveira VAM, Hayashi H, Pawlowski K;

XX WPL, 2002-083086/11.

DR P-PSDS; AA080873.

XX New caspase recruitment domain (CARD)-containing polypeptides and

PT encoding nucleic acids, useful for treating abnormal cell proliferation

PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,

PT arthritis or stroke -

XX Claim 1; Page 202-203; 216pp; English.

CC The invention relates to an isolated caspase recruitment domain (CARD)

CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain

CC from it, and the polynucleotides encoding them. Also included are a

CC recombinant vector comprising the polynucleotide, recombinant cells



CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian  
CC and insect cells) and an anti-CARD antibody. The CARD-containing  
CC polypeptide and CARD-encoding nucleic acid are useful for treating a  
CC pathology characterised by abnormal cell proliferation (e.g. cancer),  
CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In  
CC particular, the polypeptide and nucleic acid are useful for treating  
CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth  
CC muscle cell proliferation in arteries following balloon angioplasty  
CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,  
CC allergies, arthritis, lupus, Schlegel's syndrome, Crohn's disease,  
CC graft-versus-host disease, stroke, myocardial infarction, heart failure,  
CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's  
CC disease) or immunodeficiency associated disease (e.g. human  
CC immunodeficiency virus (HIV) infection). The nucleic acids are useful  
CC in a variety of diagnostic applications. The present sequence is a  
CC cDNA encoding a CARD domain containing protein.

XX  
SQ Sequence 618 BP; 194 A; 113 C; 148 G; 163 T; 0 other;

#### Alignment Scores:

Pred. No.:	1 5e-151	Length:	618
Score:	1084.00	Matches:	206
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	19.86%	Indels:	0
DB:	24	Gaps:	0

US-09-697-089-2 (1-1024) x ABR22767 (1-618)

QY 760 GlyAsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluLysAsp 779  
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DB 1 GGTAACCTTGAGAACCTTACCAAGCTCATATGATTAACATAAGATGAAGTGAAGAGAT 60  
QY 780 AlaIleLysLeuAlaGluGlyLeuLysAsnLeuLysMetCysLeuPheHisLeuThr 799  
|||  
DB 61 GCTATAAACTACTGAGAGCCCTGAAAAACCTGAAAGATGCTTATTTCAATTGACC 120  
QY 800 HisLeuSerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluPro 819  
|||  
DB 121 CACTGTCTACATTTGGAGAGGGAGATGATTAATAGTCAAGCTCTCTGTAAGTGAAGACC 180  
QY 820 CysAspLeuGluGluIleGluLeuValSerCysCysLeuSerAlaAsnAlaValLysIle 839  
|||  
DB 181 TGTGACCTTGAGAAATTCATTAAGTCTCTGCTGCTTGTCTGCAATTCAGTGAAGATC 240  
QY 840 LeuAlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyr 859  
|||  
DB 241 CTAGCTCAGAACTCTTCACATTTGGTCAAACTGAGCATCTTGAATTCAGAAAATTCAC 300  
QY 860 LeuGluLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGlu 879  
|||  
DB 301 CTGGAAAAGATGAAATGAAGCTCTTCATGAACCTGATCGACAGATGAACGTGCTAGAA 360  
QY 880 GlnLeuThrAlaLeuMetLeuProTyrPglyCysAspValGlnGlySerLeuSerSerLeu 899  
|||  
DB 361 CAGCTCACCCACTGAGATGCTGCCCTGGGGCTGTGACGTGCAAGGACACCTGAGAGAGCTG 420  
QY 900 LeuLysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrPargLeu 919  
|||  
DB 421 TTGAAACATTTGGAGGAGGCTCCACCACTGTCACAGCTGGGTGAAAACTGGAGACTC 480  
QY 920 ThrAspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPhe 939  
|||  
DB 481 ACAGATTCACAGATTAAGATTTTAAAGTCAATTTTGGAAAGAACCTCTGAAAACCTTC 540  
QY 940 GlnGlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrPheLeuAlaPheMetGly 959  
|||  
DB 541 CACGAGTTGAAATTTGGCGGGAATCGTGTGACAGATGATGATGGCTTGCCTCATGGGT 600  
QY 960 ValPheGluAsnLeuLys 965  
|||  
DB 601 GTATTGTGAAATCTTAAG 618

RESULT 11  
ID AAS26160  
AAS26160 standard; cDNA; 608 BP.  
AC AAS26160;  
XX  
DT 07-NOV-2001 (first entry)  
XX  
DE Human cDNA encoding a novel secreted protein, Seq ID 339.  
XX  
XX Human; immunosuppressive; antiarthritic; ss; antiinflammatory;  
XX cytotoxic; cardiant; vasotropic; cerebroprotective; nootropic;  
XX neuroprotective; antibacterial; virucide; fungicide; ophthalmological;  
XX vulnary; secreted protein; rheumatoid arthritis;  
XX hyperproliferative disorder; cardiovascular disorder; cardiac arrest;  
XX cerebrovascular disorder; cerebral ischaemia; angiogenesis;  
XX nervous system disorder; Alzheimer's disease; infection; ocular disorder;  
XX corneal infection; wound healing; epithelial cell proliferation;  
XX skin ageing; food additive; preservative; antiproliferative.  
XX  
OS Homo sapiens.  
XX  
PN WO200155322-A2.  
XX  
PD 02-AUG-2001.  
XX  
PF 17-JAN-2001; 2001WO-US01341.  
XX  
XX 31-JAN-2000; 2000US-0179065.  
XX 04-FEB-2000; 2000US-0180628.  
XX 24-FEB-2000; 2000US-0184664.  
XX 02-MAR-2000; 2000US-0186350.  
XX 16-MAR-2000; 2000US-0189874.  
XX 17-MAR-2000; 2000US-0190076.  
XX 18-APR-2000; 2000US-0198123.  
XX 19-MAY-2000; 2000US-0205515.  
XX 07-JUN-2000; 2000US-0209467.  
XX 28-JUN-2000; 2000US-0214886.  
XX 30-JUN-2000; 2000US-0215135.  
XX 07-JUL-2000; 2000US-0216647.  
XX 07-JUL-2000; 2000US-0216880.  
XX 11-JUL-2000; 2000US-0217487.  
XX 11-JUL-2000; 2000US-0217496.  
XX 14-JUL-2000; 2000US-0218290.  
XX 26-JUL-2000; 2000US-0220963.  
XX 26-JUL-2000; 2000US-0220964.  
XX 14-AUG-2000; 2000US-0224518.  
XX 14-AUG-2000; 2000US-0224519.  
XX 14-AUG-2000; 2000US-0224513.  
XX 14-AUG-2000; 2000US-0225213.  
XX 14-AUG-2000; 2000US-0225266.  
XX 14-AUG-2000; 2000US-0225267.  
XX 14-AUG-2000; 2000US-0225268.  
XX 14-AUG-2000; 2000US-0225270.  
XX 14-AUG-2000; 2000US-0225272.  
XX 14-AUG-2000; 2000US-0225447.  
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XX 14-AUG-2000; 2000US-0225758.  
XX 14-AUG-2000; 2000US-0225759.  
XX 18-AUG-2000; 2000US-0226279.  
XX 22-AUG-2000; 2000US-0226681.  
XX 22-AUG-2000; 2000US-0226688.  
XX 23-AUG-2000; 2000US-0227182.  
XX 23-AUG-2000; 2000US-0227009.  
XX 30-AUG-2000; 2000US-0228924.  
XX 01-SEP-2000; 2000US-0229287.  
XX 01-SEP-2000; 2000US-0229343.  
XX 01-SEP-2000; 2000US-0229344.  
XX 01-SEP-2000; 2000US-0229345.  
XX 05-SEP-2000; 2000US-0229509.  
XX 05-SEP-2000; 2000US-0229513.  
XX 06-SEP-2000; 2000US-0230437.  
XX 06-SEP-2000; 2000US-0230438.  
XX 08-SEP-2000; 2000US-0231242.

	PR	08-SEP-2000;	2000US-0231243.
	PR	08-SEP-2000;	2000US-0231244.
	PR	08-SEP-2000;	2000US-0231245.
	PR	08-SEP-2000;	2000US-0231413.
	PR	08-SEP-2000;	2000US-0231414.
	PR	08-SEP-2000;	2000US-0232080.
	PR	08-SEP-2000;	2000US-0232081.
	PR	12-SEP-2000;	2000US-0231968.
	PR	14-SEP-2000;	2000US-0233397.
	PR	14-SEP-2000;	2000US-0233398.
	PR	14-SEP-2000;	2000US-0233399.
	PR	14-SEP-2000;	2000US-0233400.
	PR	14-SEP-2000;	2000US-0233401.
	PR	14-SEP-2000;	2000US-0233063.
	PR	14-SEP-2000;	2000US-0233064.
	PR	21-SEP-2000;	2000US-0233065.
	PR	21-SEP-2000;	2000US-0234223.
	PR	25-SEP-2000;	2000US-0234274.
	PR	25-SEP-2000;	2000US-0234997.
	PR	25-SEP-2000;	2000US-0234998.
	PR	26-SEP-2000;	2000US-0235484.
	PR	27-SEP-2000;	2000US-0235834.
	PR	27-SEP-2000;	2000US-0235836.
	PR	29-SEP-2000;	2000US-0236327.
	PR	29-SEP-2000;	2000US-0236367.
	PR	29-SEP-2000;	2000US-0236368.
	PR	29-SEP-2000;	2000US-0236369.
	PR	29-SEP-2000;	2000US-0236370.
	PR	02-OCT-2000;	2000US-0236802.
	PR	02-OCT-2000;	2000US-0237037.
	PR	02-OCT-2000;	2000US-0237038.
	PR	02-OCT-2000;	2000US-0237039.
	PR	13-OCT-2000;	2000US-0239935.
	PR	13-OCT-2000;	2000US-0239937.
	PR	20-OCT-2000;	2000US-0240960.
	PR	20-OCT-2000;	2000US-0241221.
	PR	20-OCT-2000;	2000US-0241785.
	PR	20-OCT-2000;	2000US-0241786.
	PR	20-OCT-2000;	2000US-0241787.
	PR	20-OCT-2000;	2000US-0241808.
	PR	20-OCT-2000;	2000US-0241809.
	PR	20-OCT-2000;	2000US-0241826.
	PR	01-NOV-2000;	2000US-0244617.
	PR	08-NOV-2000;	2000US-0246474.
	PR	08-NOV-2000;	2000US-0246475.
	PR	08-NOV-2000;	2000US-0246476.
	PR	08-NOV-2000;	2000US-0246477.
	PR	08-NOV-2000;	2000US-0246478.
	PR	08-NOV-2000;	2000US-0246523.
	PR	08-NOV-2000;	2000US-0246524.
	PR	08-NOV-2000;	2000US-0246525.
	PR	08-NOV-2000;	2000US-0246526.
	PR	08-NOV-2000;	2000US-0246527.
	PR	08-NOV-2000;	2000US-0246528.
	PR	08-NOV-2000;	2000US-0246532.
	PR	08-NOV-2000;	2000US-0246609.
	PR	08-NOV-2000;	2000US-0246610.
	PR	08-NOV-2000;	2000US-0246611.
	PR	08-NOV-2000;	2000US-0246613.
	PR	17-NOV-2000;	2000US-0249207.
	PR	17-NOV-2000;	2000US-0249208.
	PR	17-NOV-2000;	2000US-0249209.
	PR	17-NOV-2000;	2000US-0249210.
	PR	17-NOV-2000;	2000US-0249211.
	PR	17-NOV-2000;	2000US-0249212.
	PR	17-NOV-2000;	2000US-0249213.
	PR	17-NOV-2000;	2000US-0249214.
	PR	17-NOV-2000;	2000US-0249215.
	PR	17-NOV-2000;	2000US-0249216.
	PR	17-NOV-2000;	2000US-0249217.
	PR	17-NOV-2000;	2000US-0249218.
	PR	17-NOV-2000;	2000US-0249244.
	PR	17-NOV-2000;	2000US-0249245.
	PR	17-NOV-2000;	2000US-0249246.
	PR	17-NOV-2000;	2000US-0249247.
	PR	17-NOV-2000;	2000US-0249248.
	PR	17-NOV-2000;	2000US-0249249.
	PR	17-NOV-2000;	2000US-0249250.
	PR	17-NOV-2000;	2000US-0249251.
	PR	17-NOV-2000;	2000US-0249252.
	PR	17-NOV-2000;	2000US-0249253.
	PR	17-NOV-2000;	2000US-0249254.
	PR	17-NOV-2000;	2000US-0249255.
	PR	17-NOV-2000;	2000US-0249256.
	PR	17-NOV-2000;	2000US-0249257.
	PR	17-NOV-2000;	2



DE Human cDNA encoding CLAN D.  
XX  
XX Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;  
KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;  
KW autoimmune disease; inflammation; keratinocyte hyperplasia;  
KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;  
KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;  
KW leukemia; allergy; arthritis; lupus; Schrogen's syndrome;  
KW Crohn's disease; graft-versus-host disease; stroke;  
KW myocardial infarction; heart failure; neurodegenerative disease;  
KW Parkinson's disease; Alzheimer's disease; HIV;  
KW human immunodeficiency virus infection.  
XX  
XX Homo sapiens.  
XX  
XX WO200190156-A2.  
XX  
XX 29-NOV-2001.  
XX  
XX 24-MAY-2001; 2001WO-US17158.  
XX  
XX 24-MAY-2000; 2000US-0579240.  
XX  
XX 10-OCT-2000; 2000US-0686347.  
XX  
XX 14-MAR-2001; 2001US-275960P.  
XX  
XX 23-MAY-2001; 2001US-0864921.  
XX  
XX (BURN-) BURHAM INST.  
XX  
XX Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;  
PI Oliveira VAM, Hayashl H, Pawlowski K;  
XX  
XX WPI; 2002-083086/11.  
XX  
XX P-PDB; AAU80864.  
XX  
XX New caspase recruitment domain (CARD)-containing polypeptides and  
PT encoding nucleic acids, useful for treating abnormal cell proliferation  
PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,  
PT arthritis or stroke  
XX  
XX  
XX Claim 1; Page 178-179; 216pp; English.  
XX  
XX  
XX The invention relates to an isolated caspase recruitment domain (CARD)  
CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain  
CC from it, and the polynucleotides encoding them. Also included are a  
CC recombinant vector comprising the polynucleotide, recombinant cells  
CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian  
CC and insect cells) and an anti-CARD antibody. The CARD-containing  
CC polypeptide and CARD-encoding nucleic acid are useful for treating a  
CC pathology characterised by abnormal cell proliferation (e.g. cancer),  
CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In  
CC particular, the polypeptide and nucleic acid are useful for treating  
CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth  
CC muscle cell proliferation in arteries following balloon angioplasty  
CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukemias,  
CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,  
CC graft-versus-host disease, stroke, myocardial infarction, heart failure,  
CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's  
CC disease) or immunodeficiency associated disease (e.g. human  
CC immunodeficiency virus (HIV) infection). The nucleic acids are useful  
CC in a variety of diagnostic applications. The present sequence is a  
CC cDNA encoding a CARD domain containing protein.  
XX  
XX  
XX Sequence 768 BP; 218 A; 157 C; 180 G; 213 T; 0 other;  
SQ  
XX  
XX  
XX Alignment Scores:  
Pred. No.: 7,2e-117 Length: 768  
Score: 853.00 Matches: 154  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 15.63% Indels: 0  
DB: 24 Gaps: 0  
US-09-697-089-2 (1-1024) x ABR22734 (1-768)

QY 1 MetasphelleielysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20  
Db 277 ATGAAATTCATTAAGGACATATAGCCGACCCCTTATTAAAGATGGAAATGACTGTATA 336  
QY 21 LysGlnIleThrAspAspleuPheValITrPAsnValLeuAsnArgGluValAsnIle 40  
Db 337 AAGCAAAATTCACAGATGACCTATTGTATGGAATGTCTGAAATGCGCAAGAAATTAACATC 396  
QY 41 IleGlySerGluGlyValAlaGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60  
Db 397 ATTTGCTGCCAGAGAGAGGAGGACAGATGCTGTAGAGGATCATTCATGATTTTGAAA 456  
QY 61 LysGlySerGluSerCysAsnLeuPheLeuIleYSerLeuYsguITrPAsnITrProLeu 80  
Db 457 AAGGTTTCAGAGTCCTTAACCTCTTTCTTAATCCCTTAAGAGATGAGACTATCCCTTA 516  
QY 81 PheGlnAspleuAsnGlnGlnSerLeuPheHisGlnThrSerGluGlyAspleuAspAsp 100  
Db 517 TTTCAGACCTTGAAATGAGCAAAAGCTTTTTCATCAGACATCAGAAAGAGACTTGAGCAT 576  
QY 101 LeuAlaGlnAspleuLysAspleuITrHisITrProSerPheLeuAsnPheITrProLeu 120  
Db 577 TTGGCTCAGGATTTAAAGACTGTGTACCATACCCCATCTTTTGAACTTTTATCCCTT 636  
QY 121 GlyGluAspIleAspIleIlePheAsnLeuYSerThrPheITrGluITrProValLeuITrP 140  
Db 637 GGTCAAGATATGTGACATATTATTTTAACCTGAAAAGCACTTCACAGAACTGTCTGTGG 696  
QY 141 ArgLysAspGlnHisHisArgValGluGlnLeuITrLeu 154  
Db 697 AGCAAGAGCAACACCATCACCGGTGAGACAGCTGACCTTA 738  
RESULT 14  
AAS26575  
ID AAS26575 standard; cDNA; 522 BP.  
XX  
XX AAS26575;  
AC  
XX  
XX 07-NOV-2001 (first entry)  
XX  
XX  
XX Human cDNA encoding a novel secreted protein, Seq ID 754.  
XX  
XX Human; immunosuppressive; antiarthritic; ss; antirheumatic;  
KW cytostatic; cardiant; vasotropic; cerebroprotective; nootropic;  
KW neuroprotective; antibacterial; virucide; fungicide; optalmalogical;  
KW vulnary; secreted protein; rheumatoid arthritis;  
KW hyperproliferative disorder; cardiovascular disorder; cardiac arrest;  
KW cerebrovascular disorder; cerebral ischemia; angiogenesis;  
KW nervous system disorder; Alzheimer's disease; infection; ocular disorder;  
KW corneal infection; wound healing; epithelial cell proliferation;  
KW skin ageing; food additive; preservative; antiproliferative.  
XX  
XX  
XX Homo sapiens.  
XX  
XX WO200155322-A2.  
XX  
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XX  
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XX 17-JAN-2001; 2001WO-US01341.  
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PR 01-DEC-2000; 2000US-0250160.  
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PR 08-DEC-2000; 2000US-0251856.  
PR 08-DEC-2000; 2000US-0251868.  
PR 08-DEC-2000; 2000US-0251869.  
PR 08-DEC-2000; 2000US-0251989.  
PR 08-DEC-2000; 2000US-0251990.  
PR 11-DEC-2000; 2000US-0254097.  
PR 05-JAN-2001; 2001US-0259678.  
  
(HUMA -) HUMAN GENOME SCI INC.  
Rosen CA, Barash SC, Ruben SM;  
WPI. 2001-488783/53.  
P-PSDB: AA016588.  
  
New nucleic acid molecules encoding 461 human secreted proteins for  
diagnosing, preventing, treating or ameliorating medical conditions and  
used as food additives or preservatives -  
  
Claim 1; SEQ ID NO 754; 980pp; English.  
  
The invention relates to isolated nucleic acid molecules and their  
encoded secreted proteins. The nucleic acids and proteins are used to  
prevent, treat or ameliorate a medical condition in e.g. humans, mice,  
rabbits, goats, horses, cats, dogs, chickens or sheep. They  
are also used in diagnosing a pathological condition or susceptibility  
to a pathological condition. Antibodies to the proteins can also  
be used in alleviating symptoms associated with the disorders and in  
diagnostic immunoassays e.g. radioimmunoassays or enzyme linked

CC immunosorbant assays (ELISA). Disorders which are diagnosed or treated  
CC include autoimmune diseases e.g. rheumatoid arthritis,  
CC hyperproliferative disorders e.g. neoplasms of the breast or liver,  
CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders  
CC e.g. cerebral ischaemia, angiodenesis, nervous system disorders e.g.  
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi  
CC and ocular disorders e.g. corneal infection, and many other  
CC disorders listed in the specification. The polypeptides can also  
CC be used to aid wound healing and epithelial cell proliferation, to  
CC prevent skin aging due to sunburn, to maintain organs before  
CC transplantation, for supporting cell culture of primary tissues, to  
CC regenerate tissues and in chemotaxis. The polypeptides can also be used  
CC as a food additive or preservative to increase or decrease storage  
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,  
CC minerals, cofactors and other nutritional components. The present  
CC sequence encodes a novel secreted protein of the invention.

## Alignment Scores:

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Best Local Similarity:	87.72%	Mismatches:	14
Query Match:	13.28%	Indels:	6
DB:	22	Gaps:	1

US-09-697-089-2 (1-1024) x AAS26575 (1-522)

QY 80 LEUPHEGINASPLEAASNGLYGINSERLEUPHEHISGINTHRSERGLGYASPLEUASP 99  
DB 3 CTATTTGAGACTTGAAAGGACAAAGCTTTTTCATGACATCGAAGGACACTTGAGC 62  
QY 100 ASPLAUALAGINASPLEULYSASPLEUTYRHSRPROSERPHELEUASPHETRYPRO 119  
DB 63 GATTGGGTGACGATTAAAGACTGTACCATACCCATCTTTCTGACATTTATGCC 122  
QY 120 LEUGLYGUASPILEASPILEIPEHEASNULEYSSETRHPHERTHGLUPVALLEU 139  
DB 123 CTGGTGAAAGATATGACATATTTTAACTTGAAAGACACCTTCACAGAACCTGCTCG 182  
QY 140 TRPATGLVSAPGINHSHISHSIRGVALGINSLEUINLEUTHREUASNGLYLEUENG 159  
DB 183 TGGAGGAAGGACCAACACCATCACCCTGGAGCAGCTGACCTTAATGAGCTCTGCAG 242  
QY 160 ALALEUGINSERPROCYILEIIEGLUGLYUSERSGLYLYSSETRHREULEU 179  
DB 243 GCTTTGAGAGCCCTCGCATCATTTGAAGGGAACTGGCAAGCAATCCATCTGCTG 302  
QY 180 GINATGIIIEALAMETLEUTRPGLYSERGLYSCYLSAIALEUTHREULYS-PH 199  
DB 303 CAGCCCATTTGCCATGCTCTGGGGCTCCGGAAGTCCAGAGGCTCTGACCAAGTTCAANT 362  
QY 199 EVALPHE-PHELEUARGYSEARARGALAGINGLY-GIYLEUPHGLUITHREUCYSASP 218  
DB 363 CGTCTTTCTTTCTCTCTGTTTCAGCAGGCGCCAGGGTGGGCTTTTGAACCCCTGTGTAT 422  
QY 219 GINLEULEUASPILEPROGLYTHRIIEARGLYSGINTHRPHEMETALAMETLEU 238  
DB 423 CAATTCGCG-GGTATACCGGGACA-TTCAGGAGCAGACATTCAGGCCNCGT---GCTGAG 477  
QY 239 LEUATGGINATGVALLEUPHELEULEU 247  
DB 478 GTGCGGACAGAGGCTTTCTTTCTTCTTG 504

## RESULT 15

ABK22733 standard; CDNA; 578 BP.

AC ABK22733;

DT 26-MAR-2002 (first entry)

DE Human cDNA encoding CLAN C.

XX

KW Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;  
KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;  
KW autoimmune disease; inflammation; keratinocyte hyperplasia;  
KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;  
KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;  
KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;  
KW Crohn's disease; graft-versus-host disease; stroke;  
KW myocardial infarction; heart failure; neurodegenerative disease;  
KW Parkinson's disease; Alzheimer's disease; HIV;  
KW human immunodeficiency virus infection.

Homo sapiens.

WO200190156-A2.

29-NOV-2001.

24-MAY-2001; 2001WO-US17158.

24-MAY-2000; 2000US-0579240.

10-OCT-2000; 2000US-0686347.

14-MAR-2001; 2001US-275980P.

23-MAY-2001; 2001US-0864921.

(BURN-) BURNHAM INST.

Reed JC, Plo FF, Godzik A, Stehlik C, Damiano JS, Lee SH;  
Oliveira VAM, Hayashi H, Pawlowski K;  
P-PSDB; AAU80863.

WP1; 2002-083086/11.

New caspase recruitment domain (CARD)-containing polypeptides and  
encoding nucleic acids, useful for treating abnormal cell proliferation  
or cell death, autoimmune diseases or inflammation, e.g. carcinomas,  
arthritis or stroke.

Claim 1; Page 177; 216pp; English.

The invention relates to an isolated caspase recruitment domain (CARD)  
-containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain  
from it, and the polynucleotides encoding them. Also included are a  
recombinant vector comprising the polynucleotide, recombinant cells  
containing the vector (e.g. bacteria, yeast, plant, animal, mammalian  
and insect cells) and an anti-CARD antibody. The CARD-containing  
polypeptide and CARD-encoding nucleic acid are useful for treating a  
pathology characterised by abnormal cell proliferation (e.g. cancer). In  
abnormal cell death (apoptosis), autoimmune diseases or inflammation. In  
particular, the polypeptide and nucleic acid are useful for treating  
keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth  
muscle cell proliferation in arteries following balloon angioplasty  
(restenosis), gliomas, carcinomas, sarcomas, melanomas, leukemias,  
allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,  
graft-versus-host disease, stroke, myocardial infarction, heart failure,  
neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's  
disease) or immunodeficiency associated disease (e.g. human  
immunodeficiency virus (HIV) infection). The nucleic acids are useful  
in a variety of diagnostic applications. The present sequence is a  
cDNA encoding a CARD domain containing protein.

Sequence 578 BP; 172 A; 106 C; 143 G; 157 T; 0 other;

## Alignment Scores:

Pred. No.:	3.46e-63	Length:	578
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Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	9.03%	Indels:	0
DB:	24	Gaps:	0

US-09-697-089-2 (1-1024) x ABK22733 (1-578)

QY 1 Metasphelelelyaspanserargalaleuileglnargmetcglymetrhvalle 20



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Db 277 ATGATTTTCATAAGCACAATAGCCGAGCCCTTATTCAAGAATGGGAATGACTGTTATA 336
QY 21 LysGlnIleThrAspAspLeuPheValITrpAsnValLeuAsnArgGluGluValAsnIle 40
Db 337 AAGCAATACACAGATGACCTATTGTATGGAATGTTCTGAAATCGCGAAGAAAGTAAACATC 396
QY 41 IleCysCysGluIuysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
Db 397 ATTGCTGGGAGAGAGTGAGAGATGCTGCTAGAGGAGATCATTCACATGATTTTGAAA 456
QY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluITrpAsnTyrProLeu 80
Db 457 AAGGTTTCAGAGTCCCTGTAACCTTTCTTAATCCCTTAAGGAGTGAAGAACTATCCTCTA 516
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Search completed: January 31, 2003, 08:55:35  
Job time : 532 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 31, 2003, 08:44:56 ; Search time 3285 Seconds

(without alignments)  
5048.456 Million cell updates/sec

Title: US-09-697-089-2  
Perfect score: 5459  
Sequence: 1 MNFIKDNSRALIQMGWTVI.....WQFDDDDLSVTGAFKLVT A 1024

Scoring table:  
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Ygapop 4.0 , Ygapext 12.0  
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Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 33308132

Minimum DB seq length: 0  
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Listing first 45 summaries

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9: gb\_est1: \*  
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24: em\_gss\_mus: \*  
25: em\_gss\_other: \*  
26: em\_gss\_pro: \*  
27: em\_gss\_rod: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	872	16.0	650	10 BB627584	BB627584 BB627584
4	853	15.6	741	13 B1824482	B1824482 603038854
5	837	15.3	480	10 AV719179	AV719179 AV719179
6	826	15.1	748	13 B1908869	B1908869 603066455
7	824	15.1	602	17 AZ360053	AZ360053 IM0103H11
8	739	13.5	518	17 BH348412	BH348412 CH230-42F
9	644	11.8	619	17 BH267158	BH267158 CH230-19B
10	628	11.5	775	13 B1854236	B1854236 603381263
11	613	11.2	817	17 BH358172	BH358172 CH230-18E
12	609	11.2	364	9 A1263294	A1263294 qx57B01.x
13	586	10.7	371	10 AV656315	AV656315 AV656315
14	547	10.0	719	14 BQ204082	BQ204082 UT-R-DN1-
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29	208	3.8	577	13 B1037401	B1037401 B1037401
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33	177	3.2	625	17 AZ614134	AZ614134 IM0442N17
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38	122	2.2	429	17 AZ484615	AZ484615 IM0311P08
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40	117	2.1	342	17 AZ805292	AZ805292 2M0066B12
41	116	2.1	586	13 BG994334	BG994334 PMO-HT116
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#### ALIGNMENTS

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CH230-44G15.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone  
ACCESSION BH293386  
VERSION BH293386  
KEYWORDS CH230-44G15, DNA sequence.  
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Norway rat.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
REFERENCE 1 (bases 1 to 697)  
Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn

,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de  
Jong,P. and Fraser,C.M.  
Rat BAC End Sequences from Library CHORI-230 EcoRI segment  
Unpublished (1999)  
Other\_GSSS: CH230-44G15.TU  
COMMENT

Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhao@tigr.org  
Clones are derived from the rat BAC library CHORI-230  
(http://www.chori.org/bacpac/rat230.htm). For BAC library  
availability, please contact Pieter de Jong (pdejong@mail.cho.org).  
Clones may be purchased from BACPAC Resources  
(http://www.chori.org/bacpac/or\_eirng\_info.htm). BAC end  
page: http://www.tigr.org/tdb/bac\_ends/rat\_bac\_end\_intro.html  
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/clone\_lib="CHORI-230 Segment 1"  
/sex="Female"  
/cell\_type="Brain"  
/note="Vector: pTRABAC2.1; Site\_1: EcoRI; Site\_2: EcoRI;  
CHORI-230 Rat (BN/SSNhd/MCW) BAC library produced by  
Pieter de Jong"  
BASE COUNT 182 a 165 c 190 g 160 t  
ORIGIN

Alignment Scores:  
Pred. No.: 5.66e-136 Length: 697  
Score: 996.00 Matches: 185  
Percent Similarity: 91.27% Conservative: 24  
Best Local Similarity: 80.79% Mismatches: 20  
Query Match: 18.25% Indels: 1  
DB: 17 Gaps: 0

US-09-697-089-2 (1-1024) x BH293386 (1-697)

QY 266 LysGluSnhHsArgPheLysASnMetValILleValThrThrThrGluCysLeuArg 285  
DB 11 AAGGAAAACCATCG-TTTAAGAACATGGTCTATTGTCAACACACCGAGCGCTGAGG 69  
QY 286 HistLeaArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMetThrGluAspSerAla 305  
DB 70 CACATGACACACGTTGGCCCTGACTGTGAGAGTGGAGATATGACCGAAGACAGCCG 129  
QY 306 GlnAlaLeuLeuLeaArgGluValLeuLeuLysGluLeuAlaGluGlyLeuLeuGlnIle 325  
DB 130 CGAGTTCTCAATCCGGAAGTGTGATTAATGACTGGCTGAAGGCTGTGTCCAGATG 189  
QY 326 GlnLysSerArgCysLeuAlaGlnLeuMetLysThrProLeuPheValValIleThrCys 345  
DB 190 CAGAGATCCAGAGTCTGTGAGAAATCTGATGAGAGCCCTCTCTCTGTGTGATTAACCTGT 249  
QY 346 AlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnThrThrLeuPheHisThr 365  
DB 250 GCCATTCAGATGGGCACTGAGGAATTCACAGCTCAACAGCTCTTCCAAAC 309  
QY 366 PheTyrAspLeuLeuIleGlnLysAsnLysHisLysHisLysGlyValAlaAlaSerAsp 385  
DB 310 TTTCAGACACCTCGTGAATACAGAAAAACAGGCGACAGACACAGTGAAGAACTTCAGTGTAT 369  
QY 386 PheIleArgSerLeuAspRHisCysGlyAspLeuAlaLeuGluGlyValPheSerHisLys 405  
DB 370 TTTCAGAGGAGCCATGACTCTGTGAGAGACCTGCGCCCTGGAAGGTGTGTCTCCACAAAG 429

QY 406 PheAspPheGlnLeuGlnAspValSerSerValAsnGluAspValLeuLeuThrGly 425  
DB 430 TTTGATTTCCAGACTTGGAGAGTGTGACAGCATGAATAGACGCTCTGGTACAGACGGG 489  
QY 426 LeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLysPhePheHisLysSer 445  
DB 490 CTCTCTGTAGTACAGCGGCTCAGAGCCTGAGCCCACTTAATTCCTTTCATTAATTC 549  
QY 446 PheGlnGluTyrThrAlaArgArgLeuSerSerLeuLeuThrSerHisGluProGlu 465  
DB 550 TTTCAGAGTACACAGAGGCTGGAGACTCAGCACTTGTGAACTCAGAGCCAGAG 609  
QY 466 GlnValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIleSerAspIleThrSer 485  
DB 610 GAGGTGACCAAGGAGATAGCTACTTGAAGAAATGTTTCCATCTCCGACATCATCC 669  
QY 486 ThrTyrSerSerLeuLeuArgTyrThr 494  
DB 670 CTGTATGTATCTGCTCTGACACT 696

RESULT 2  
AO309404/c 552 bp DNA linear GSS 22-DEC-1998  
LOCUS  
DEFINITION  
DNA sequence.  
ACCESSION  
AO309404  
VERSION  
AO309404.1 GI:4041438  
KEYWORDS  
GSS.  
SOURCE  
human.  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (bases 1 to 552)  
Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,  
Berry,K., Granger,D., Sun,E., Wible,C., Shizuya,H., Simon,M. and  
Venter,J.C.  
Map Building  
Use of a random human BAC End Sequence Database for Sequence-Ready  
Unpublished (1998)  
OTHER\_GSSS: CITBI-EL-2528J13.TR  
CONTACT: Shaying Zhao, William Nierman, Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: hbe@tigr.org  
Clones are available from Research Genetics (info@resgen.com). BAC  
end search page:  
http://www.tigr.org/tdb/humgen/bac\_end\_search/bac\_end\_search.html.  
Seq primer: M13-21  
Class: BAC ends.

# FEATURES

source location/Qualifiers  
1..552  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="2528J13"  
/clone\_lib="CITBI-EL"  
/sex="male"  
/cell\_type="sperm"  
/note="Vector: pBelOBAC11; Site\_1: EcoRI; Site\_2: EcoRI;  
Caltech Human BAC Library D"  
BASE COUNT 144 a 121 c 130 g 157 t  
ORIGIN

Alignment Scores:  
Pred. No.: 7.52e-133 Length: 552  
Score: 974.00 Matches: 183  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 17.84% Indels: 0  
DB: 17 Gaps: 0



```

Db 62 GTGAGCAGCTGACTTTGGGACGCTCTCGAGGCTCTGAAGAGCCCTGCTGATTGAA 121
QY 169 GYGLUserGLysGLysSerThrLeuLeuInArgIleAlaMetLeuTrpGLys 188
    |||||
Db 122 GGGGAGCTGGCAAGGAGAGTCCACCTGCTGAGAGAAATCGTATGCTCTGGGCTCT 181
QY 189 GYLYScysIleAlaLeuThrLysPheLysPheValPhePheLeuArgLeuSerArgAla 208
    |||||
Db 182 GGGGGCTGCAGGCTCTGAGAGGGCTTCAGATTAGCTCTTCATCCACCTGAGAGCGCC 241
QY 209 GYGLULeuPheGluThrLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 228
    |||||
Db 242 ATGGGGGAGCTATCGAAACCTGTACATGCTCTGAACTACCGGACTTCATGACG 301
QY 229 LysGlnThrPheMetAlaMetLeuLeuLeuLeuArgGlnArgValLeuPheLeuLeuAsp 248
    |||||
Db 302 AAGCCGACCTTCAAGGCTGCTGCTGAGCTACACAGAGAGGTCCTCTTCTCTGAT 361
QY 249 GYTYTrsGlnLysPheLysPheLysPheLysPheLysPheLysPheLysPheLys 268
    |||||
Db 362 GGTTCACATGATTCATCCACCCAGAACTGCCAGAAATTGAAAGCCCTGATTAAGAAAC 421
QY 269 HisArgPheLysAsnMetValIleValIleThrThrThrThrGluCysLeuArgHisIleArg 288
    |||||
Db 422 CATGCTTCAAGACATGCTATGTCACCAACGAGAGTGCCTGAGGATATGAGA 481
QY 289 GlnPheGlyAlaLeuThrAlaGluValAlaGlyAspMetThrGluAspSerAlaGlnAlaLeu 308
    |||||
Db 482 CATGTTGGCGCCCTGATGCGGAGGTGGAGATGTGACCGAAGACATGCCAAGATCTC 541
QY 309 IleArgIleValLeuIleLysGlnLeuAlaGluGlyLeuLeuLeuGlnIleGlnLysSer 328
    |||||
Db 542 ATCGAGCAGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 601
QY 329 ArgCysLeuArgAsnLeuMetLysThrProLeuPheValIleThr 344
    |||||
Db 602 AGGTGCTGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 649
    |||||

RESULT 4
BI824482 741 bp mRNA linear EST 04-OCT-2001
LOCUS 603038854F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5179909 5',
DEFINITION mRNA sequence.
ACCESSION BI824482
VERSION BI824482.1 GI:15936032
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 741)
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: c9apbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: ILAM1148 row: k column: 14
High quality sequence start: 3
High quality sequence stop: 705.
location/Qualifiers
    1..741
FEATURES
    source
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /clone="IMAGE:5179909"
        /clone_lib="NIH_MGC_115"
        /lab_host="DH10B"

```

```

/note="Organ: pooled brain, lung, testis; Vector:
PCMV-SpORF6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH MGC Library."

BASE COUNT      233 a      147 c      164 g      197 t
ORIGIN

Alignment Scores:
Pred. No.:      9,29e-115      Length:      741
Score:          853.00      Matches:      168
Percent Similarity: 96.55%      Conservative: 0
Best Local Similarity: 96.55%      Mismatches: 1
Query Match:     15.63%      Indels:      6
DB:              13      Gaps:      0

US-09-697-089-2 (1-1024) x BI824482 (1-741)
QY 1 MetAsnPheIleLysAspAsnSerArg--AlaLeuIleGlnArgMetGlyMetThrValI 20
    |||||
Db 228 ATGAAATTCATTAAGACAAATAGCCGAGCCCTTATTCAAGAAATGGAATGACTGTTA 287
QY 20 IeLysGlnIleThrAspAspLeuPheValIleTrpAsnValLeuAsnArgGlnGluValAsnI 40
    |||||
Db 288 TAAAGCAATATCACAGATGACTTATTGTATGAAATGTTCTGAAATCGCGAAGAAATTAACA 347
QY 40 IeIeCysCysGluLysValAlaGluGlnAspAlaAlaArgIleIleHisMetIleLeuI 60
    |||||
Db 348 TCATTTCCTGCGAAGAGTGGAGCAGATGCTGTAGAGGATCATTCACATGATTTTGA 407
QY 60 YsLysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTrpProI 80
    |||||
Db 408 AAAAGGTTACAGAGTCCGTGTAACCTCTTCTTAATCCCTTAAGAGTGAACATATCCTC 467
QY 80 eupheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAspA 100
    |||||
Db 468 TATTTCAGGACTTAATGAGACAAAGTCTTTTTCATCGACACTGAGAGAGACATTGAGCG 527
QY 100 spleuAlaGlnAspLeu--LysAspLeuTyHisThrProSerPheLeuAsnPheTyProI 119
    |||||
Db 528 ATTGGCTCAGAGATTTCAGAGACTTGTACCATACCCCATTTTTCGAACTTTTATCCC 587
QY 120 LeuGlyGluAspIleAspIleIlePheAsnLeuLysSerThrPheTrpGluProVal--Le 139
    |||||
Db 588 CTTGTGAGAGATATTGACATTAATTTTAACTTGAAGAACCTTCACAGAACCTGTCTCT 647
QY 139 uTPArgLysAspGlnHisHisArgValAlaGluGlnLeuThrLeuAsn--GlyLeuLeuG 159
    |||||
Db 648 GTGAGAGAGAGACCAACACCATCACCGGTGAGCAGCTGACCTGAAATGGGTCTCTGC 707
QY 159 InAlaLeuGlnSerProCysIleIleGluGly 169
    |||||
Db 708 AAGCTTCACAGAG--CCCTGCATCATTTGAAGCG 738
    |||||

RESULT 5
AV719179/c 480 bp mRNA linear EST 16-OCT-2000
LOCUS AV719179 GLC Homo sapiens cDNA clone GICEDAL0 5', mRNA sequence.
DEFINITION AV719179
ACCESSION AV719179
VERSION AV719179.1 GI:10816331
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 480)
AUTHORS Qian,B., Wu,T., Huang,Q., Kang,B., Gao,X., Xu,Z., Xiao,H.,
    , Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z., Zeng,L.,

```



Xu,S., Gu,W., Tu,Y., Jia,D., Fu,G., Ren,S., Zhong,M., Lu,G., Yang  
Y., Gu,Y., Chen,Z. and Han,Z.  
Homo sapiens cDNA GLC clones  
Unpublished (2000)  
JOURNAL  
COMMENT

Contact: Zeguang Han  
Chinese National Human Genome Center at Shanghai  
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai  
201203, P. R. China  
Tel: 86-21-50801919(ex.45)  
Fax: 86-21-50801922  
Email: hanzg@chgc.sh.cn

This clone is available at CHGC in Shanghai.

## FEATURES

Location/Qualifiers

1..480  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="GLCEQA10"  
/clone\_1id="GLC"  
/tissue\_type="corresponding non cancerous liver tissue"  
/dev\_stage="Adult"  
/lab\_host="SOLR"  
/note="Vector: pBluescript sk(-); Site\_1: EcoRI; Site\_2:  
XhoI"

BASE COUNT 138 a 120 c 85 g 137 t

## ORIGIN

## Alignment Scores:

Pred. No.: 1.22e-112 Length: 480  
Score: 837.00 Matches: 156  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 15.33% Indels: 0  
Gaps: 0

US-09-697-089-2 (1-1024) x AV719179 (1-480)

OY 869 Hlsglualeuileaspargmetasnvalleugluinleuthralaleuemetleuprtrp 888  
DB 480 CATGACATGATCGACAGATGACGTGCTAGACAGCTCACCACGCTATGCTGCTGG 421  
OY 889 glycysaspvalglinglyserleuserleuileuylshislenugluvalprolin 908  
DB 420 GGCTGTGACGTGCAAGCAGCCTGAGCAGCTGTGAACAATTGGAGAGAGTCCACAA 361  
OY 909 leuvallyslleuglyleuylasnttrpargleuthrparthrgluilaleugly 928  
DB 360 CTCGTCAAGCTTGGGTTGAAAACTGGAGACTCACAGATACAGATTAGATTAGGT 301  
OY 929 Alaphhegilylysasnproleuylasnpheglingluinleuylasleuylasna 948  
DB 300 GCATTTTGGAAAGAACCCCTCTGAAAAACTTCCAGCATTTGGCGGAAATCGT 241  
OY 949 valseraseraspglytrpaleualaphemetglyvalphegluasnleuylsleuval 968  
DB 240 GTGAGCACTGATGATGATGCTGCTTCATGGTGTATTGGAATCTTAAGCAATTAGTG 181  
OY 969 phepheasprheserthlyslupheleuproasprrfoalaleuvalaarglyseuser 988  
DB 180 TTTTGTGCTTAGTACTAAAGAAATTTCTACCTGATCCAGATTAGTCAGAAAACTTAGC 121  
OY 989 Gluvalleuserlyleuthrphelenglingluilaleuvalaarglyleuval 1008  
DB 120 CAAGGTATATCCAACTTAATCTTCTGCAAGAGCTAGGCTTGGTGGCAATTTGAT 61  
OY 1009 aspsaspaspleuservalillethrclyalaphelyleuvalthrila 1024  
DB 60 GATGATGATCTCAGTGTATTACAGAGAGCTTTTAAACTAGTAAGTACTGCT 13

## RESULT 6

LOCUS B1908869 748 bp mRNA linear EST 16-OCT-2001  
DEFINITION 603066455F1 NIH\_MGC\_118 Homo sapiens cDNA clone IMAGE:521569 5',  
mRNA sequence.

ACCESSION B1908869  
VERSION B1908869.1 GI:16171950  
KEYWORDS EST.  
SOURCE human.

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

1 (bases 1 to 748)  
NIH-MGC <http://mgc.nci.nih.gov/>.

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

## FEATURES

## SOURCE

NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.lnl.gov>  
plate: LLM11541 row: m column: 14  
High quality sequence start: 7  
High quality sequence stop: 744.  
Location/Qualifiers

## ORIGIN

1..748  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:521569"  
/clone\_1id="NIH\_MGC\_118"  
/tissue\_type="leukocyte"  
/lab\_host="DH10B"  
/note="Vector: pCMV-Sport6; Site\_1: NotI; Site\_2: EcoRV  
(destroyed); RNA source leukocytes from anonymous pool of  
non-activated adult donors. Library is oligo-dT primed  
and directionally cloned (EcoRV site is destroyed upon  
cloning). Average insert size 1.7 kb, insert size range  
1.2-3.3 kb. Library is normalized and enriched for  
full-length clones and was constructed by C. Gruber  
(Invitrogen). Research Genetics tracking code 027. Note:  
this is a NIH\_MGC Library."

BASE COUNT 236 a 148 c 166 g 198 t

## ORIGIN

## Alignment Scores:

Pred. No.: 9.38e-111 Length: 748  
Score: 826.00 Matches: 160  
Percent Similarity: 96.41% Conservative: 1  
Best Local Similarity: 95.81% Mismatches: 4  
Query Match: 15.13% Indels: 4  
Gaps: 0

US-09-697-089-2 (1-1024) x B1908869 (1-748)

OY 1 Metasnphelileysaspasnserrargalaleuileglnatrgmetglymethrvalille 20  
DB 252 ATGATTTTCATTAAGGACAAATAGCCGACCTTATTCAAAGAAATGGAATGACTTTATA 311  
OY 21 lysglinlethrparaspaspleurphevalitrpasnvalleuasnargylugluvalasntle 40  
DB 312 AAGCAATACACAGATGACCTATTGTATGAAATGTTTGAATCCGGAAGATTAACATC 371  
OY 41 ilcyscysgilylvalygluinspralaalaargylillelleillemelleleuyls 60  
DB 372 ATTTCCTCGAGAAAGGTGAGCAGATCTCTCTAAGGAGATTCACATGATATTTTGAAA 431  
OY 61 lysglyserglysercysasnleupheleuylsleuylsleuylsleuylsleuyls 80  
DB 432 AAGGTTACAGACTCTGTAACTCTTTTCTTAATCCCTTAAGAGATGGAATATCTCTTA 491  
OY 81 pheglnaspleuasnglylnserleuphehlsgrlnrsergluglylaspleuaspsasp 100  
DB 492 TTTTCAGACTGAAATGAGCAAAAGTCTTTTCATCAGACATCAGAAAGAGACTTGAGCAT 551



TITLE  
Jong, P. and Fraser, C.M.  
Rat BAC End Sequences from Library CHORI-230 EcoRI segment  
Unpublished (1999)  
JOURNAL  
Other\_GSSs: CH230-42F7.TV  
COMMENT  
Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230  
(http://www.chori.org/bacpac/rat230.htm). For BAC library  
availability, please contact Pieter de Jong (pdejong@mail.cho.org).  
Clones may be purchased from BACPAC Resources  
(http://www.chori.org/bacpac/orering\_information.htm). BAC end  
page: http://www.tigr.org/tldb/bac\_ends/rat/bac\_end\_intro.html  
Plate: 42 row: F column: 7  
Seq primer: T7  
Class: BAC ends.

# FEATURES

Source Location/Qualifiers  
1. 518  
/organism="Rattus norvegicus"  
/strain="BN/SENHsd/MCM"  
/db\_xref="taxon:10116"  
/clone="CH230-42F7"  
/clone\_1lb="CHORI-230 Segment 1"  
/sex="Female"  
/cell\_type="Brain"  
/note="Vector: PTARBAC2.1; Site\_1: EcoRI; Site\_2: EcoRI;  
CHORI-230 Rat (BN/SENHsd/MCM) BAC library produced by  
Pieter de Jong"  
BASE COUNT 133 a 124 c 146 g 115 t  
ORIGIN

## Alignment Scores:

Pred. No.: 4.42e-98 Length: 518  
Score: 739.00 Matches: 135  
Percent Similarity: 91.72% Conservative: 20  
Best Local Similarity: 79.88% Mismatches: 13  
Query Match: 13.54% Indels: 1  
Gaps: 0

US-09-697-089-2 (1-1024) x BH348412 (1-518)

OY 261 lllcglualaleuileysgluasnhisarphelysasmetvalillevalthrthrthr 280  
|||||  
Db 2 ATCGAGCCCTGTGTAAGAAACCATGCTTCAAGACATGTCATGTCACCCACACC 61  
OY 281 ThrGlucysleuArghisIleArgGlnpheGlyAlaLeuThrAlaGluValGlyAspMet 300  
|||||  
Db 62 ACGAGTCCCTGAGGACATCATGACCTGTGGCCCTGACTGTGGAGGTGGAGCATATG 121  
OY 301 ThrGluAspSerAlaGlnAlaLeuIleArgGluValleuileysgluasleuAlaGluGly 320  
|||||  
Db 122 ACCGAGACACGCCCGGAGTCTCATCGGAGAGTGGCTGATTAATGAACCTGGCTGAAGGC 181  
OY 321 LeuLeuLeuGlnIleGlnIleSerArgCysLeuArgAsnLeuMetIleThrProLeuPhe 340  
|||||  
Db 182 TTGTTGTTCCAGATGACAGAGTCCAGGTGCTTGAGAAATCTGATGAGAGACCCCTCTCTC 241  
OY 341 ValValIleThrCys-AlaIleGlnMetGlyGluSerIleuPheHisSerHisThrGlnTh 360  
Db 242 GTGGTGATTAACCTGTGACATCTCTGATACAGAAAACAGGCCACACACAGTGG 301  
OY 360 rThrIleuPheHisThrPheTyraSpLeuLeuIleGlnIleAsnIleHisIleHisIleGly 380  
|||||  
Db 302 CATGCTCTTCCAAACCTTCTACGACCTCTGATACAGAAAACAGGCCACACACAGTGG 361  
OY 380 yValAlaIleSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGly 400  
|||||  
Db 362 AGGAACCTCAGGTATTTGTTCAGAGAGCTTACACTGAGAGACCTGGCCCTGGAAGG 421

OY 400 yValPheSerHisIleAspPheIleuPheGluLeuGlnAspValSerSerValAsnGluAspVal 420  
|||||  
Db 422 TGTGTTCTCCCAAGATTGATTTGCACTTGAGATGTGTCACCATGAATGAGACGT 481  
OY 420 lIleuLeuThrThrGlyLeuLeuCys 428  
|||||  
Db 482 CCTGCTGAGACGCGGCTCTCTGT 506

RESULT 9  
BH267158/c 619 bp DNA linear GSS 30-NOV-2001  
LOCUS  
DEFINITION  
CH230-19B22.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone  
CH230-19B22, DNA sequence.  
ACCESSION  
BH267158  
VERSION  
BH267158.1 GI:17179098  
KEYWORDS  
GSS.  
SOURCE  
Norway rat.  
Rattus norvegicus  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
REFERENCE  
1 (bases 1 to 619)  
Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn,  
A., Gebregorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de  
Jong, P. and Fraser, C.M.  
Rat BAC End Sequences from Library CHORI-230 EcoRI segment  
Unpublished (1999)  
Other\_GSSs: CH230-19B22.TV  
COMMENT  
Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230  
(http://www.chori.org/bacpac/rat230.htm). For BAC library  
availability, please contact Pieter de Jong (pdejong@mail.cho.org).  
Clones may be purchased from BACPAC Resources  
(http://www.chori.org/bacpac/orering\_information.htm). BAC end  
page: http://www.tigr.org/tldb/bac\_ends/rat/bac\_end\_intro.html  
Plate: 19 row: B column: 22  
Seq primer: SP6  
Class: BAC ends.

# FEATURES

Source Location/Qualifiers  
1. 619  
/organism="Rattus norvegicus"  
/strain="BN/SENHsd/MCM"  
/db\_xref="taxon:10116"  
/clone="CH230-19B22"  
/clone\_1lb="CHORI-230 Segment 1"  
/sex="Female"  
/cell\_type="Brain"  
/note="Vector: PTARBAC2.1; Site\_1: EcoRI; Site\_2: EcoRI;  
CHORI-230 Rat (BN/SENHsd/MCM) BAC library produced by  
Pieter de Jong"  
BASE COUNT 163 a 141 c 158 g 157 t  
ORIGIN

Alignment Scores:  
Pred. No.: 6.59e-84 Length: 619  
Score: 644.00 Matches: 115  
Percent Similarity: 84.38% Conservative: 20  
Best Local Similarity: 71.88% Mismatches: 25  
Query Match: 11.80% Indels: 0  
Gaps: 0

US-09-697-089-2 (1-1024) x BH267158 (1-619)

OY 88 SerLeuPheHisGlnThrSerGluGlyAspLeuAspSerAlaGlnAspLeuIleAsp 107  
|||||  
Db 482 GGTCTTTTTCATCAGAACTTGAAGAGACTTGGATGTTCTGGCCAGAGTCTAAAGAC 423



Fax: 301 838 0208  
Email: szhoo@tigr.org  
Clones are derived from the rat BAC library CHORI-230  
(http://www.chori.org/bacpac/rat230.htm). For BAC library  
availability, please contact Pieter de Jong (pdejong@mail.cho.org).  
Clones may be purchased from BACPAC Resources  
(http://www.chori.org/bacpac/or\_ering\_information.htm). BAC end  
page: http://www.tigr.org/tldb/Bac\_ends/rat/Bac\_end\_intro.html  
Plate: 18 row: E column: 7  
Seq primer: SP6  
Class: BAC ends.

#### FEATURES

source

Location/Qualifiers  
1..817  
/organism="Rattus norvegicus"  
/strain="BN/SSNHsd/MCW"  
/db\_xref="taxon:10116"  
/clone\_1id="CH230-18E7"  
/clone\_1lb="CHORI-230 Segment 1"  
/sex="Female"  
/cell\_type="Brain"  
/note="Vector: pTRABAC2.1; Site\_1: EcoRI; Site\_2: EcoRI;  
CHORI-230 Rat (BN/SSNHsd/MCW) BAC library produced by  
Pieter de Jong"

BASE COUNT 211 a 182 c 199 g 225 t

#### ORIGIN

##### Alignment Scores:

Pred. No.: 3,72e-79 Length: 817  
Score: 613.00 Matches: 115  
Percent Similarity: 84.91% Conservative: 20  
Best Local Similarity: 72.33% Mismatches: 24  
Query Match: 11.23% Indels: 2  
DB: 17 Gaps: 0

US-09-697-089-2 (1-1024) x BH358172 (1-817)

OY 88 SerLeuPheHISGlnThrSerGluGlyAspLeuAspLeuAlaGlnAspLeuLysAsp 107  
DB 475 GGTCTTTTTCATCAGACTGAGAGAGAGCTTGATGTTCTGGCCAGAGCTTAAGAGC 416  
OY 108 LeuTYrHISThrProSerPheLeuAsnPheTYrProLeuGlyGluAspIleAspIleIle 127  
DB 415 TTATACACAGAGCCGCTTTTAAAGACTCTTCTCGGCGGAGAGATATGACATCATC 356  
OY 128 PheAsnLeuLysSerThrPheThrGluProValLeuTrpArgLysAspGlnHisHis 147  
DB 355 TTCAATCTGCAGATCATTCTACAGAACCTCTCTGTGAGAGAGAGACCATCATCAGC 296  
OY 148 ArgValGlnGlnLeuThrLeuAsnGlyLeuGlnAlaIleGlnSerProCysIleIle 167  
DB 295 CGAGTAGAGCAGATGACCTGGGAGAGCTGAGAGCTGTGAAGATGCTGCTCAT 236  
OY 168 GlnGlyGluSerGlyLysGlyLysSerThrLeuLeuGlnArgIleAlaMetLeuTrpGly 187  
DB 235 GAAGGGAGGTGCGGCAAGGAGATCCACCGCTGCAGCAAAATTCATGCTGAGGCC 176  
OY 188 SerGlyLysCysLysAlaLeuThrLysPheLysPheValPhePheLeuArgLysSerArg 207  
DB 175 TCTGGAGATGCGCCAGCTGTGAACAGATTGCTCTCTCATCGGCTGAGCAGT 116  
OY 208 AlaGlnGlyGlyLeuPheGlnThrLeuGlyCysAspGlnLeuLeuAspIleProGlyThrIle 227  
DB 115 GCTAAGGGTGGCTGTTGAAACATTTGA-TATCAGCTGCTGTAACATTCATCATCAGC 57  
OY 228 ArgLysGlnThrPheMetAlaMetLeuLeuLysArgGlnArgValLeuPheLeu 246  
DB 56 AGCAACACCAACCTTCAGGGCTCTGCTGCT-AACTTACACAGAAAGTCTCTTTCTC 1

RESULT 12  
A1263294/c A1263294 364 bp mRNA linear EST 03-FEB-1999  
LOCUS qx57b01.x1 NCI\_CGAP\_Pan1 Homo sapiens cDNA clone IMAGE:2005417 3',  
DEFINITION mRNA sequence.

ACCESSION A1263294  
VERSION A1263294.1 GI:3871497  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
TITLE NCI-CCAP http://www.ncbi.nlm.nih.gov/nciccap.  
TUMOR Gene Index  
Tumor Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
National Cancer Institute, (1997)

JOURNAL  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgap@briemail.nih.gov  
Life Technologies catalog #: 11548-013

DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CCAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html  
Insert Length: 2146 Std Error: 0.00  
Seq primer: -400P from Glbco  
High quality sequence stop: 364.  
location/Qualifiers

#### FEATURES

source

1..364  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_1id="IMAGE:2005417"  
/clone\_1lb="NCI\_CGAP\_Pan1"  
/tissue\_type="adenocarcinoma"  
/lab\_host="DH10B"  
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site\_1: SalI;  
Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.72 kb. Life Technologies catalog #:  
11548-013"

BASE COUNT 117 a 84 c 55 g 108 t

#### ORIGIN

##### Alignment Scores:

Pred. No.: 4.97e-79 Length: 364  
Score: 609.00 Matches: 114  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 11.16% Indels: 0  
DB: 9 Gaps: 0

US-09-697-089-2 (1-1024) x A1263294 (1-364)

OY 911 LysLeuGlyLeuLysAsnTrpArgLeuThrAspThrGluIleArgIleLeuGlyAlaPhe 930  
DB 364 AAGCTTGGGTGAAAAGAGGAGACTCACAGATACAGAGATTAGATTAGTGCATTT 305  
OY 931 PheGlyLysAsnProLeuLysAsnPheGlnGlnLeuAsnLeuAlaGlyAsnArgValSer 950  
DB 304 TTGGAAAGAACCCCTGTGAAGAACTTCACAGCAGTTGATTTGGCGGAATGCTGAGC 245  
OY 951 SerAspGlyTrpLeuAlaPheMetGlyValPheGluAsnLeuLysGlnLeuValPhePhe 970  
DB 244 AGTAGTAGATGCTGCTTCATGCGGTGATTTGAGAACTTAAACCAATTAGTCTTTT 185  
OY 971 AspPheSerThrLysGlnPheLeuProAspProAlaLeuValArgLysLeuSerIleVal 990  
DB 184 GACTTAGTACTAAAGAAATTTCTACCTGATCCAGCATTAAGTCAGAAACTTAGCCAGTG 125  
OY 991 LeuSerLysLeuThrPheLeuGlnGlnAlaArgLeuValGlyTrpGlnPheAspAsp 1010  
DB 124 TTATCCAGTAGTAATCTTCTGCAAGAGCTAGGCTGTGGGTGCAATTTGATGATGAT 65  
OY 1011 AspLeuSerValIleThrGlyAlaPheLysLeuValIleThrAla 1024  
DB 64 GATCTCAGTGTATTATACAGGCTTTTAACTAGTAAGTCTGT 23

RESULT 13  
AV656315

LOCUS AV656315 371 bp mRNA linear EST 16-JAN-2002  
 DEFINITION AV656315 GLC Homo sapiens cDNA clone GICEQA10 3', mRNA sequence.  
 ACCESSION AV656315  
 VERSION AV656315.1 GI:9877329  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 371)  
 AUTHORS Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X., Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W., Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X., Hu, G., Gu, J., Chen, Z., and Han, Z.  
 TITLE Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)  
 MEDLINE 21625106  
 COMMENT Contact: Zeguang Han  
 Chinese National Human Genome Center at Shanghai  
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China  
 Tel: 86-21-50801919 (ex.45)  
 Fax: 86-21-50801922  
 Email: hanzg@chgc.sh.cn  
 This clone is available at CHGC in Shanghai.  
 FEATURES  
 source  
 1..371  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="GICEQA10"  
 /clone\_1lb="GIC"  
 /tissue\_type="corresponding non cancerous liver tissue"  
 /dev\_stage="Adult"  
 /lab\_host="SOLR"  
 /note="Vector: pBluescript sk(-); Site\_1: EcoRI; Site\_2: XhoI"  
 BASE COUNT 112 a 85 c 91 g 82 t 1 others  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 1.3e-75 Length: 371  
 Score: 586.00 Matches: 114  
 Percent Similarity: 98.31% Conservative: 2  
 Best Local Similarity: 96.61% Mismatches: 2  
 Query Match: 10.73% Indels: 0  
 DB: 10 Gaps: 0  
 US-09-697-089-2 (1-1024) x AV656315 (1-371)  
 QY 625 GUAUYSALAAAGUASPThrGlyGlyLeuIleHisMetGluAlaProGluThrTyrIle 644  
 Db 1 GAANAAGGTGAGAAAGACAGGTGGAATCCACATGGAAGAGCCGCCGAACCTACTT 60  
 QY 645 ProSerAlaValSerLeuPheAsnTrpLysGlnGluPheArgThrLeuGluVal 664  
 Db 61 CCCAGAGAGGCTGATCTTTGTTCTTCACTGGAAGCAGAACTCAGACTCTGGAGGTC 120  
 QY 665 ThrLeuArgPheSerLysLeuAsnLysGlnAspIleThrTyrLeuGlyLysIlePhe 684  
 Db 121 ACACCTCGGGGATTTCAGCAAGTGAATTAAGCAATATCAATATCTGGGAAATATTC 180  
 QY 685 SerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyValAlaGlySerLeu 704  
 Db 181 AGCTCTGCCAAGAGCTCTAGGCTGCAATTAAGAGATGTGCTGGTGGTGAAGCCTC 240  
 QY 705 SerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGluAlaSerProLeu 724  
 Db 241 AGTTTGCTCCACACCTGTAAGAACATTTATCTCTCACTGAGGGAAGCCAGTCCCTC 300  
 QY 725 ThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThrLeuSer 742  
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 ::::::::::::::

Db 301 ACCATAGAGATGAGAGGACATCAATCTGTAAACAACCTGGACAGCTTGCGT 354  
 RESULT 14  
 LOCUS BQ204082/c 719 bp mRNA linear EST 02-MAY-2002  
 DEFINITION BQ204082 UI-R-DNI-cmv-e-08-0-UI-S1 UI-R-DNI Rattus norvegicus cDNA clone  
 ACCESSION BQ204082  
 VERSION BQ204082.1 GI:20420547  
 KEYWORDS EST.  
 SOURCE Norway rat.  
 ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 REFERENCE 1 (bases 1 to 719)  
 AUTHORS Bonaldo, M.F., Lennon, G., and Soares, M.B.  
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery  
 JOURNAL Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE 97044477  
 COMMENT Contact: Soares, MB  
 Program for Rat Gene Discovery and Mapping  
 University of Iowa  
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: msoares@blue.weeg.uiowa.edu  
 The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the normalized distal colon library cDNA library preparation: M.B. Soares lab clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 12-210, >L1B3#LINE/L1 Seq primer: M13 forward  
 POLY=yes.  
 FEATURES  
 source  
 1..719  
 Location/Qualifiers  
 /organism="Rattus norvegicus"  
 /strain="Sprague-Dawley"  
 /db\_xref="taxon:10116"  
 /clone="UI-R-DNI-cmv-e-08-0-UI"  
 /clone\_1lb="UI-R-DNI"  
 /dev\_stage="adult"  
 /lab\_host="DH10B (Life Technologies)"  
 /note="Vector: p773D-Pac (Pharmacia) with a modified polylinker. Site\_1: Not I; Site\_2: Eco RI; The UI-R-DNI library is a normalized Rat Distal Colon library (nRDC) constructed in p7377 PAC vector according to the procedure described by Bonaldo, Lennon & Soares (Normalization and Subtraction: Two Approaches to Facilitate Gene Discovery. Genome Research 6: 791-806, 1996). The oligonucleotide used to prime first strand synthesis contained the sequence tag GAAGTCTCC between the Not I cloning site and DRI8 stretch. The Rat Distal Colon tissue was provided by Tom Freeman of the Sanger Center.  
 TAG\_LIB=UI-R-DNI  
 TAG\_TISSUE=distal colon  
 TAG\_SEQ=GAAGTCTCC"  
 BASE COUNT 184 a 185 c 146 g 203 t 1 others  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 1.87e-69 Length: 719  
 Score: 547.00 Matches: 104  
 Percent Similarity: 82.64% Conservative: 15  
 Best Local Similarity: 72.22% Mismatches: 25  
 Query Match: 10.02% Indels: 0  
 DB: 14 Gaps: 0



US-09-697-089-2 (1-1024) x BQ204082 (1-719)

```

OY 881 LeuThralaleuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerLeuLeu 900
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 718 CTAACGGCTTGATCTGCTGCTGGTGGATGGCTACATCATGCTGCCAATCTGCTG 659
OY 901 LysHisLeuGlnGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThr 920
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 658 AAGCAACGTGAGGGGAGCCCAAGGGCTTGTCAAACTTGATTAATAAAGCTGAGGCTCAGA 599
OY 921 AsphTrgUuIleArgIleLeuGlnValAphPheGlyLysAsnProLeuLysAsnDheGln 940
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 598 GACGAGAGATTAGAAAGTTTCGGTGAATTTTGGAGATGAACCTCTGAGAACCTTGGCAG 539
OY 941 GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGlyVal 960
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 538 CAGTTGGATTTCACGACGACGCTGTGAGCATGATGAGTGGCTTCTTCATGGAGTGG 479
OY 961 PheGlnAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGlnPheLeuProAsp 980
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 478 TTTGAGAAATCTTAACGACATGTTATTTTGGCTTCGGCAGCTGAGAGATCTTACAGAC 419
OY 981 ProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGluAla 1000
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 418 GCAGCGCTGTGGAGGAACCTCGCTCAAGTGTATTAAGCTAACCTGCTGCAGAGAGCA 359
OY 1001 ArgLeuValGlyTrpGlnPheAspAspAspLeuSerValIleThrGlyAlaPheLys 1020
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 358 AGGCTCACAGGCTGGAGCTGTGATGATCATATGATTAATTAAGGAACCTTTTAA 299
OY 1021 LeuValThrAla 1024
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 298 CTAGTACTGCT 287

RESULT 15
LOCUS AL639997 637 bp mRNA linear EST 12-DEC-2001
DEFINITION AL639997 XGC-neurula Silurana tropicalis cDNA clone TNeu003d13 5',
mRNA sequence.
ACCESSION AL639997.1 GI:16792128
VERSION AL639997.1
KEYWORDS EST.
SOURCE western clawed frog.
ORGANISM Silurana tropicalis
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Silurana.
1 (bases 1 to 637)
Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J.
Sanger Xenopus tropicalis EST project 2001 (10_2001)
Unpublished (2001)
Contact: Huckle E
Sanger Centre
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: tropesanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TNeu003d13.sp6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
FEATURES
    source
        1..637
            /organism="Silurana tropicalis"
            /db_xref="taxon:8364"
            /clone="TNeu003d13"
            /clone_lib="XGC-neurula"
            /dev_stage="neurula"
            /lab_host="Escherichia coli DH10B"
            /note="Vector: PCS107; Site 1: EcoRI; Site 2: NotI; cDNA
was oligo dT primed from 5' of poly A+ RNA from neurula.
EcoRI-NotI cut cDNA was then ligated into PCS107 with
EcoRI at the 5' end and NotI at the 3' end."
BASE COUNT 226 a 93 c 132 g 185 t 1 others

```

# ORIGIN

Alignment Scores: 8.04e-66 Length: 637  
 Pred. No.: 522.00 Matches: 105  
 Score: 73.63% Conservative: 43  
 Percent Similarity: 52.24% Mismatches: 5  
 Best Local Similarity: 9.56% Indels: 0  
 Query Match: 9 Gaps: 0

US-09-697-089-2 (1-1024) x AL639997 (1-637)

```

OY 641 GlnThrTrpIleProSerArgAlaValSerLeuPheAsnTrpLysGlnGluPheArg 660
    ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 24 GACAAATTATATTCAGAGAAACAGTCAATATATTTTGGATGGAAATCAGCAATTCAG 83
OY 661 ThrLeuGlnValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTrpLeu 680
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 84 ACTTTGGAGGTTACACTCAGAGATTTTCCAAATTAATAAAGATATAAATATACCTG 143
OY 681 GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVal 700
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 144 GGCAGAAATATGTGTGCTCCGCTGACAGTCTCGACGTAACATTAAAGAGTTACAGAAAT 203
OY 701 AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleLysSerLeuMetValGlu 720
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 204 ACTGATCTCTTGTTGGTGGCTTTTGGAAATCCCTGTAAGATATATCAAGATTTAAATGTCAT 263
OY 721 AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr 740
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 264 AGCAGCAAACTAAGCATTAAGATGAGAGAAATTTGTAACAATGACAGAGATGAAGAA 323
OY 741 LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly 760
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 324 CTGAGTATATTAACCTACACAGTACATGCAAGGTGACTTTAGAGGGATTTGCT 383
OY 761 AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGlnGluAspAla 780
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 384 AATCTAGTAGGGCTTGAAAAATTTGTTTCCATTAATTAATAAGACAGAAATGATGCA 443
OY 781 IleLysLeuAlaGlnGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis 800
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 444 AAAACTCTGGCTGAGAGCATTTTAAGCTGGAAGAGTTAAAGAGCTTATCCATATCAT 503
OY 801 LeuSerAspIleGlyGlnGlyMetAspTrpIleValLysSerLeuSerSerLeuProCys 820
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 504 ATCTCAACATTGGAGATGGCATGAGATATTGCAGAAATCAATTTCTTATGTTGCCAT 563
OY 821 AspLeuGlnGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu 840
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 564 GAGCTTAAGAACTGAATTAATGACGTGTGTTTGAGTGTGAAGAGCTCTCNAAGGTCTT 623
OY 841 Ala 841
    |||
Db 624 GCA 626

```

Search completed: January 31, 2003, 11:41:08  
 Job time : 3292 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus.p2n model

Run on: January 31, 2003, 08:40:36 ; Search time 85 seconds  
(without alignments) 3694.553 Million cell updates/sec

Title: US-09-697-089-2

Perfect score: 5459

Sequence: 1 MNFKDNRSLRIQRMGMTVL.....WQFDDDLSTVTGAFKLVTG 1024

Scoring table:

PAM120	4.0	Xgapex	12.0
Xgapop	4.0	Ygapex	12.0
Ygapop	6.0	Fgapex	7.0
Delop	6.0	Delext	7.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+P2n.model -DEV=xlh  
-O=/cgn2\_1/USPTO.spool/US09697089/runat\_29012003\_092505\_19177/app\_query.fasta.1.1223  
-DB=Issued\_Patents\_NA -QEMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPEXT=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=pam120 -TRANS=human40.cdi  
-LIST=45 -DOCCALIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09697089 -RCGN\_1.1.46 -rcgnat\_29012003\_092505\_19177 -NCPU=6 -ICPU=3  
-NO\_XLPTX -NO\_MMAP -LARGEQUERY -NEG.SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120  
-WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=4 -XGAPEXT=12 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=4 -YGAPEXT=12 -DELOP=6 -DELEXT=7

Database :

1: Issued\_Patents\_NA:\*  
2: /cgn2\_6/ptodata/2/1na/5A.COMB.seq:\*  
3: /cgn2\_6/ptodata/2/1na/5B.COMB.seq:\*  
4: /cgn2\_6/ptodata/2/1na/6A.COMB.seq:\*  
5: /cgn2\_6/ptodata/2/1na/6B.COMB.seq:\*  
6: /cgn2\_6/ptodata/2/1na/Backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	279	5.1	5502	3	US-08-836-134-1
2	279	5.1	5502	4	US-09-493-784-1
3	95	1.7	3573	4	US-09-353-585-4
4	95	1.7	3573	4	US-09-353-585-1
5	94	1.7	1386	2	US-08-910-731-5
6	82	1.5	250	2	US-08-824-701A-8
7	82	1.5	2568	4	US-09-228-986-2
8	81	1.5	1470	4	US-09-099-041A-27
9	81	1.5	1470	4	US-09-245-281-27
10	81	1.5	1470	4	US-09-207-359B-27
11	81	1.5	2859	4	US-09-099-041A-9
12	81	1.5	2859	4	US-09-245-281-9

13	81	1.5	2859	4	US-09-207-359B-9	Sequence 9, Appli
14	81	1.5	3080	4	US-09-099-041A-25	Sequence 25, Appl
15	81	1.5	3080	4	US-09-245-281-25	Sequence 25, Appl
16	81	1.5	3080	4	US-09-207-359B-25	Sequence 25, Appl
17	81	1.5	3382	4	US-09-099-041A-7	Sequence 7, Appli
18	81	1.5	3382	4	US-09-245-281-7	Sequence 7, Appli
19	81	1.5	3382	4	US-09-207-359B-7	Sequence 7, Appli
20	81	1.5	3979	4	US-09-180-439-1	Sequence 2, Appli
21	81	1.5	3979	4	US-09-180-439-2	Sequence 2, Appli
22	81	1.5	32042	4	US-09-245-281-44	Sequence 44, Appl
23	80	1.5	4141	4	US-09-245-281-42	Sequence 42, Appl
24	80	1.5	4141	4	US-09-207-359B-42	Sequence 42, Appl
25	79	1.4	4123	4	US-09-180-439-7	Sequence 7, Appli
26	77	1.4	3541	4	US-09-180-439-5	Sequence 5, Appli
27	76	1.4	1435	5	PCT-US95-05322A-1	Sequence 1, Appli
28	76	1.4	2589	4	US-08-569-749-1	Sequence 1, Appli
29	76	1.4	2589	5	PCT-US96-12860-1	Sequence 1, Appli
30	76	1.4	3532	2	US-09-205-204-1	Sequence 1, Appli
31	76	1.4	3732	3	US-09-212-971-7	Sequence 7, Appli
32	76	1.4	3732	3	US-08-800-929A-7	Sequence 7, Appli
33	76	1.4	3732	4	US-09-617-053A-7	Sequence 7, Appli
34	75	1.4	1058	4	US-08-238-163-1	Sequence 13, Appl
35	75	1.4	2862	4	US-08-569-749-13	Sequence 13, Appl
36	75	1.4	2862	5	PCT-US96-12860-13	Sequence 13, Appl
37	75	1.4	3151	3	US-09-212-971-13	Sequence 13, Appl
38	75	1.4	3151	3	US-08-800-929A-13	Sequence 13, Appl
39	75	1.4	3151	3	US-09-617-053A-13	Sequence 13, Appl
40	74	1.4	626	3	US-09-019-942-4	Sequence 4, Appli
41	74	1.4	626	4	US-09-470-271-4	Sequence 4, Appli
42	74	1.4	1185	2	US-08-391-916A-3	Sequence 3, Appli
43	74	1.4	1215	1	US-08-242-663A-1	Sequence 1, Appli
44	74	1.4	1215	3	US-08-954-536-17	Sequence 17, Appl
45	74	1.4	1215	4	US-08-748-547-1	Sequence 1, Appli

#### ALIGNMENTS

RESULT 1  
US-08-836-134-1  
; Sequence 1, Application US/08836134A  
; Patent No. 6020127  
; GENERAL INFORMATION:  
; APPLICANT: Mackenzie, Alex E.  
; APPLICANT: Korneluk, Robert G.  
; APPLICANT: Mahadevan, Mani S.  
; APPLICANT: McLean, Michael  
; APPLICANT: Roy, Natalie  
; APPLICANT: Ikeda, John  
; TITLE OF INVENTION: Neuronal Apoptosis Inhibitor Protein, Gene Sequence and  
; Patent No. 6020127  
; TITLE OF INVENTION: Mutations Causative of Spinal Muscular Atrophy  
; FILE REFERENCE: 3477-112, 033477/139914  
; CURRENT APPLICATION NUMBER: US/08/836,134A  
; CURRENT FILING DATE: 1997-06-20  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: Patentia Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 5502  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-08-836-134-1  
Alignment Scores:  
Pred. No.: 2.39e-31 Length: 5502  
Score: 279.00 Matches: 120  
Percent Similarity: 53.80% Conservative: 78  
Best Local Similarity: 32.61% Mismatches: 156  
Query Match: 5.11% Indels: 15  
DB: Gaps: 6  
US-09-697-089-2 (1-1024) x US-08-836-134-1 (1-5502)  
OY 150 GUGINLeuThrLeuAsnGlyLeuLeuGlnAlaLeuGlnSerProCysIleIleGluGly 169





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:
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
:
: CURRENT APPLICATION DATA:
:   APPLICATION NUMBER: US/09/353,585
:   FILING DATE: 15-Jul-1999
:   CLASSIFICATION: C12N 15/29, 15/82, A01H 5/00, A01N 65/00, C12Q
:   1/68
:
: PRIOR APPLICATION DATA:
:   APPLICATION NUMBER: US 08/930,277
:   FILING DATE: 27-OCT-1997
:   APPLICATION NUMBER: PCT/GB96/00785
:   FILING DATE: 01-APR-1996
:   APPLICATION NUMBER: GB 9506658.5
:   FILING DATE: 31-MAR-1995
:   ATTORNEY/AGENT INFORMATION:
:     NAME: Ms Mary J Wilson
:     REGISTRATION NUMBER: 32,955
:     REFERENCE/DOCKET NUMBER: 620-69
:   TELECOMMUNICATION INFORMATION:
:     TELEPHONE: (703) 816-4000
:     TELEFAX: (703) 816-4100
:   INFORMATION FOR SEQ ID NO: 1:
:     SEQUENCE CHARACTERISTICS:
:       LENGTH: 6471 base pairs
:       TYPE: nucleic acid
:       STRANDEDNESS: double
:       TOPOLOGY: linear
:     MOLECULE TYPE: DNA (genomic)
:     HYPOTHETICAL: NO
:     ORIGINAL SOURCE:
:       ORGANISM: Tomato
:       STRAIN: Cf2
:     FEATURE:
:       NAME/KEY: mat_peptide
:       LOCATION: 1754..5012
:     FEATURE:
:       NAME/KEY: sig_peptide
:       LOCATION: 1677..1753
:     SEQUENCE DESCRIPTION: SEQ ID NO: 1:
:
: US-09-353-585-1
:
: Alignment Scores:
:   Pred. No.: 0.00403 Length: 6471
:   Score: 95.00 Matches: 24
:   Percent Similarity: 66.15% Conservative: 19
:   Best Local Similarity: 36.92% Mismatches: 21
:   Query Match: 1.74% Indels: 1
:   DB: 4 Gaps: 1
:
: US-09-697-089-2 (1-1024) x US-09-353-585-1 (1-6471)
:
: QY 733 ThrservAlThAsnleuylsThrIeuSerIlleHlAspLseuGlnAsnGlnArgIeuPro 752
:   :::::::::::||||| ||||| ::::| | | ::::|:::
: Db 2661 GCTTATATGGGAACCTGTAAAACTGCTACGTTGAACCTGTAAATTAATACGTTTCT 2720
:
: QY 753 GlyGlyLeuThrAspSerIeuGlnAsnleuLysAsnLeuThrLysIeuLeuMetAspAsn 772
:   ||:::|:::| ||||| |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
: Db 2721 GGCCTATATCCGCTTCATGGGGAATCTGAAACAACCTTGTCTATGTGTGATCTTTACAT 2780
:
: QY 773 IleLysMetAsnGlnGlnAspAlaIleLysIeuAlaGlnGlyLeuLysAsnleuLysLys 792
:   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
: Db 2781 AACCAAGCTTTCGCGCATTCTCTGCTTCATTTGGGGAAT---CTGAACAACATTGTCTATG 2837
:
: QY 793 MetCysIeuPheHis 797
:   ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
: Db 2838 TTGTATCTTTACAT 2852
:
: RESULT 5
: US-08-910-731-5
:   Sequence 5, Application US/08910731
:   Patent No. 5932440
:   GENERAL INFORMATION:
:   APPLICANT: CHATTERJEE, DEB K.

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1 APPLICANT : SHANDILYA, HARINI
2 TITLE OF INVENTION : Mammalian Ribonuclease Inhibitors and Use Thereof
3 NUMBER OF SEQUENCES : 16
4 CORRESPONDENCE ADDRESS :
5 ADDRESSEE : STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
6 STREET : 1100 NEW YORK AVE., N.W., SUITE 600
7 CITY : WASHINGTON
8 STATE : D.C.
9 COUNTRY : USA
10 ZIP : 20005-3934
11
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE: Floppy disk
14 COMPUTER: IBM PC compatible
15 OPERATING SYSTEM: PC-DOS/MS-DOS
16 SOFTWARE: PatentIn Release #1.0, Version #1.30
17 CURRENT APPLICATION DATA:
18 APPLICATION NUMBER: US/08/910,731
19 FILING DATE: (Herewith)
20 CLASSIFICATION: 435
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: 08/795,395
23 FILING DATE: 04-FEB-1997
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: 08/794,546
26 FILING DATE: 03-FEB-1997
27 PRIOR APPLICATION DATA:
28 APPLICATION NUMBER: 60/024,057
29 FILING DATE: 16-AUG-1996
30 ATTORNEY/AGENT INFORMATION:
31 NAME: ESMOND, ROBERT W.
32 REGISTRATION NUMBER: 32,893
33 REFERENCE/DOCKET NUMBER: 0942.3440003
34 TELECOMMUNICATION INFORMATION:
35 TELEPHONE: 202-371-2600
36 TELEFAX: 202-371-2540
37
38 INFORMATION FOR SEQ ID NO: 5:
39
40 SEQUENCE CHARACTERISTICS:
41 LENGTH: 1386 base pairs
42 TYPE: nucleic acid
43 STRANDEDNESS: both
44 TOPOLOGY: both
45 MOLECULE TYPE: cDNA
46
47 US-08-910-731-5
48
49 Alignment Scores:
50 Pred. No.: 0.000672 Length: 1386
51 Score: 94.00 Matches: 27
52 Percent Similarity: 59.78% Conservative: 28
53 Best Local Similarity: 29.35% Mismatches: 34
54 Query Match: 1.72% Indels: 3
55 DB: 2 Gaps: 1
56
57 US-09-697-089-2 (1-1024) x US-08-910-731-5 (1-1386)
58
59 Oy GlyMetAspTyrIleValIleAllySerLeuSerGlnUbpProCysAspLeuGluGluIleGln 826
60 |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||::: 826
61 Db 214 GGCGTCGATTCGCTGCCTCCAGGGCGCTCAACCCCCCTCTGCAAGATCCAGAAGCTGAGC 273
62 |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||::: 273
63 Oy 827 LeuValSerCysLeuSerAlaAsnAlaValIleLeuAlaGlnAsnLeuHisAsn 846
64 |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||::: 846
65 Db 274 CTCGAGAACTCTGCTCCAGGGGGCGGCTCGCGGGCTCTGTCCAGCACACTACGCCACC 333
66 |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||::: 333
67 Oy 847 LeuValIleuSerIleLeuAspLeuSerGlnAsnTyrIleuLuluyAspGlyAsnGlu 866
68 |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||::: 866
69 Db 334 CTGGCCACCCTGCAGAGAGCTGCACCTCAGCGACAACCTTTGGGGGATGCGGGCTGCAG 393
70 |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||::: 393
71 Oy 867 AlaLeuHisGlu--LeuIleAspArgMetAsnValLeuGluGluIleu--ThrAlaLeuM 885
72 |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||::: 885
73 Db 394 CTGCTCTGCGAAGAGACACTCGAGACCCCCCAATGCGCGCTGGAAAAGCTGCAGCTGAGATA 453
74 |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||::: 453
75 Oy 885 etLeuProTIpGlyCysAspValGlnGlySer 895
76 ::::|:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||::: 895
77 Db 454 TGCAGCGCTCTGCGCTGCAGCTGGAGACCCCCT 485
78 ::::|:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||::: 485

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RESULT 6
US-08-824-701A-8
: Sequence 8, Application US/08824701A
: Patient No. 5882868
: GENERAL INFORMATION:
: APPLICANT: Funanage, Vicky L.
: APPLICANT: Scavina, Mena
: TITLE OF INVENTION: Method of Diagnosing Spinal Muscular Atrophy
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Jeffrey C. Lew
: STREET: 501 Silverside Road Suite 124
: City: Wilmington
: STATE: Delaware
: COUNTRY: USA
: ZIP: 19809
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette 3.5 inch, 1.44 Mb storage
: COMPUTER: IBM PC/XT/AT
: OPERATING SYSTEM: Windows for Workgroups 3.11
: SOFTWARE: Ami Pro 3.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/824,701A
: FILING DATE: 14-APR-1997
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Lew, Jeffrey C.
: REGISTRATION NUMBER: 35935
: REFERENCE/DOCKET NUMBER: 47066
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (302) 798-0700
: TELEFAX: (302) 798-5970
: INFORMATION FOR SEQ. ID NO.: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 250 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: Genomic DNA
: HYPOTHEICAL: no
US-08-824-701A-8

Alignment Scores:
Pred. No.: 0 00423 length: 250
Score: 82.00 Matches: 23
Percent Similarity: 54.79% Conservative: 17
Best Local Similarity: 31.51% Mismatches: 32
Query Match: 1.50% Indels: 1
DB: 2 Gaps: 1

US-09-697-089-2 (1-1024) x US-08-824-701A-8 (1-250)

QY 218 AspGlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetalaMetLeu 2377
|||||
Db 2 GACCAGCTCCTAGGAAGAAGATGTCGTACGAAATGTGCATGAGACCATTTATCCAG 61
|||||

QY 238 LysLeuArgGlnArgValIleuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsn 257
|||||
Db 62 CAGTTAAAGATCAGGCTTATTCCTTTGTAGATGACTCAAAATAATGTCAATCCCT 121
|||||

QY 258 CysProGluIleGluAlaIleuIleLysGluAsnHisArgPheLysAsnMetValIleVal 2777
|||||
Db 122 ---CAACTCATAGGAAGAACTGATTCAAAAAAACACATTATCCCGGACCTGCTATTGATT 178
|||||

QY 278 ThrThrThrThrGluCysLeuArgHisIleArgGlnPhe 290
:::
Db 179 GCTGTCGTACAAACAGGCGCCAGGACATCCTCCGCGATAC 217
:::

RESULT 7
US-09-228-986-2
Sequence 2, Application US/09228986
Patient No. 6359198

```

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: GENERAL INFORMATION:
: APPLICANT: Strabala, Timothy
: APPLICANT: Nieuwenhuizen, Niels
: TITLE OF INVENTION: Compositions Isolated from Plant Cells
: TITLE OF INVENTION: and their use in the Modification of Plant Cell Signalling
: FILE REFERENCE: 11000/1020
: CURRENT APPLICATION NUMBER: US/09/228, 986
: CURRENT FILING DATE: 1999-01-12
: NUMBER OF SEQ ID NOS: 130
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 2
: LENGTH: 2568
: TYPE: DNA
: ORGANISM: Eucalyptus grandis
US-09-228-986-2

Alignment Scores:
Pred. No.: 0.108 Length: 2568
Score: 82.00 Matches: 18
Percent Similarity: 64.15% Conservative: 16
Best Local Similarity: 33.96% Mismatches: 19
Query Match: 1.508 Indels: 0
DB: 4 Gaps: 0

US-09-697-089-2 (1-1024) x US-09-228-986-2 (1-2568)
OY 733 ThrSerValThrAsnLeuysThrIleuseIleHisAspIleuInsnGlnArgLeuPro 752
Db 508 ACAAAAGCTGGGATCTGTGAAGAGCTGAGTGTCTTGCTGTGCAATCAATACAGCTACT 567
OY 753 GlyGlyLeuThrAspSerLeuGlnAsnLeuLysAsnLeuThrLysLeuIleMetAspAsn 772
Db 568 GCGCGAATACCGGCAAGATTAGGTGACCTGGCGGACGTTGACGAGGTTATATTGAGTTTC 627
OY 773 IleLysMetAsnGlnGlnAspAlaIleLysLeuAlaGlu 785
Db 628 AATCGCCTCTTGCTGCCTGATTCACATGAAGATAGCCGAT 666

RESULT 8
US-09-099-041A-27
: Sequence 27, Application US/09099041A
: Patent No. 6340576
: GENERAL INFORMATION:
: APPLICANT: Bertin, John
: TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
: TITLE OF INVENTION: PROTEIN FAMILY AND USNS THEREOF
: FILE REFERENCE: 07334-076001
: CURRENT APPLICATION NUMBER: US/09/099, 041A
: CURRENT FILING DATE: 1998-06-17
: PRIOR APPLICATION NUMBER: 09/019, 942
: PRIOR FILING DATE: 1998-02-06
: NUMBER OF SEQ ID NOS: 37
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 27
: LENGTH: 1470
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-099-041A-27

Alignment Scores:
Pred. No.: 0.0708 Length: 1470
Score: 81.00 Matches: 20
Percent Similarity: 58.70% Conservative: 7
Best Local Similarity: 43.48% Mismatches: 19
Query Match: 1.488 Indels: 0
DB: 4 Gaps: 0

US-09-697-089-2 (1-1024) x US-09-099-041A-27 (1-1470)
OY 156 GlyLeuLeuGlnAlaLeuGlnSerProCysIleIleGlnGlyGluSerGlyLysGlyLys 175
Db 448 GGCATCTCTAATGACACGAGGTGACAGACCATCTTCATCTCGGTGATCATCTCGGTGGCCAG 507

```





; Patent No. 6369196  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY  
; FILE REFERENCE: 0734/118001  
; CURRENT FILING DATE: 1999-02-05  
; EARLIER APPLICATION NUMBER: US/09/245,281  
; EARLIER FILING DATE: 1998-12-08  
; EARLIER APPLICATION NUMBER: US/09/099,041  
; EARLIER FILING DATE: 1998-06-17  
; EARLIER APPLICATION NUMBER: US/09/019,942  
; EARLIER FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 2859  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-245-281-9

Alignment Scores:  
Pred. No.: 0.179 Length: 2859  
Score: 81.00 Matches: 20  
Percent Similarity: 58.70% Conservative: 7  
Best Local Similarity: 43.48% Mismatches: 19  
Query Match: 1.48% Indels: 0  
DB: 4 Gaps: 0

US-09-697-089-2 (1-1024) x US-09-245-281-9 (1-2859)

Oy 156 GlyLeuLeuGlnAlaLeuGlnSerProCysIleIleGluGlyGlnSerGlyLysGlyLys 175  
Db 565 GGCATCCTCAATGACAGCGGTGAGACCATCTTCATCTGCGGTGGGCAAG 624  
Oy 176 SerThrLeuLeuGlnArgIleAlaLeuTleuTrpGlySerGlyLysCysLysAlaLeuThr 195  
Db 625 TCATGCTGCTACAGCGGCTGCGAGACCTCTGCGCCACGGCGCTAGACGAGGGGTC 684

Oy 196 LysPheLysPheValPhe 201  
Db 685 AAATCTCTCTCCACTTT 702

RESULT 13

US-09-207-359B-9  
; Sequence 9, Application US/09207359B  
; Patent No. 6469140  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
; FILE REFERENCE: 0734-112001  
; CURRENT FILING DATE: 1998-12-08  
; PRIOR APPLICATION NUMBER: US/09/207,359B  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: US/09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 2859  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-207-359B-9

Alignment Scores:  
Pred. No.: 0.179 Length: 2859  
Score: 81.00 Matches: 20  
Percent Similarity: 58.70% Conservative: 7  
Best Local Similarity: 43.48% Mismatches: 19  
Query Match: 1.48% Indels: 0

DB: 4 Gaps: 0

US-09-697-089-2 (1-1024) x US-09-207-359B-9 (1-2859)

Oy 156 GlyLeuLeuGlnAlaLeuGlnSerProCysIleIleGluGlyGlnSerGlyLysGlyLys 175  
Db 565 GGCATCCTCAATGACAGCGGTGAGACCATCTTCATCTGCGGTGGGCAAG 624  
Oy 176 SerThrLeuLeuGlnArgIleAlaLeuTleuTrpGlySerGlyLysCysLysAlaLeuThr 195  
Db 625 TCATGCTGCTACAGCGGCTGCGAGACCTCTGCGCCACGGCGCTAGACGAGGGGTC 684  
Oy 196 LysPheLysPheValPhe 201  
Db 685 AAATCTCTCTCCACTTT 702

RESULT 14  
US-09-099-041A-25

; Sequence 25, Application US/09099041A  
; Patent No. 6340576  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
; FILE REFERENCE: 0734-076001  
; CURRENT FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: US/09/099,041A  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 25  
; LENGTH: 3080  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1470)  
US-09-099-041A-25

Alignment Scores:  
Pred. No.: 0.198 Length: 3080  
Score: 81.00 Matches: 20  
Percent Similarity: 58.70% Conservative: 7  
Best Local Similarity: 43.48% Mismatches: 19  
Query Match: 1.48% Indels: 0  
DB: 4 Gaps: 0

US-09-697-089-2 (1-1024) x US-09-099-041A-25 (1-3080)

Oy 156 GlyLeuLeuGlnAlaLeuGlnSerProCysIleIleGluGlyGlnSerGlyLysGlyLys 175  
Db 448 GGCATCCTCAATGACAGCGGTGAGACCATCTTCATCTGCGGTGGGCAAG 507  
Oy 176 SerThrLeuLeuGlnArgIleAlaLeuTleuTrpGlySerGlyLysCysLysAlaLeuThr 195  
Db 508 TCATGCTGCTACAGCGGCTGCGAGACCTCTGCGCCACGGCGCTAGACGAGGGGTC 567  
Oy 196 LysPheLysPheValPhe 201  
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RESULT 15  
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; Sequence 25, Application US/09245281  
; Patent No. 6369196  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY  
; FILE REFERENCE: 0734/118001  
; CURRENT FILING DATE: 1999-02-05



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OM protein - nucleic search, using frame\_plus.p2n model

Run on: January 31, 2003, 08:47:16 ; Search time 111 Seconds  
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Title: US-09-697-089-2

Sequence: 1 MNFKDNRALIQRMGMVTI.....MQPDDDLSTVITGAFKLYTA 1024

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Searched: 396772 segs, 224632407 residues

Total number of hits satisfying chosen parameters: 793544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	5188	95.0	3612	10	US-09-841-739-6

5	5188	95.0	3615	10	US-09-841-739-4	Sequence 4, Appli
6	5188	95.0	3615	10	US-09-841-739-12	Sequence 12, Appli
7	1598	29.3	891	9	US-09-864-921-179	Sequence 179, App
8	1424	26.1	1395	9	US-09-864-921-98	Sequence 98, Appli
9	1084	19.9	618	9	US-09-864-921-181	Sequence 181, App
10	1005	18.4	608	10	US-09-864-921-339	Sequence 339, App
11	853	15.6	768	9	US-09-864-921-102	Sequence 102, App
12	725	13.3	522	10	US-09-864-921-754	Sequence 754, App
13	493	9.0	578	9	US-09-864-921-100	Sequence 100, App
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16	391	7.2	220	10	US-09-864-761-20988	Sequence 20988, A
17	369	6.8	483	10	US-09-728-445-337	Sequence 337, App
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20	279	5.1	6124	8	US-08-913-322-21	Sequence 21, Appli
21	279	5.1	6124	10	US-09-967-768A-184	Sequence 184, App
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27	114	2.1	526	10	US-09-917-265-19	Sequence 19, Appli
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#### ALIGNMENTS

RESULT 1  
US-09-841-739-3  
; Sequence 3, Application US/09841739  
; Patent No. US20020034784A1  
GENERAL INFORMATION:  
APPLICANT: Bertin, John  
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES TH  
FILE REFERENCE: 07334-329001  
CURRENT APPLICATION NUMBER: US/09/841,739  
CURRENT FILING DATE: 2001-08-29  
PRIOR APPLICATION NUMBER: US 09/697,089  
PRIOR FILING DATE: 2000-10-26  
PRIOR APPLICATION NUMBER: US 60/161,822  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 3072  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-841-739-3

Alignment Scores:  
Pred. No.: 0  
Score: 5459.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%

Length: 3072  
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Conservative: 0  
Mismatches: 0  
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Oy 61 LysGlySerGlnSerCysAsnLeuPheLeuLysSerIleuLysGlnTPrasnTProLeu 80  
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Oy 81 PheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGlnGlyAspLeuAspAsp 100  
Db 241 TTTCAGGACTTGAATGAGCAAAAGTCTTTTTCATCAGACATCAGAAAGAGACTTGGACAT 300  
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RESULT 2  
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; Sequence 1, Application US/09841739  
; Patent No. US20020034784A1  
; GENERAL INFORMATION:  
; APPLICANT: Berlin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE

; FILE REFERENCE: 07334-329001  
; CURRENT APPLICATION NUMBER: US/09/841,739  
; CURRENT FILING DATE: 2001-08-29  
; PRIOR APPLICATION NUMBER: US 09/697,089  
; PRIOR FILING DATE: 2000-10-26  
; PRIOR APPLICATION NUMBER: US 60/161,822  
; PRIOR FILING DATE: 1999-10-27  
; NUMBER OF SEQ ID NOS: 16  
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; SEQ ID NO 1  
; LENGTH: 3133  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (36)..(3107)  
US-09-841-739-1  
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Score: 5459.00 Matches: 1024  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
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Db 696 CTGGATATACCTGGCACAAATCAGAGAACAGACATTCATGGCCATGCTGAACCTCGG 755  
 Qy 241 GlnArgValIleuPheIleuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 260  
 Db 756 CAGAGGGTCTCTTTCCTCTTGTGATGCTACATTAATTCAGCCCGCAAGCTGCCAGAA 815  
 Qy 261 IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThrThr 280  
 Db 816 ATGCAACCCCGATGAAGAAAGAAACACCGCTTCAAGAAACATGGTCATCGTCACACATAC 875  
 Qy 281 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 300  
 Db 876 ACTAGAGCTCTGAGGACAAATACGGCAGATTGGTCCCTGACTGCTGAGGTGGGGATATG 935  
 Qy 301 ThrGluAspSerAlaGlnAlaLeuIleArgGluValIleuIleLysGluLeuAlaGluGly 320  
 Db 936 ACAGAAACAGACGCCAGGCTCTATCCGAGAAAGTGGATCAAGAGAGCTTGAGAGGC 995  
 Qy 321 LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe 340  
 Db 996 TTGTTGGTCCAAATTCAGAAATCCAGGAGCTTGAGGAATCTCATGAAGACCCCTCTCTT 1055  
 Qy 341 ValValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnThr 360  
 Db 1056 GTGGTCATCACTTGCAATCCAGATGGGTGAAAGTGAATGCCACTCCACACACAAACA 1115  
 Qy 361 ThrIleuPheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysGly 380  
 Db 1116 ACCGTGTTCCATACCTTCTATGATCTGTTCATACAGAAACAAACACAAACATTAAGT 1175  
 Qy 381 ValAlaAlaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGly 400  
 Db 1176 GTGGCTCAAGTACTTCATTCATCGGAGCCTGAGCACCTGTGAGACCTAGCTCTGAGAGCT 1235  
 Qy 401 ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal 420  
 Db 1236 GTGTTCCTCCACAAAGTTGATTTGAACTGCAAGATGTGTCCACGCTGAAGAGAGATGTC 1295  
 Qy 421 LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys 440  
 Db 1296 CTGCTGACAACTGGCTCCCTCTGTAAATATACACTCAAGTCCAAAGTCCAAAGCTATATAA 1355  
 Qy 441 PhePheHisLysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerSerLeuLeuThr 460  
 Db 1356 TTCTTTTACAAAGTCAATTCACAGAGTACACACAGAGAGACACAGAGTATATGACG 1415  
 Qy 461 SerHisGluProGlnGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle 480  
 Db 1416 TCTCATGAGCCAGAGAGAGGTACCAAGGGAGATGTTACTTGCAAGAAATGGTTCCATT 1475  
 Qy 481 SerAspIleThrSerThrTyrSerSerSerLeuLeuArgTyrThrCysGlySerSerValGlu 500  
 Db 1476 TCGCAACATTAATCACTTAATAGCAGCGCTGCTCCGGTACACTGtGGGTACTGTGTGAA 1535  
 Qy 501 AlaThrArgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuLeuGly 520  
 Db 1536 GCCACCAAGGCGCTGTATATAGACACCTCCGACAGAGTATCAACACAGCGCTGCTTCCGA 1595  
 Qy 521 LeuSerIleAlaLysArgProLeuThrParGlnGlnLysLeuGlnLysSerValLysAsnThr 540  
 Db 1596 CTTTTCATCGCCAGAGAGCGCTCTGAGAGACAGAAATCTTGGCAAAAGTAAAAAACCC 1655  
 Qy 541 ThrGlnGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHis 560  
 Db 1656 ACTAGACAGAAATTCGAAAGCCATTAACATCAATTCCTTTGTAGAGTGTGGCATCCAT 1715  
 Qy 561 LeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePheGln 580  
 Db 1716 TTATATCAAGAGATACATCCAAATTCAGCCCTGAGCCCAAGAAATTTGAAGCTTTCTTCAA 1775  
 Qy 581 GlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPheGlu 600

Db 1776 GGTAAAGCTTATATATCAACTCAGGAGACATCCCGATTACTATTGACTCTTTGAA 1835  
 Qy 601 HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyAla 620  
 Db 1836 CATTGGCCCAATTTGCAAGTGTCTGTGACTTCAATTAACTGACCTTTATGGGGAGCT 1895  
 Qy 621 MetAlaSerTyrPglLysAlaAlaGluAspThrGlyGlyIleHisMetGluGluAlaPro 640  
 Db 1896 ATGCTTCATGCGAAAGGCTCGAGAGACACAGAGTGAATCCCATGAGAAAGAGCCCA 1955  
 Qy 641 GluThrTyrIleProSerArgAlaValSerLeuPheAsnThrPylsGlnGluPheArg 660  
 Db 1956 GAAACCTACATTCCTCCACAGGCGTGTATCTTTGTCTTCAACTGGAAGAGGAATTCAGG 2015  
 Qy 661 ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeu 680  
 Db 2016 ACTCTGGAGGTACACCTCCGGGATTTACAGCAAGTTGAATTAAGCAAGATACACATATCTG 2075  
 Qy 681 GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVal 700  
 Db 2076 GCGAAATATATTCAGCTCTGCGCACAGCCTCAGGCTGCAAAATTAAGAGATGTGCTGTG 2135  
 Qy 701 AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGlu 720  
 Db 2136 GCTGGAAGCCCTCAGATTGGTCTTCAGCACTGTAAAGCAATTAATTCATGATGTGGA 2195  
 Qy 721 AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr 740  
 Db 2196 GCCAGTCCCTCACCATTAAGAGATGAGAGGACATCACTGTATACAAACCTGAAACCC 2255  
 Qy 741 LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyLeuThrAspSerLeuGly 760  
 Db 2256 TTGAGTATTCATGACCTACAGAAATCAACGGCTCGGGGTGTCTGACTGCACGCTTGCTG 2315  
 Qy 761 AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluAspAla 780  
 Db 2316 AACTTGAAGAACTTACAAAGCTCATTAATGATACATAAAGATGAAGAAAGATGCT 2375  
 Qy 781 IleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis 800  
 Db 2376 ATAAACCTAGCTGAAGGCTGAAAAACCTGAAGAAAGTGTATTTCATTGATTAACCCAC 2435  
 Qy 801 LeuSerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCys 820  
 Db 2436 TTGTCTGACATTTGAGAGGAGATGATTACATTAATCAAGTCTGTCAAGGAAGCCCTGT 2495  
 Qy 821 AspLeuGlnGluIleGlnLeuValSerCysLysSerLeuSerAlaAsnAlaValLysIleLeu 840  
 Db 2496 GACCTTGAAGAAATTCATTTAGTCTCTCTGCTGCTGTCTGTGCAAAATGCAAGTCAAAATCTTA 2555  
 Qy 841 AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeu 860  
 Db 2556 GCTCAGAAATCTTCACAATTTGGTCAAACTGAGCATTTCTGTATATATGAGAAATTAACCTG 2615  
 Qy 861 GluLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetLysValIleGluGln 880  
 Db 2616 GAAAAAGATGGAATGAAGCTTTCATGAACCTGATCAACAGAGTGAACAGTGTGAACAAG 2675  
 Qy 881 LeuThrAlaLeuMetLeuProTyrGlyCysAspValGlnLysSerLeuSerSerLeuLeu 900  
 Db 2676 CTCACCCGACATGATGCTCCCTGGGGCTGTGACCTGCAAGGACACCTGACAGACGCTGTG 2735  
 Qy 901 LysHisLeuGlnGluValProGlnLeuValLysLeuGlnLysLysAsnTyrParGluThr 920  
 Db 2736 AAACCTTTGAGAGGAGGTCCCAACCTGCAAGCTTGAGGTGAAAACTGAGACTCACA 2795  
 Qy 921 AspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln 940  
 Db 2796 GATACAGAGATTAGAAATTTTGGTGCAATTTTGGAAAGAACCTCGCAAAACCTTCCAG 2855  
 Qy 941 GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrPleuAlaPheMetGlyVal 960  
 Db 2856 CAGTTGAATTTGGCGGGAATCGTGTAGCAGTGTGATGCTTGCCCTTCAATGGGTGTA 2915





OY	421	LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys	440
Db	1537	CTGCTGCAACTGGGCTCCCTGTAATATACAGCTCAAGGTTCAAGCCAAAGTATAA	1596
OY	441	PhePheHisLysSerPheGlnGlnTyrThrAlaGlyArgLeuSerSerLeuLeuThr	460
Db	1597	TTCTTTCCACAGTCATTTCCAGAGTACACAGCAGAGCAAGACTCAGCAGTTTATTAGC	1656
OY	461	SerHisGluProGlnGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle	480
Db	1657	TCTATGAGCCACGAGGAGGAGGACCAGGGGAAGTGTACTTCCAAAAATGGTTTCCAT	1716
OY	481	SerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu	500
Db	1717	TCCGACATTAATCCACTTTATACAGCTGCTCTCGGTACACTGTGGGTCATCTGTGAA	1776
OY	501	AlaThrArgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuLeuGly	520
Db	1777	GCCACCCAGGGGTGTATGAAGCACCTCCGACAGCTGATCAACACGGCTGCTTCGGA	1836
OY	521	LeuSerIleAlaLysArgProLeuThrPArgGlnGlnSerLeuGlnSerValLysAsnThr	540
Db	1837	CTTTCCATCCGCAAGAGGCTCTCTGGACACAGGAATCTTTCCAAAGTGTAAATACCC	1896
OY	541	ThrGlnGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHis	560
Db	1897	ACTGAGCAAGAAATTCGAAAGCCATTAACATCAATTCCTTGTGAGTGGTGCATCAT	1956
OY	561	LeuTyrGlnGlnSerThrSerLysSerAlaLeuSerGlnGlnPheGlnAlaPheGln	580
Db	1957	TTTATATCAGAGATATCATCCAAATCAGCCCTGAGCCAAATTTGAAGCTTCTTTCAA	2016
OY	581	GlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPheGln	600
Db	2017	GGTAAAGCTTATATATCACTCAGGAAACATCCCGGATTTATTTGACTTCTTTGAA	2076
OY	601	HisLeuProAsnGlyAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyAla	620
Db	2077	CATTGGCCCAATGTGCAAGTCCCTGGACTTCATTAAACTGGACTTTATGGGGAGCT	2136
OY	621	MetAlaSerTyrGluLysAlaIleGlnAspThrGlyGlyIleHisMetGlnGluValPro	640
Db	2137	ATGGCTTCATGGGAAAGGCTGCAGAAACACACAGCGTGAATCCACATGGAGAGGCCCA	2196
OY	641	GluThrTyrIleProSerArgAlaValSerLeuPheAsnTTPlyGlnGluPheArg	660
Db	2197	GAACCTACATTCCTCCACAGGGCTGTATCTTCTTCACTGAGACAGCAATTCAGG	2256
OY	661	ThrLeuGlnValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeu	680
Db	2257	ACTCTGAGAGTCAACATCCCGGATTTCCAGCAAGTTAAATACCAAGATTCAGATATCTG	2316
OY	681	GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVal	700
Db	2317	GGGAAATATTCACACTCTGCCACAGCGTCAAGCTCAATTAAGAGATGCTCTGTGTG	2376
OY	701	AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerIleMetValGlu	720
Db	2377	GCTGGAAAGCTCACTTTGGTCTCCACACCTGTAAACAACTTATATTTCTCTCATGGTGAA	2436
OY	721	AlaSerProLeuThrIleGlnAspGlnArgHisIleThrSerValThrAsnLeuLysThr	740
Db	2437	GCCAGTCCCTCCACCATAGAAGATGAGAGCACAATCACTCTGTAAACAACCTGAAAAC	2496
OY	741	LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly	760
Db	2497	TTTGAGTATTCATGACTACAGAAATCAACGGCTCCCGGCTGCTCACTACAGACTTGGGT	2556
OY	761	AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGlnGluAspAla	780
Db	2557	AACTTGAAGAACCTTACAAAGCTCTATATGGAATACATTAAGATGAATGAAGAAGATCT	2616

QY	781	lleuylsleuAlaIgluGlyLeuLysAsnleuLysMetCysLeuPheHis	800
Db	2617	ATAAAACTAGCTGAAGGGCTGAAAAACCTGAAGAAGATGTTATTCATTTGACCCAC	2676
QY	801	leuSerAspIleGlyGlyIleMetAspTyrIleValLysSerLeuSerSerGluProCys	820
Db	2677	TTGTCTGCATTTGGAGAGGAATGGAATTCATAGTCAGAGTCTGTCTCAAGTGAACCTGT	2736
QY	821	AspLeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu	840
Db	2737	GACCTTGAAGAAATTCATTTAGTCTCTGCTGCTGTCTGCAAAATGCAGTGAATACTCTA	2796
QY	841	AlaGlnAsnleuHisAsnLeuValLysleuSerIleLeuAspLeuSerGluAsnTyrLeu	860
Db	2797	GCTCAAACTCTTCACAAATTTGGTCAAACTGAGCATCTTGATTTATACAGAAAATTTACCTG	2856
QY	861	GluLysAspGlyAsnGluAlaIleuHisGluLeuIleAspArgMetAsnValLeuGluGln	880
Db	2857	GAAAAAGATGGAAATGAAGCTCTTCATGACTGATCGACAGATGAAGACGTCTGGAACAG	2916
QY	881	LeuThrAlaLeuMetLeuProTropGlyCysAspValGlnGlySerLeuSerSerLeuLeu	900
Db	2917	CTCACCGCACTGATCTCTCCCTGGGGCTGTGACGTGCAAGCGACACCTGAGCAGCCTGTG	2976
QY	901	LysHisLeuGluGluValProGlnleuValLysLeuGlyLeuLysAsnTyrArgLeuThr	920
Db	2977	AAACATTTGGAGAGAGGTCCCACTCGTCAAGCTTGAGTTGAAAACCTGAGACTCA	3036
QY	921	AspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln	940
Db	3037	GATACAGAGATTAGAAATTTTAACTGTCATTTTGGAAAGAACCTCTGAAAAACTTCAG	3096
QY	941	GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrPheAlaPheMetGlyVal	960
Db	3097	CAGTTGAATTTGGCGCGGAAATCGTGTGAGCAGTGTGATGGCTTCATCGGGGTGA	3156
QY	961	PheGluAsnleuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuProAsp	980
Db	3157	TTTGGAAATCTTAAACCAATAGTGTGTTTTTAACTTAAAGAAATTTCTACCTGAT	3216
QY	981	ProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGluAla	1000
Db	3217	CCAGATTATAGTCAGAAAACCTTAGCAAGTGTATCCAAAGTTACTTTTCTCAGAAAGCT	3276
QY	1001	ArgLeuValGlyTyrGlnPheAspAspAspLeuSerValIleThrGlyAlaPheLys	1020
Db	3277	AGCGTTGTTGGGTGCAATTTGATGATGATGATCACTGATTATACAGCGCTTTAAA	3336
QY	1021	leuValThrAla	1024
Db	3337	CTAGTAACTGCT	3348

**Alignment Scores:**

Pred. No.:	0	Length:	3612
Score:	5188.00	Matches:	1014
Percent Similarity:	98.16%	Conservative:	1
Best local Similarity:	98.07%	Mismatches:	1
Query Match:	95.04%	Indels:	18
DB:	10	Gaps:	1

US-09-697-089-2 (1-1024) x US-09-841-739-6 (1-3612)

QY	1	Mesnpshellelyspansserrargalaleuileglarngmetcllyethrvallie	20
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Db	418	GTGAAATTCTAAAGGACAATAGCCAGCCCTTATTCAAAGAAATGGGAATGACTGTATA	477
QY	21	LygslnllenthraspspleuphevaltrpasvvalleuasnarglucluvaleuAsnile	40
Db	478	AAGCAATCAACATGACCTATTTGTATGTGAATGTTCTGAATCGCAGACAGAAAGTAAACATC	537
QY	41	lleCysCysgluLysvalgluInaspaalalaarglyllellehismetileuLys	60
Db	538	ATTGTGCGAGAAAGGTGGAGCAGATGCTGTAGAGGAGCATCATCATGATTTGAAA	597
QY	61	LygslYsergluSerCysasnleupheleuLysSerleuLysgluLrpsnsnYproleu	80
Db	598	AAGGCTTACAGTCCTETAACCTCTTCTTAAATCCCTTAAGAGTGAACATACTCTTA	657
QY	81	PheglAspleuansnglYlnSer-----	88
Db	658	TTTCAGACCTTGATGAGCAAACTTTTGAGAGACACAGAAATTGGGCTCTTTAAACATC	717
QY	89	-----LeuphehlsGlnThrSerGluglYAspleuAspleuala	102
Db	718	ACCTCTCTCTAATAGGCTCTTTTCATCAGACATCAGAAAGAGACTTGGACATTTGGCT	777
QY	103	GlAspleuLysAspleuYrHsIstHrProSerPheleuAsnpheryProleuLysglu	122
Db	778	CAGGATTTAAAGGCTGTACCAATACCCACTCTTCTGTGACTTATATCCCTTGGTGAA	837
QY	123	AspIleAspIlellepheasneuleuLysSerThrPheThrGluProvalleuTrpArgLys	142
Db	838	GATATTGACATATTATTTTAACTTGAAAGACCTTCACAGAACCCTGCTGGAGAGAG	897
QY	143	AspGlnHsIstHsIstargValgluInleuThrLeuAsnglYleuLcglalaleuGln	162
Db	898	GACCAACACCATACCGCGTGGAGAGCTGACCCCTAAATGGCCTCTCGAGGCTCTTCAG	957
QY	163	SerProCysIlellegluLysSerglYysglYlySerThrleuenglnArgile	182
Db	958	AGCCCTCGCATCTAGAGGGAAATTCGCAAAAGCAATCCACTTCTGTCAGACCAATT	101
QY	183	AlaMetLeuTrpLyserylYsCysLysalaLeuThrLysPheLysPheValPhephe	202
Db	1018	GCCATGCTCGGGGCTCCGGAAGTGCAGAGGCTGACCAAGTTCAAATTCGCTCTTC	1077
QY	203	LeuArgLeuSerTrpAlaglnnglyleuPhegluThrleuCysaspIleuLeuasp	222
Db	1078	CTCCGTCGCGAGGGGCCAGGGTGAACCTTTTGAACCTCTGTATCAACCTCCGAT	1137
QY	223	lleProglYthrIleargLysgluThrPheMetAlaMetleuLeuLysLeuArglnarg	242
Db	1138	ATACCTGGCACAATCAGGAAGCAGACATTCATGGCCATGCTGTGAAGCTGGGGCAGAG	1197
QY	243	ValleuPheleuLeuAspLyIYrAsngluPheLysPProglInAsnCysProgluIleglu	262
Db	1198	GTTCCTTTCCTTATGTGCTCAATGAATTCACCCCCAGACAGTCCCAAAATCGAA	1257
QY	263	AlaLeuIleLysgluAsnHsIstargPheLysAsnMetValIleValInThrThrProglu	282
Db	1258	GCCTGTAAAGAAACCAACCCCTTCAGAGACATGTGATGTCACCACTACCACTGAG	1317
QY	283	CysLeuArgHsIleleargInPheglYalaLeuThrAlaGluValglYsPheThrGlu	302
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QY 663 GluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeuGlyLys 682
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QY 683 IlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyValAlaGly 702
DB 2518 ATATTCAGCTTCGCCACAAAGCCTCAGCTGCMAATTAAGAATATGTGCTGGTGGCTGGA 2577
QY 703 SerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGlnAlaSer 722
DB 2578 AGCTTCAGTTGGTCCACAGACCTGTAGAACATTTATTTCTTCATGGTGGAAAGCCAGT 2637
QY 723 ProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThrLeuSer 742
DB 2638 CCCCTCACATAGAAAGATGAGAGGCACATCATCTGTAAACAACCTGAAACCTTGAGT 2697
QY 743 IleHisAspLeuGlnAsnGlnArgLeuProGlyLeuThrAspSerLeuGlyAsnLeu 762
DB 2698 ATTATGACCTACAGAAATCAACGGCTCGCGGTGCTGACTGACAGCTTGGTAAACTTG 2757
QY 763 LysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGlnLysAlaIleLys 782
DB 2758 AAGAAGCTTAAAGCTCATATATGATACATTAAGATGAATGAAGAAGATGCTATATAA 2817
QY 783 LeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeuSer 802
DB 2818 CTACCTGAGAGGCTGAAAAACCTGAGAAAGATGTTTATTTATTTGATTTGACCACCTTGCT 2877
QY 803 AspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAspLeu 822
DB 2878 GACATTCGAGAGGAATGGAATGATATGATCAAGTCTGTCAGTCAAGTGAACCTTGACCTT 2937
QY 823 GluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAlaGln 842
DB 2938 GAAAGAAATTCATATAGTCTCTGCTGCTGTCTGCAAAATGCAAGTGAATAATCTTAGCTAG 2997
QY 843 AsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGluLys 862
DB 2998 AATCTTCACAATTTGGTCAAACTGAGCATCTTGATTTATCAGAAATATTAACCTGAAAAA 3057
QY 863 AspLysAsnGlnAlaLeuHisGlnLeuIleAspArgMetAsnValLeuGluGlnLeuThr 882
DB 3058 GATGAAATGAAGCTTTCAAGAACTGATGTCACAGAGAAAGTGAAGAACACTCTCAC 3117
QY 883 AlaLeuMetLeuProTyrGlyCysAspValGlnGlySerLeuSerSerLeuLeuLysHis 902
DB 3118 GCACCTGATGCTGCCCTGGGCTGTGACCTGCAGAGCAGCCTGAGCAGCCTTTGAAACAT 3177
QY 903 LeuGluGlnValProGlnLeuValLysLeuGlyLeuLysAsnTyrPargLeuThrAspThr 922
DB 3178 TTGGAGAGGCTCCCAACCTGTCAGGCTTGGTTGAAAACTGGAGACCTCACAGATCA 3237
QY 923 GluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnIleu 942
DB 3238 GAGATTTAAATTTTAAAGTGCATTTTGTGAAAGAACCTTGAAAAATTTCCACAGATTTG 3297
QY 943 AsnLeuAlaGlnAsnArgValSerSerAspGlyTyrPheuAlaPheMetGlyValPheGlu 962
DB 3298 AATTTGGCGGAAATCTGTGTAGCAGATGATGATGCTTGCCTTCATGGGTGATTTGAG 3357
QY 963 AsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuProAspProAla 982
DB 3358 AATCTTAAGCAATTAAGTGTGTTTGGACTTGTAGTAAAGAAATTTTCACCGATCCAGCA 3417
QY 983 LeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnAlaArgLeu 1002
DB 3418 TTAGTTCAGAAATCTTACCAAGGTGTATCCAAAGTTAACTTTTCGCAAGAGCTAGGCTT 3477
QY 1003 ValGlyTyrPargIlePheAspAspAspLeuSerValIleThr 1016
DB 3478 GTTGGGTGGCAATTTGATGATGATGATCTCAGTGTATTATACA 3519

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RESULT 5
US-09-841-739-4
: Sequence 4, Application US/09841739
: Patent No. US20020034784A1
: GENERAL INFORMATION:
: APPLICANT: Bertin, John
: TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES TH
: FILE REFERENCE: 0734-329001
: CURRENT APPLICATION NUMBER: US/09/841,739
: PRIOR FILING DATE: 2001-08-29
: PRIOR APPLICATION NUMBER: US 09/697,089
: PRIOR FILING DATE: 2000-10-26
: PRIOR APPLICATION NUMBER: US 60/161,822
: NUMBER OF SEQ ID NOS: 16
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 4
: LENGTH: 3615
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)...(3612)
US-09-841-739-4

Alignment Scores:
Pred. No.: 0 Length: 3615
Score: 5188.00 Matches: 1014
Percent Similarity: 98.16% Conservative: 1
Best Local Similarity: 98.07% Mismatches: 1
Query Match: 95.04% Indels: 18
DB: Gaps: 1

US-09-697-089-2 (1-1024) x US-09-841-739-4 (1-3615)
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QY 21 LysGlnIleThrAspAspLeuPheValThrAsnValLeuAsnArgGluValAsnIle 40
DB 478 AAGCAAAATCACAGATGACCTATTGTTGTATGCAATTTCTGAAATCCCGAAGAAAGTAAACATC 537
QY 41 IleCysCysGluLysValGlnGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
DB 538 ATTGTCGCGAGAAAGTGGAGACAGATGCTGTGAGAGGATCATCATGATTTTGAAA 597
QY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTyrPargLeu 80
DB 598 AAGGTTTCAGAGTCTGTAACTCTTTCTTAAATCCCTTAAAGAGTGAACCTATCCCTCA 657
QY 81 PheGlnAspLeuAsnGlyGlnSer----- 88
DB 658 TTTTCAAGACTTGAATGAGACAAAGTTTGGAGAGACACAGAAATTTGGCTTTTAACATC 717
QY 89 -----LeuPheHisGlnThrSerGluLysAspLeuAspAspLeuAla 102
DB 718 ACCTCTTCTAATAGGCTTTTTCATCAGACATCAAGAAAGACTTGGAGCATTTGGCT 777
QY 103 GlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPhetYrProLeuGlyGlu 122
DB 778 CAGGATTTAAAGACTTGTACATACCAATCCCATCTTTTGTGAACCTTTTATCCCTTGGTGA 837
QY 123 AspIleAspIleIlePheAsnLeuLysSerThrPheThrGluProValIleuTyrPargL 142
DB 838 GATATTGACATTAATTTTAACTTGAAGAAAGCACTTCACAGAACTGTCTGTGGAGGAG 897
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DB 898 GACCAACACATCACCGCGGTGGAGACCTGACCTGAAATGGCTTCCGCGAGGCTTTCAG 957
QY 163 SerProCysIleIleGlyGluGlySerGlyLysGlyLysSerThrLeuLeuGlnArgIle 182

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Dh 958 AGCCCTGCATCATTTGAAGGGAATCTGGCAAGCAAGTCCACTCTGCTGACGCATTT 1017  
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Db 1018 GCCATGCTGGGGCTCCCGAAAGTGCAGAGCTGCACCAAGTTCAAATTCCTCTCTTC 1077  
Qy 203 LeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuCysAspGlnLeuAsp 222  
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Qy 223 LLeProGlyThrLLeArgLysGlnThrPheMeLAlaMeLeuLeuLysLeuArgGlnArg 242  
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Qy 283 CysLeuArgHisLLeArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMetThrGlu 302  
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Qy 303 AspSerAlaGlnAlaLeuLLeArgGluValIleuIleLysGlnLeuAlaGluLysLeuLeu 322  
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Qy 583 SerLeuTyrLLeAsnSerGlyAsnLLeProAspTyrLeuPheAspPheGlnHisLeu 602  
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Qy 603 ProAsnCysAlaSerAlaLeuAspPheLLeLysLeuAspPheTyrGlyLysAlaMetAla 622  
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RESULT 6  
US-09-841-739-12/c  
; Sequence 12, Application US/09841739  
; Patent NO. US20020034784A1  
; GENERAL INFORMATION:  
; APPLICANT: Berlin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
; FILE REFERENCE: 07334-329001  
; CURRENT APPLICATION NUMBER: US/09/841,739  
; PRIOR FILING DATE: 2001-08-29  
; PRIOR APPLICATION NUMBER: US 09/697,089  
; PRIOR FILING DATE: 2000-10-26  
; PRIOR APPLICATION NUMBER: US 60/161,822  
; PRIOR FILING DATE: 1999-10-27  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 3615  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-841-739-12

Alignment Scores:  
Pred. No.: 0 Length: 3615  
Score: 5188.00 Matches: 1014  
Percent Similarity: 98.16% Conservative: 1  
Best Local Similarity: 98.07% Mismatches: 1  
Query Match: 95.04% Indels: 18  
DB: 10 Gaps: 1

US-09-697-089-2 (1-1024) x US-09-841-739-12 (1-3615)

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QY 89 -----LeuPheHisGlnThrSerGluGlyAspLeuAspLeuAla 102  
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QY 103 GlnAspLeuLysAspLeuThrHisThrProSerPheLeuAsnPheTrpProLeuGlyL 122  
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Db 1998 GCAAGTACTTCATTTGGAGGCTGAGACACCTGTGAGAACCTGTGAGAGGTGTGTC 1939  
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QY 463 GluProGlnGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerLysSerAsp 482  
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QY 483 IleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGluAlaThr 502  
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Db 1638 AGGGCTGTATGAGCACCCTCGACAGAGTATCAACACGGCTGCTTCTCGGACTTCC 1579  
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QY 743 IleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGlyAsnLeu 762  
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RESULT 7  
US-09-864-921-179  
; Sequence 179, Application US/09864921  
; Patent No. US20020176853A1  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John C.  
; APPLICANT: Pio, Frederick F.  
; APPLICANT: Godzik, Adam  
; APPLICANT: Stehlik, Christian  
; APPLICANT: Damiano, Jason S.  
; APPLICANT: Lee, Sung-Hyung  
; APPLICANT: Oliveira, Vasco A.  
; APPLICANT: Hayashi, Hideki  
; APPLICANT: Pawlowski, Krzysztof  
; TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing  
; TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods of Use  
; FILE REFERENCE: P-LJ 4752  
; CURRENT APPLICATION NUMBER: US/09/864, 921  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 09/579, 240  
; PRIOR FILING DATE: 2000-05-24  
; PRIOR APPLICATION NUMBER: US 09/686, 347  
; PRIOR FILING DATE: 2000-10-10  
; PRIOR APPLICATION NUMBER: US 60/275, 980  
; NUMBER OF SEQ ID NOS: 195  
; SOFTWARE: FastSeq for Windows Version 4. 0  
; SEQ ID NO 179



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;      NAME/KEY: CDS
;      LOCATION: (1) .. (891)
;
US-09-864-921-179

```

Alignment Scores:	
pred. No.:	4.62e-229
Score:	1598.00
Percent Similarity:	99.66%
Best Local Similarity:	99.66%
Query Match:	29.27%
DB:	9
Gaps:	0
Length:	891
Matches:	286
Conservative:	0
Mismatches:	1
Indels:	0
Gaps:	0

US-09-697-089-2 (1-1024) x US-09-864-921-179 (1-891)

QY	161	LeGInSerProCysIIleAGInGIVGInSerCIVlySGIVlySGIVlySerThrIleuGIn	160
Db	1	CTTCAGAGCCCCCTGCATCTTGAAGAGGGAATCTGGCAAGGCAAGTCACTCTGGCTGAG	60
QY	181	ArgIIleAlaMetIeuTrpGlySerCIVlySGIVlySAlaIleuThrIlyPheIlyPheVal	200
Db	61	CGCATTTGCCATGCTCTGGGGCTCCGGAAAGTCAAGAGCTCTGACCAAGTTCAAAATTGCTC	120
QY	201	PhePheIeuArgIleuSerArgAlaInGInGIVlyIleuPheGIVuThrIleuCysAspGInIleu	220
Db	121	TTTCTTCCTCCCTCTCAGAGGGGCCCAAGGGTGGACTTTTGTAAACCCCTCTGTGATCAACTC	180
QY	221	IleuAspIleProGIVlyThrIleArgIVlySGIVuThrPheMetAlaMetIleuIleuIlyLeuArg	240
Db	181	CTGGATTTACTCTGGCACATCTAGGAACAGACATTTATGGCCATGCTGCTGAAGCTGGG	240
QY	241	GInArgValIleuPheIleuLeuAspGIVlyTyrAsnGIVuPheIlyProGInAsnCysProGIVu	260
Db	241	CAGAGGGTCTTCTTCTCTCTTGAGGGCTTACATGAATTCAGAGCCCCAGAACTGGCCAGAA	300
QY	261	IIleGIVuAlaIleuIleIlySGIVuAsnHisArgPheIlyAsnMetValIIleValIIThrThrThr	280
Db	301	ATTCAGAGCCCTGATTAAGGAAGAAACCCAGCCCTTCAAGAACATGGCATCTGTACACCACTACC	360
QY	281	ThrGIVuCysIleuArgHisIleArgGIVuPheGIVuAlaIleuThrAlaIleuValGIVuAspMet	300
Db	361	ACTGAGTGCCTGAGAGCAATACGCGAGTTTGGTCCCTGACTGCTGAGGIVGGGGAGATG	420
QY	301	ThrGIVuAspSerAlaGInAlaIleuIIleArgGIVuAlaIleuIIleIlySGIVuIleuAlaGIVuGIVu	320
Db	421	ACAAGAAGCACAGCCGCGAGGCTCTATCCGAGAACTGCTGATCAAGAGAGCTTCTGTGAAGGC	480
QY	321	IleuIleuIeuGInIIleGInIlySGIVuSerArgCysIleuArgAsnIleuIlyThrProIleuPhe	340
Db	481	TTGTGTCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGAGCCCCCTCTCTTT	540
QY	341	ValValIIleThrCysAlaIIleGInMetGIVuSerGIVuPheHisSerHisThrGInThr	360
Db	541	GTGCTCATCACTGTGCATTCACAGATGGGGAAGTGATGCCACTGCACACACAACA	600
QY	361	ThrIleuPheHisThrPheTyrAspIleuIleIIleGInIlySGIVuAsnIlySGIVuHisIlySGIVu	380
Db	601	ACGGTGTTCATACCTCTCTGTGATCTTTGATACGAAAAACAACAACAACAACAACAACAAGT	660
QY	381	ValIIleAlaSerAspPheIIleArgSerIleuAspHisCysGIVuIlySGIVuAlaIleuGInGIVu	400
Db	661	GTGGCTCCAGATGACTTCATTCGGAGCCTGGACCAAGCTGGAAGCTTACGCTTGGAGGGT	720
QY	401	ValPheSerHisIlySGIVuPheAspPheGIVuIleuGInAspValSerSerValAsnGIVuAspVal	420
Db	721	GTTGTTCTCCACAGATTGATTTGAACTCAGAGATGTGTCCAGCGGATGAGAGATGTC	780
QY	421	IleuIleuThrThrGIVuIleuIleuCysIlySGIVuTyrThrAlaGInArgPheIlySGIVuTyrIlySGIVu	440
Db	781	CTGTGTGCAACTGGGCTCTCTGTGAATATATACAGCTCAAGGTTCAAGCCAAAGTGTATAA	840

Qy 441 PhePheHisLysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerSer 457  
+ + + + +  
Db 841 TTCCTTTACAGATCATTTCCAGGAGTACACAGCAGGAGCAACTCAGCAGT 891

RESULT 8  
US-09-864-921-98  
: Sequence 98, Application US/09864921

```

: GENERAL INFORMATION:
: APPLICANT: Reed, John C.
: APPLICANT: Pio, Frederick F.
: APPLICANT: Godzik, Adam
: APPLICANT: Stenlik, Christian
: APPLICANT: Damiano, Jason S.
: APPLICANT: Lee, Sug-Hyung
: APPLICANT: Oliveira, Vasco A.
: APPLICANT: Hayashi, Hideki
: APPLICANT: Pawlowski, Krzysztof
: TITLE OF INVENTION: No. US2002017685A1e1 Card Domain Containing
: FILE REFERENCE: P-IJ 4752
: CURRENT APPLICATION NUMBER: US/09/864,921
: CURRENT FILING DATE: 2001-05-23
: PRIOR APPLICATION NUMBER: US 09/579,240
: PRIOR FILING DATE: 2000-05-24
: PRIOR APPLICATION NUMBER: US 09/686,347
: PRIOR FILING DATE: 2000-10-10
: PRIOR APPLICATION NUMBER: US 60/275,980
: PRIOR FILING DATE: 2001-03-14
: NUMBER OF SEQ. ID NOS: 195
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ. ID NO 98

```

Alignment Scores:	
Pred. No.:	9_58e-203
Score:	1424.00
Percent Similarity:	100.00%
Best Local Similarity:	99.63%
Query Match:	26.09%
DB:	9
	length: 1395
	Matches: 271
	Conservative: 1
	Mismatches: 0
	Indels: 0
	Gaps: 0

US-09-697-089-2 (1-1024) x US-09-864-921-98 (1-1395)

QY	753	GlygyleuThrAspSerLeuGlyAsnLeuLysAsnLeuThrLysLeuIleMetAspAsn	772
Db	538	AGTGGTCGACTGCACCTGGGTAACCTTGAAAGCACTTCAAAGCCATCAATAGGATAC	597
QY	773	IleLysMetAsnGluGluAspAlaIleLysLeuAlaGluGlyLeuLysAsnLeuLys	792
Db	598	ATAAGATGATGAAAGAAAGATGCCTATTAACCTAGCTAAGGCCCGAAAACCTGAAGAC	657
QY	793	MetCysLeuPheHisLeuThrHisLeuSerAspIleGlyGluGlyMetAspTyrIleVal	812
Db	658	ATGCTTTATTTCAATTGGACCCACTTGTCTGCACATTTGGAAGGAAAGCATTCATCATGTC	717
QY	813	LysSerLeuSerSerGluProCysAspLeuGluIleGluLeuValLysCysLeu	832
Db	718	AAGTCCTGTCACATGGAACCCCTGGACCTTGAAACAATTCATAATGACCTCCCTGCTTG	777
QY	833	SerIAsnAlaValLysIleLeuAlaGluAsnLeuHisAsnLeuValLysSerIle	852
Db	778	TCTGCAATGACAGTGAAGAATCTTAGCTCAGATCTTACATATTTGGTCAAACTGAGCATT	837
QY	853	LeuAspLeuSerGluAsnTyrLeuGluLysAspLysGluAlaLeuHisGluLeuIle	872

Db 838 CTTGATTATACAGAAAATTACTGTGAAAAAGATGAAATGAACTCTTACATGAACTGATC 897  
Qy 873 AspArgMetAsnValIleuGluGlnIleuThrAlaIleuMetIleuProTrpGlyCysAspVal 892  
Db 898 GACAGGATGAACTGCTAGAACAGCTCACCGCACTGATGCTGCGGCGCTGTGACGTG 957  
Qy 893 GlnGlySerLeuSerSerLeuLeuLysHisLeuGlnGluValProGlnIleuValLysLeu 912  
Db 958 CAAGGACGCTGAGCAGCCGCTTGAAACATTGGAGAGAGTCCACACACTGCTCAAGCTT 1017  
Qy 913 GlyLeuLysAsnTrpArgIleuThrAspTrpHisIleArgIleuGlnGlyAlaPhePheGly 932  
Db 1018 GGGTTAAAAAATCGAGACTCACAGATACAGAGATTAGAAATTTAGTGCATTTTGGGA 1077  
Qy 933 LysAsnProLeuLysAsnPheGlnIleuAsnLeuAlaGlyAsnArgValLysSerSerAsp 952  
Db 1078 AAAAAACCTTGAAAAAATCTGCAGCACTGAAATTTGGCGGAAATCTGTGACACAGTAT 1137  
Qy 953 GlyTrpLeuAlaPheMetGlyValPheGluAsnLeuLysGlnIleuValPhePheAspPhe 972  
Db 1138 GGATGGCTTCCTTCATGAGGTGATTTGACAACTTACAGCAATTTAGTGTTCCTTTGACTTT 1197  
Qy 973 SerThrLysGluPheLeuProAspProAlaLeuValArgLysLeuSerGlnValLysSer 992  
Db 1198 AGTACTAAAGAAATTTCTACCTGATCCAGCATTTAGTCAGAAACTTACCCAAAGTGTATCC 1257  
Qy 993 LysLeuThrPheLeuGlnGluAlaArgLeuValGlyTrpGlnPheAspAspAspLeu 1012  
Db 1258 AACTTAACTTTTCTGCAGAGAGCTAGGCTGTGGGGCAATTTGATGATGATCTC 1317  
Qy 1013 SerValIleThrGlyAlaPheLysLeuValThrAla 1024  
Db 1318 AGTGTTATTACAGTGTCTTTTAAACTAGTACTGCT 1353

RESULT 9  
US-09-864-921-181  
; Sequence 181, Application US/09864921  
; Patent No. US20020176853A1  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John C.  
; APPLICANT: Pio, Frederick F.  
; APPLICANT: Godzik, Adam  
; APPLICANT: Stehlik, Christian  
; APPLICANT: Damiano, Jason S.  
; APPLICANT: Lee, Sung-Hyung  
; APPLICANT: Oliveira, Vasco A.  
; APPLICANT: Pawlowski, Krzysztof  
; TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing  
; TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods of Use  
; FILE REFERENCE: P-1L 4752  
; CURRENT APPLICATION NUMBER: US/09/864,921  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 09/579,240  
; PRIOR FILING DATE: 2000-05-24  
; PRIOR APPLICATION NUMBER: US 09/686,347  
; PRIOR FILING DATE: 2000-10-10  
; PRIOR APPLICATION NUMBER: US 60/275,980  
; PRIOR FILING DATE: 2001-03-14  
; NUMBER OF SEQ ID NOS: 195  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 181  
; LENGTH: 618  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(618)  
US-09-864-921-181

Alignment Scores: 2.42e-152 Length: 618  
Pred. No.: 1084.00 Matches: 206  
Score:

Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 19.86% Indels: 0  
DB: 9 Gaps: 0

US-09-697-089-2 (1-1024) x US-09-864-921-181 (1-618)

Qy 760 GlyAsnLeuLysAsnLeuThrLysLeuIleMetAspAsnLysLeuMetAsnGlnGluAsp 779  
Db 1 GGTAACTTGAAAGAACTTACAAAGCTCATATATGATATACATTAAGATGATGAAGAGAT 60  
Qy 780 AlaIleLysLeuAlaGlnGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThr 799  
Db 61 GCTATAAATACTAGCTGAAGGCTGAAAAAACCCTGAAGAAAGATGATTATTTCAATTCACC 120  
Qy 800 HisLeuSerAspIleGlyGlnGlyMetAspTrpIleValLysSerLeuSerGluPro 819  
Db 121 CACTTGCTGTACATTGAGAGGGAATGATTAATGATCAATGTCATGCTGTCAAGTGAACCC 180  
Qy 820 CysAspLeuGlnGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIle 839  
Db 181 TGTGACCTTGAAAGAAATTCATTATAGTCTCCTGCTGTGCTCAAAATGCAAGTGAATC 240  
Qy 840 LeuAlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTrp 859  
Db 241 CTAGCTCAGAAATCTTCACATTTTGGTCAAACTGACGATTTCTGATTTATCAGAAAAATTAC 300  
Qy 860 LeuGlnLysAspGlyAsnGlnAlaLeuHisGlnLeuIleAspArgMetAsnValLeuGlu 879  
Db 301 CTGAAAAAAGATGAAATGAAATGAACTTTCATGATGATGATGATGAAAGTGAACCTGTAGAA 360  
Qy 880 GlnLeuThrAlaLeuMetIleuProTrpGlyCysAspValGlnIleSerLeuSerSerLeu 899  
Db 361 CAGCTCAGCCGCACTGAGTGCCTCGGCGGTGAGCTGCAAGCGACGCTGACACCTG 420  
Qy 900 LeuLysHisLeuGlnGluValProGlnLeuValLysLeuGlnLysLeuAsnTrpArgLeu 919  
Db 421 TTGAACATTTGAGAGAGGCTCCACAACTGCTACAGCTTGAGTGAAGAACTGAGACATC 480  
Qy 920 ThrAspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPhe 939  
Db 481 ACAGATACAGAGATTGAAATTTAGTGATTTTGGAAAGAACTCTGAAAAAATCTTC 540  
Qy 940 GlnGlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGly 959  
Db 541 CACGAGTTGAATTTGCGGGGAAATCGTGAAGAGTGAATGATGCTTGCGCTTCATGCGGT 600  
Qy 960 ValPheGluAsnLeuLys 965  
Db 601 GTAATTGAGAACTTTAAG 618

RESULT 10  
US-09-764-864-339  
; Sequence 339, Application US/09764864  
; Patent No. US20020132753A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PT223  
; CURRENT APPLICATION NUMBER: US/09/764,864  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 1792  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 339  
; LENGTH: 608  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (20)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE

```

; LOCATION: (23)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (26)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (86)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-864-339

Alignment Scores:
Pred. No.: 1.58e-140 Length: 608
Score: 1005.00 Matches: 189
Percent Similarity: 98.45% Conservative: 1
Best Local Similarity: 97.93% Mismatches: 3
Query Match: 18.41% Indels: 0
DB: 10 Gaps: 0

US-09-697-089-2 (1-1024) x US-09-764-864-339 (1-608)
QY 479 SerIleSerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSer
DB 28 GCCATTTCGCCCATTCATCCACTATATACAGCTCTCCGGTACCTCTGGGTATMT 87
QY 499 ValGluAlaThrArgAlaValMetCysHisLeuAlaAlaValTyrGlnHisGlyCysLeu
DB 88 GTGGAAGCCACACAGGCTCTTATGAGCACCTCGCAGCTGATCAACACGCTCCCT 147
QY 519 LeuGlyLeuSerIleAlaLysArgProLeuTyrArgGlnGluSerLeuInsValCys
DB 148 CTCGGACTTTCATCCCTCCCAAGAGGCTCTCTGGAGACAGGAATCTTGAAGGTGAAA 207
QY 539 AsnThrThrGluGlnGluIleLeuLysAlaAlaLeuAsnIleAsnSerPheValGluCysGly
DB 208 AACACACACAGACAGAAATTCGAAAGCCATTAACATCAATCTCTTTAGAGTGTGC 267
QY 559 IleHisLeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhe
DB 268 ATCCCTTTATATATCAAGAGGTGATCATCCAAATCAGCCCTGAGCCCAAGAAATTTGAAGCTTTC 327
QY 579 PheGlnGlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrIlePheAspPhe
DB 328 TTTCAGAGTAAAGCTTATATATCAACTACAGGAAACATCCCGATTACTTATTTGACTTC 387
QY 599 PheGluHisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGly
DB 388 TTGTAACATTTGCCCAATTTGCAAGTGTCTGGACTTCATTAACCTGACTTTTATGCG 447
QY 619 GlyAlaMetAlaSerTyrGluLysAlaAlaGluAspThrGlyGlyIleHisMetGluGlu
DB 448 GGAGCTATGGCTTTCATGGGAAAAGGCTGCAGAAACACAGGAGATCCACATGGAAGAG 507
QY 639 AlaProGluThrTyrIleProSerArgAlaValSerLeuPheAsnThrPryLysGlnGlu
DB 508 GCCCCAGAAACCTACATTCCTCCAGCAGGCTGTATCTTCTTCAACTGGAAGCAGAA 567
QY 659 PheArgThrLeuGluValThrLeuArgAspPheSerLys 671
DB 568 TTCAGAGACTCGAGGTCACACTCCGCGGATTCACGCAAG 606

RESULT 11
US-09-864-921-102
; Sequence 102, Application US/09864921
; Patent No. US20020176853A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Plo, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stelianik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sung-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
```

```

; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing
; FILE REFERENCE: P-LI 4752
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102
; LENGTH: 768
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (277)...(744)
US-09-864-921-102

Alignment Scores:
Pred. No.: 1.24e-117 Length: 768
Score: 853.00 Matches: 154
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 15.63% Indels: 0
DB: 9 Gaps: 0

US-09-697-089-2 (1-1024) x US-09-864-921-102 (1-768)
QY 1 MetAsnPheIleLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20
DB 277 ATGATTTTATTAAGACATTAAGCCAGCCCTTATTCAAAGATGGATGACTGTATA 336
QY 21 LysGlnIleThrAspAspLeuPheValTyrAsnValLeuAsnArgGluValAlaSnile 40
DB 337 AAGCAATACAGATGACCTATTGTATGGAATGTTCTGAATCCGCAAGATTAACATC 396
QY 41 IleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
DB 397 ATTTGCTCGAAGAGGTGAGCAGATGCTGCTAGAGGATCATTCATGATTTTGAAA 456
QY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTyrAsnTyrProLeu 80
DB 457 AAGGTTTCAGAGTCTCTTAACCTCTTTCTTAATCTTAAGAGATGGAATATCTCTTA 516
QY 81 PheGlnAspLeuAsnGlyLysSerLeuPheHisGlnThrSerGluGlyAspLeuAspAsp 100
DB 517 TTTCAGAGCTTGATGACAAAGTCTTTTCATCAGACATCAGAAGAGACATTTGAGCAT 576
QY 101 LeuAlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTyrProLeu 120
DB 577 TTGGCTCAGAGATTTAAAGACATTTGATACCATTCATCCATCTTCTGAACTTATATCCCTT 636
QY 121 GlyGluAspIleAspIleIlePheAsnLeuLysSerThrPheThrGluProValLeuTyr 140
DB 637 GGTGAAGATATTGACATTTATTTTAACTTGAAAAGACACTTACAGAACCTGTCTGTGG 696
QY 141 ArgLysAspGlnHisHisHisArgValGluGlnLeuThrLeu 154
DB 697 AGGAAGACCAACACATCACCAGCGGTGAGCAGAGCTGACCTTA 738

RESULT 12
US-09-764-864-754
; Sequence 754, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
```

```
; CURRENT APPLICATION NUMBER: US/09/764, 864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1782
; SOFTWARE: Patentn Ver. 2.0
; SEQ ID NO 754
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (360)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (468)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (499)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (505)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-864-754
```

```
Alignment Scores:
Pred. No.: 1,05e-98 Length: 522
Score: 725.00 Matches: 150
Percent Similarity: 89.47% Conservative: 3
Best Local Similarity: 87.72% Mismatches: 14
Query Match: 13.28% Indels: 6
DB: 10 Gaps: 1
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US-09-697-089-2 (1-1024) x US-09-764-864-754 (1-522)

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QY 80 LeuPheGlnAspLeuAnGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAnp 99
Db 3 CTATTTCAGAGCTTGAATGAGACAAAGTCTTTTCATCAGACATCAGAGAGACCTTGAGC 62
QY 100 AspLeuAlaGlnAspLeuLysAspLeuYrHisThrProSerPheLeuAnpPheYrPro 119
Db 63 GATTGGCTCAGATTAAAGGACTGTACATACCCCATCTTTCTGACCTTTATCCC 122
QY 120 LeuGlyGlnAspLeuAspLeuIlePheAsnLeuLysSerThrPheThrGluProValLeu 139
Db 123 CTGTGTGAGATATTGACATATTATTAACTTGAAAACACCTTCACAGAACCTGCTG 182
QY 140 TrpArgLysAspGlnHisHisHisArgValGluGlnLeuThrLeuAnGlyLeuLeuGln 159
Db 183 TGGAGAGAGGACCAACACCATCACCGCGTGAGCAGCTGACCTGAATGGCTCCTGCGAG 242
QY 160 AlaLeuGlnSerProCysIleIleGluGlyGlnSerGlyLysGlyLysSerThrLeuLeu 179
Db 243 GCTCTTCAGACCCCTGATCATTTGAAGGGAATCTGGCAAGGCAATCCATCTCTGCTG 302
QY 180 GlnArgIleAlaMetLeuTrpGlySerGlyLysCysIysAlaLeuThrLysPheLys-PH 199
Db 303 CAGGCGCATGCGCATGCTGTGGGCTCCGGAAGTGCAAGGCTTGACCAATTTCAANTT 362
QY 199 eValPhe-PheLeuArgLeuSerArgAlaGlnGly-GlyLeuPheGluThrLeuCysAsp 218
Db 363 CGTCTTCTTCTCTCTGTTCCAGAGGCGCCAGGGTGAGCTTTTGAACCCCTCTGTAT 422
QY 219 GlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLys 238
Db 423 CAATTCGC-GGTATACCGGGACA-TTCAGGAGGAGACATTACAGCCNGGT--GCTGAG 477
QY 239 LeuArgGlnArgValLeuPheLeuLeu 247
Db 478 GTGGCGGAGAGGCTTCTTTNTCTTG 504
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RESULT 13  
US-09-864-921-100  
; Sequence 100, Application US/09864921

```
; Patent No. US20020176853A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Pio, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: No. US20020176853A1e1 Card Domain Containing
; FILE REFERENCE: P-LJ 4752
; CURRENT APPLICATION NUMBER: US/09/864, 921
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579, 240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686, 347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275, 980
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 100
; LENGTH: 578
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (277)...(552)
US-09-864-921-100
```

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Alignment Scores:
Pred. No.: 6.46e-64 Length: 578
Score: 493.00 Matches: 89
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.03% Indels: 0
DB: 9 Gaps: 0
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US-09-697-089-2 (1-1024) x US-09-864-921-100 (1-578)

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Db 337 AAGCAATACACAGATGACCTATTGTATGAAATGTTGAAATCGGAAAGTAACATC 396
QY 41 IleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
Db 397 ATTTGCTCGGAGAGGTGAGCAGATGCTCTGAGAGGATCATTCACATATTTTGAAA 456
QY 61 LysGlySerGlnSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnThrProLeu 80
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Db 517 TTTGAGGACTTGAATGAGCAAAATGCTT 543
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RESULT 14  
US-09-864-921-177  
; Sequence 177, Application US/09864921  
; Patent No. US20020176853A1  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John C.  
; APPLICANT: Pio, Frederick F.  
; APPLICANT: Godzik, Adam  
; APPLICANT: Stehlik, Christian  
; APPLICANT: Damiano, Jason S.

APPLICANT: Lee, Sug-Hyung  
APPLICANT: Oliveira, Vasco A.  
APPLICANT: Hayashi, Hideki  
APPLICANT: Pawlowski, Krzysztof  
TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing  
TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods of Use  
FILE REFERENCE: P-LJ 4752  
CURRENT APPLICATION NUMBER: US/09/864,921  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 09/579,240  
PRIOR FILING DATE: 2000-05-24  
PRIOR APPLICATION NUMBER: US 09/686,347  
PRIOR FILING DATE: 2000-10-10  
PRIOR APPLICATION NUMBER: US 60/275,980  
PRIOR FILING DATE: 2001-03-14  
NUMBER OF SEQ ID NOS: 195  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 177  
LENGTH: 261  
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ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)...(261)  
US-09-864-921-177  
  
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DB 121 ATTGCGTCCGAGAGAGGAGGAGAGATGCTGCTAGAGGATCATTCACATGATTTGAAA 180  
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QY 81 PheglinspleuAsnlygln 87  
DB 241 TTTTCAGGACTTGAAATGACAA 261  
  
RESULT 15  
US-09-864-761-4236  
Sequence 4236, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
FILE REFERENCE: Aecm1ca-x-1  
CURRENT APPLICATION NUMBER: US/09/864,761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
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PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
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PRIOR FILING DATE: 2001-01-30  
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PRIOR FILING DATE: 2001-01-30  
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PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
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PRIOR FILING DATE: 2001-01-29  
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SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 4236  
LENGTH: 421  
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ORGANISM: Homo sapiens  
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OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2  
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US-09-864-761-4236  
  
Alignment Scores:  
Pred. No.: 2e-55 Length: 421  
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Percent Similarity: 100.00% Conservative: 0  
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Query Match: 7.97% Indels: 0  
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DB 241 CGTGTAGCAGTGTATGATGGCTTCTTCATGCGTGTATTTGGAATCTTAAGCAATTA 300  
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Db 301 GTGTTTTGACTTAGTACTAAGAAATTTCACCTGATCCAGCATTTACTCAGAAACTT 360  
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Job time : 154 secs

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Mon Feb 3 14:11:37 2003

US-09-697-089-2.p2n.rapn

Pending Nucleic Acid and/or Pending Amino Acid database searches now generate two sets of results. These databases were split into to two parts to reduce the time needed to update the databases daily. The split freed up more machine time for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions, **.rnpn** and **.rapn**  
Searches run against the Amino Acid Pending database produce two sets of results, with the extensions, **.rapn** and **.rapn**

*The Pending database search results should not be left in the case because they contain data that is confidential.*

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GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 31, 2003, 10:46:26 : Search time 5176 Seconds  
(without alignments)  
4974.093 Million cell updates/sec

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Delop	6.0 , Delext 7.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0  
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Post-processing: Minimum Match 08  
Maximum Match 1008  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	5459	100.0	3133	1	PCT-US00-29643-1
5	5459	100.0	3133	27	US-09-697-089-1
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7 5453 99.9 3075 41 US-10-156-733-1 Sequence 1, Appl1  
8 5453 99.9 3219 41 US-10-156-733-14 Sequence 23, Appl1  
9 5448 99.8 3213 42 PCT-US01-07143-23 Sequence 14, Appl1  
10 5448 99.8 3213 42 US-10-221-097-23 Sequence 23, Appl1  
11 5441 99.7 3260 1 PCT-US01-14826-66 Sequence 66, Appl1  
12 5441 99.7 3260 26 US-09-667-298-66 Sequence 66, Appl1  
13 5438 99.6 3396 33 US-09-864-921-96 Sequence 96, Appl1  
14 5438 99.6 3545 18 US-09-491-404-1319 Sequence 1319, Ap  
15 5438 99.6 3545 34 US-09-922-279-1319 Sequence 1319, Ap  
16 5438 99.6 3545 34 US-09-922-279A-1319 Sequence 1319, Ap  
17 5425 99.4 3396 27 US-09-686-347-96 Sequence 96, Appl1  
18 5188 95.0 3612 27 US-09-687-089-6 Sequence 6, Appl1  
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27 4030 73.8 6012 22 US-09-557-676-917 Sequence 917, App  
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29 4030 73.8 6012 38 US-10-042-938-917 Sequence 917, App  
30 4023 73.7 2343 22 US-09-578-789-15 Sequence 15, Appl1  
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34 4019 73.6 2415 22 US-09-579-240-17 Sequence 17, Appl1  
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36 3950 72.4 2215 42 US-10-221-097-22 Sequence 22, Appl1  
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39 3735 68.4 4098 22 US-09-557-676-912 Sequence 912, App  
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41 3735 68.4 4098 38 US-10-042-938-912 Sequence 912, App  
42 3566 65.3 3435 80 US-60-360-207-4654 Sequence 4654, Ap  
c 43 3543 64.9 2002 38 US-10-029-386-25135 Sequence 25135, A  
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45 3543 64.9 6900 22 US-09-579-240-73 Sequence 73, Appl1

## ALIGNMENTS

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GENERAL INFORMATION:  
APPLICANT: Millennium Pharmaceuticals, Inc.  
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
FILE REFERENCE: 07334-136W01  
CURRENT APPLICATION NUMBER: PCT/US00/29643  
CURRENT FILING DATE: 2000-10-26  
PRIOR APPLICATION NUMBER: US 60/161, 822  
PRIOR FILING DATE: 1999-10-27  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 3072  
TYPE: DNA  
ORGANISM: Homo sapiens  
PCT-US00-29643-3

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QY 101 LeuAlaglnaspleuLyaspLeuTythrProserPheleuasPheTyProleu 120  
DB 301 TTGGCTCAGCATTTAAAGACTTGACCATACCCATCTTTTCGAACTTTATCCCTT 360  
QY 121 gllylaspilaspilielepheasleuysSerThrPheThrGluProvalleuTrp 140  
DB 361 GGTGAAGATATGACATATTTTAACTTGAAGAACCTTCACAGAACCTGCTCCTGCG 420  
QY 141 ArglysaSrglnhshishisargvalgluglinsleuTrleuasngllyleuclnla 160  
DB 421 AGGAAGGACCAACACATCACCGCGTGAGAGCTGACCTGAAATGGCTCTCGAGGCT 480  
QY 161 LeuglnserProCysilleileglugllySergllySergllySergllySergllySergl 180  
DB 481 CTTCAGACCCCTGATATGATTAAGGGAATCTGGCAAGGCAAGTCACACTGCTGAG 540  
QY 181 ArglllealmetleuTrpGlySergllyscylsalsaleuThrLysPheLysPheVal 200  
DB 541 CGCATTCGCAATGCTCTGGGCGCTCGGAAAGTGCAAGGCTCGACCAATGTAATTCGCTC 600  
QY 201 PhePheleuargleuSerargalaglgllyleuphegluThrleuCyaspGlnleu 220  
DB 601 TTCTTCCTCCGCTCAGAGAGGCCGAGGCTGACTTTTGAACCTCTGTGATCACTC 660  
QY 221 LeuasplleProGlyThrilearglysglnThrPheMetaleuLeuLysleuarg 240  
DB 661 CTGCATATACCTGGCACAATCAGAGACATTCAGCCATGCGCTGACACTGCGG 720  
QY 241 GlnatgvalleupheleuLeuaspllytyrnsnglupheLysProGlnAsnCyPProglu 260  
DB 721 CAGAGGTTCTTTCTCTTCTGTATGGCTACATGAAATTCAGCCCAACTGCCAGAA 780  
QY 261 lilegualaleuilelygluasnhisargPheLysasnmetvalilevalThrThr 280  
DB 781 ATCGAAGCCCTGATRAAGAAACACCGCTTCAAGAACATGGTCATCGTACACACATCC 840  
QY 281 ThrGlucysleuarghislleargglaphegllyalaleuThrAlagluValGlyaspMet 300  
DB 841 ACTGAGTCCCTGAGGACATACGAGGAGTTGCTGCTGCTGCTGAGAGTGGGAGATG 900  
QY 301 ThrGluspserAlaglnAlaleuileargglivalleuilelysglileuAlagluGly 320  
DB 901 ACAGAAAGACAGCCCGCAGCTCTCTCCGAGAAAGTGCATCAGAGACTTGCTGAAGC 960  
QY 321 LeuileuaglnlileglnlyserargCysleuargasnleuMetLysThrProleuphe 340  
DB 961 TTGTTGCTCCAAATTCAGAAATCCAGTGCTTGAGAAATTCATGAGAACCCCTCTCTTT 1020  
QY 341 ValValliethrCysAlaileglnmetgllyusergluphehshisSerhshisThrGlnThr 360  
DB 1021 GTGGTCATCACTTGTCATATCAGATCGAGTGAAGTGAAGTTCACATCTCACACACAAACA 1080  
QY 361 ThrleuphehshisThrPheTytraspLeuLeuileglnlysaSnLysLysLysGly 380

|||||  
Db 1081 ACCGCTTCACATCTTATGATCTGTGATACAGAAAAACAACAACTAAGGT 1140  
QY 381 ValAlaAlaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGly 400  
Db 1141 GGGCGGCAAGGACACTTCTGGAGCCCTGGACACTGTGGAGACTTCTGGAGGGGT 1200  
QY 401 ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal 420  
Db 1201 GGTCTTCCACACAGTTTATTTCCAGCTGCAGAGATGTCTCCAGCTGATGAGATGTC 1260  
QY 421 LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys 440  
Db 1261 CAGCTGACAACTGGGCTCTCTGTAAATATACAGCTCAAGGTTCAAGCCAAAGTATATA 1320  
QY 441 PhePheHisLysSerPheGlnGlyThrAlaGlyArgLeuSerSerLeuLeuThr 460  
Db 1321 TTTCTTTCACAAATGCATCTCAGAGGTACACAGCAGCAGAACTCAGCAAGTTTATTGAGC 1380  
QY 461 SerHisGluProGlnGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle 480  
Db 1381 TCTCATGACCGACAGAGAGGTGACCAAGGGAATGTTACTTGCAGAAAAATGGTTCCATT 1440  
QY 481 SerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu 500  
Db 1441 TCGGACATTACATCCACTTATACAGCTGCTCGGTACACCTGGGTGATCTGTGAA 1500  
QY 501 AlaThrArgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuLeuGly 520  
Db 1501 GCCACAGGGGCTGTATGAGGACCTCGCAGCAGCTGTATCAACCGCTTCCTTCGGA 1560  
QY 521 LeuSerIleAlaLysArgProLeuThrArgGlnGlnSerLeuGlnSerValLysAsnThr 540  
Db 1561 CTTTCATGCGCAAGAGGCTCTCTGGAGACAGAAATCTTGGAAAGTGGAACAAACCC 1620  
QY 541 ThrGlnGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHis 560  
Db 1621 ACTGACACAGAAATCTGAAAGCCATAAACATCAATCTTGTGTAAAGTGGCAATCCAT 1680  
QY 561 LeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePheGln 580  
Db 1681 TTATATCAAGAGAGTACATCAATCAATCAGCCCTGAGCCAAAGAAATTTGAACTTCTTCAA 1740  
QY 581 GlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPheGlu 600  
Db 1741 GGTAAAGCTTATATATCACTCAGGGAACATCCCGATTAATTAATTAATCTTGTGAA 1800  
QY 601 HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyAla 620  
Db 1801 CATTTGCCCAATTTGCAAGTCTCTGCACTTCATTAACTGGACTTTTATGGGAGCT 1860  
QY 621 MetAlaSerTyrGluLysAlaAlaGluAspThrGlyGlyIleHisMetGlnGluAlaPro 640  
Db 1861 ATGGCTTCATGGGAAAGGCTCCAGAGACACAGGTGAATCCACATGGAAGAGGCCCA 1920  
QY 641 GluThrTyrIleProSerArgAlaValSerLeuPhePheAsnTyrLysGlnGluPheArg 660  
Db 1921 GAAACCTTACATTCACAGCGGGCTGTATCTTGTCTTAACTGGAAGAGGAATTCAGG 1980  
QY 661 ThrLeuGlnValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeu 680  
Db 1981 ACTCTGAGAGTACACACTCGGGATTTTCACCAAGTTGAATTAACCAATATTCATATCG 2040  
QY 681 GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVal 700  
Db 2041 GGGAAAAATATTCAGCTCTGCCCAAGGCCCTCAGGCTGCAATTAAGAGATGCTGTGTG 2100  
QY 701 AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGlu 720  
Db 2101 GCTGGAAGCTCAGTGTGCTCTCAGCACCTGTAAAGAAATTAATCTCTCATGGGGAA 2160  
QY 721 AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr 740  
|||||

Db 2161 GCCAGTCCCTCCATCATTAGAGATGAGAGGCACATCATCTGTAAACAACTGAAACCC 2220  
QY 741 LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyIleuThrAspSerLeuGly 760  
Db 2221 TTGAGTATTCATGACCTTACAGAAATCAAGCGCTCCGGGTGTCTGTACAGCTTGGGT 2280  
QY 761 AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluAspAla 780  
Db 2281 AACTTAAAGACCTTCAAAAGCTCATATGATGATACATTAAGATGAATGAGAGATGCT 2340  
QY 781 IleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis 800  
Db 2341 ATAAACATGCTGAAAGGCTGAAAAACCTGAAGAAAGATGTGTTTATTCATTGACCCAC 2400  
QY 801 LeuSerAspIleGlyLysLysMetAspTyrIleValLysSerLeuSerSerGluProCys 820  
Db 2401 TTGTCTGACATTGGAAGGAAATGGAATTCATAGTCAATGCTCTGTCAAGTGAACCTGT 2460  
QY 821 AspLeuGluGluIleGlnLeuValSerCysLysSerAlaAsnAlaValLysIleLeu 840  
Db 2461 GACCTTGAAGAAATTAATTAATGATCTCTCTGCTTGTCTGCAATGCAGTGAACATCTA 2520  
QY 841 AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeu 860  
Db 2521 GCTCAGAAATCTCACAAATTTGGTCAAACTGAGCATCTTGATTTATCAGAAATTAATCTG 2580  
QY 861 GluLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGln 880  
Db 2581 GAAAAAGATGGAATTAACCTCTTCATGAACTGATCGAAGATGAACCTGTGTAAGACAG 2640  
QY 881 LeuThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerLeuSerSerLeuLeu 900  
Db 2641 CTCACCGCATGATGCTGCTCGGCTGAGCTGTGACGTGCAAGCCAGCTGACACCTGTGG 2700  
QY 901 LysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrArgLeuThr 920  
Db 2701 AAACATTTGGAGAGGTCCACAACTGTCAGACTTGGGTGGAAGAACTGGAGACTGACA 2760  
QY 921 AspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln 940  
Db 2761 GATACAGAAATTAAGAAATTTAGGTGATTTTGGTGAAGAACCCCTGAAAAAATCTCCAG 2820  
QY 941 GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrLeuAlaPheMetGlyVal 960  
Db 2821 CAGTTGAATTTGGCGGGAATGCTGTGACAGATGATGATGGCTTGCCTTCAATGGGTGA 2880  
QY 961 PheGluAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuProAsp 980  
Db 2881 TTTGAAATCTTAAGCAATTAAGTGTTTTGAATTAAGTAAAGAAATTTCTACCTGAT 2940  
QY 981 ProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGluAla 1000  
Db 2941 CCAGCATTTAGTCAGAAATCTTGAAGCAAGTGTATCCAAATTAATCTTCTGCAAGAGCT 3000  
QY 1001 ArgLeuValGlyTyrGlnPheAspAspAspAspLeuSerValIlePheGlyAlaPheLys 1020  
Db 3001 AGGCTTGTGGGGCAATTTGATGATGATGATCTCAGTGTATTACAGGTGCTTTTAAA 3060  
QY 1021 LeuValThrAla 1024  
Db 3061 CTAGTACTGCT 3072

RESULT 2  
US-09-697-089-3  
; Sequence 3, Application US/09697089  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
; FILE REFERENCE: 07334-136001  
; CURRENT APPLICATION NUMBER: US/09/697,089  
; CURRENT FILING DATE: 2000-10-26

:	PRIOR APPLICATION NUMBER:	US 60/161,822	
:	PRIOR FILING DATE:	1999-10-27	
:	NUMBER OF SEQ ID NOS:	12	
:	SOFTWARE:	FastSeq for Windows Version 4.0	
:	SEQ ID NO 3		
:	LENGTH:	3072	
:	TYPE:	DNA	
:	ORGANISM:	Homo sapiens	
:	US-09-697-089-3		
:	Alignment Scores:		
:	Pred. NO.:	0	
:	Score:	5459.00	
:	Percent Similarity:	100.00%	
:	Best Local Similarity:	100.00%	
:	Query Match:	100.00%	
:	DB:	Gaps: 0	
:	US-09-697-089-2 (1-1024) x US-09-697-089-3 (1-3072)		
OY	1	Melnsnphelellysaspsnseraralaleuileglnargetglymethrvalile	20
Db	1	ATGATTTTCATMAAGGACAAATGCGGACCTTATTCMAAGAAATGGGAAATGACTGTATA	60
OY	21	Lysglnietrrasparpleuhevaltropanvalleuansnarrggluglivaalaenile	40
Db	61	AAGCAATACACAGATGACCTTATTTGTATGGAAATTTCTGATGCGGAAGATTAACATC	120
OY	41	Ilecscysglulysvalgluglnasplalalaaraglylleileihismetilelelys	60
Db	121	ATTGCTCTCGAAGAGGTGGACAGATGCTGCTAGAGGATCATTCACATGATTTGGAA	180
OY	61	Lysglyserglusercysasnleupheuleulysserleulysglutrrpantyrproleu	80
Db	181	AAGGTTTCAGAGCTCTGTAACCTTTCTTAAATCCCTTAAGGAGTGAACCTATCCTTA	240
OY	81	Pheglnaspleuansnglylserleuphehiesglnthrsergluglnaspleuaspasp	100
Db	241	TTTCAGAGACTTGATGACAAAGCTTTTTCATCAGACATCAGAGAGACTTGGACAT	300
OY	101	Leualaaglnaspleulysaspleutyrrhisthrproserpheleuasnphetyrproleu	120
Db	301	TTGGCTCAGGATTTTAAAGGACTTTTACCATACCCCATCTTTTCGAACTTTTATCCCTT	360
OY	121	Glygluasplileasplilellephasnleulysserthrphenhrgluprovalleutrp	140
Db	361	GGTGAAGATATGACATTTATTTTAACTTGAAAGCACCTTCACAGAACTGTCTGTGG	420
OY	141	Argllysaspspnhshshsarsarvalgluglnleuphrleuansnglyleuleuglnala	160
Db	421	AGGAAGGACCAACACCATACCGGCTGGAGAGCTGACCTCGAATGGCTCTCTGGAGGCT	480
OY	161	Leuglnaserprocyllleileglnlglylusercyllysglyllysserthrleuagln	180
Db	481	CTTCGAGACCCCTCGATCATTTGAAGGGGAATCTGGCAAAAGCAATCCTGCTGTCAG	540
OY	181	Arglilealawettleutrrpglysercyllyscyslysalaleuthrlyspheulyspheval	200
Db	541	CGCATTTGCCATGCTCTGGGGCTCCGGAAAGCAAGGCTCGACCAAGTTCAAATTGCTC	600
OY	201	Phepheleuargyleuserararalaglnlglyllyleuheglutrrhrleucysaspsglnleu	220
Db	601	TTCTTCCTCCCTCTCACGAGGGCCCAAGGTGGACTTTTGTAAACCCCTCTGTGATCAATC	660
OY	221	Leuaspliepproglythrilearglysglnthrphelevalawettleuleulysleuarg	240
Db	661	CTGGATATACCTGGCACATAGAGAACACATTTCAATGCCATGCTGCTGAAGCTGGG	720
OY	241	Glnarrrvalleupheleuleuaspglytyrrasnglubheulysproglinaancysproglu	260
Db	721	CAGAGGGTCTTTTCTCTTCTTGATGAGGCTACAAATTAATTCAGACCCCAAGACTGCCAGAA	780
OY	261	Ileagualaleuileylsgluasnhsiargrphelysasmetvalilevalthrthr	280

Db	781	ATCGAAGCCCTGATTAAGGAAACCACCGCTTAAAGAACATGGTCACTGCTACCACTAC	840
Qy	281	ThrGluCysLeuArgHisIleArgGlnPheGlyAlaIleuThrAlaGluValGlyAspMet	300
Db	841	ACTGAGTGCCTGAGGACATACGCGACATTTGGTGGCCCTGACCTGACTGAGGTGGGATATAG	900
Qy	301	ThrGluAspSerAlaGlnAlaIleuIleArgGluValLeuIleLysGluLeuAlaGluLys	320
Db	901	ACAGAAGACACGGCCAGAGGCTCTCATCCGAAAGTCTATCAAGAGCTGTCTCAAGGC	960
Qy	321	LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnMetLysThrProLeuPhe	340
Db	961	TTGTGGCTCCAAATTCGAAATCCAGGTGCTTAGGAAATCTATGAAGACCCCTCTCTT	1020
Qy	341	ValValIleThrCysAlaIleGlnMetGlyLysGluPheHisSerHisThrGlnThr	360
Db	1021	GTGGCATCACTGTGGCAATCAGATGGTGAAAGTAGATGTCACCTCACACAAACA	1080
Qy	361	ThrLeuPheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysGly	380
Db	1081	ACGGCTGTCATACCTCTTAAGATCTGTGATACAAAAACAAACCAACATTAAGCT	1140
Qy	381	ValAlaIleAspSerPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluLys	400
Db	1141	GTGGCTGCAATGACTTCATTCGAGGCTGGACACTGTGGAGACCTTACTTGGAGGCT	1200
Qy	401	ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspAl	420
Db	1201	GTGCTCTCCCAAGATTGATTTGCAACTCGAGATGTGTCCAGCTGAATAGAGATGTC	1260
Qy	421	LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys	440
Db	1261	CTGGCGAACACTGGGCTCTCTTGAAATATACAGCTCAAGAGTTCAAGCCAAAGTATAA	1320
Qy	441	PhePheHisLysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerLeuLeuThr	460
Db	1321	TTCTTTCCACAGTCACTTCCAGAGATACACAGCAGAGCAAGATCAGCATTTATTTAGCG	1380
Qy	461	SerHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle	480
Db	1381	TCTCATGAGCCAGAGAGAGGTGACCAAGGGAAAGTGTACTTGCAGAAAATGGTTTCCATT	1440
Qy	481	SerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysLysSerValGlu	500
Db	1441	TGCGACATTTACATCCACTTAATAGCAGGCTCTCCGGTACCCGTGGGCATCTGTGAA	1500
Qy	501	AlaThrArgAlaValMetLysHisLeuAlaIleValTyrGlnIleGlyCysLeuGluLys	520
Db	1501	GCCACCAAGGCTGTTATGAGACACTCTGCAGCAGTGTATCAACACGGCTTCTCCGA	1560
Qy	521	LeuSerIleAlaLysArgProLeuThrPArgGlnLysSerLeuGlnSerValLysAsnThr	540
Db	1561	CTTTCATTCGCGCAAGAGGCTCTCTGGAGACAGAAATCTTTGCAAGGTGAAAAACCC	1620
Qy	541	ThrGluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHis	560
Db	1621	ACTGAGCAAGAAATTCGAAAGCCATTAACATCAATCTCTTTGTAAAGTGTGGCATTCAT	1680
Qy	561	LeuTyrGlnLysSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePheGln	580
Db	1681	TTATATCAAGAGACATCAATCCAAATTCAGCCCTGAGCCCAAGAAATTTAAACCTTTCTTCA	1740
Qy	581	GlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPheGlu	600
Db	1741	GGTAAACACTTATATATCAACTCAGGGAACAATCCCGATTACTTATTTTACCTTTTGA	1800
Qy	601	HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyAla	620
Db	1801	CATTTGGCCAAATTGTGCAAGGCTCTGGACTCATTTAACTGCACTTTATGTGGGAGACT	1860
Qy	621	MetalAserTTPGluLysAlaAlaGluAspThrGlyGlyIleHisMetGluAlaPro	640

Db 1861 ATGGCTCATGGGAAAAGGCTGACAGAGACACAGGTGGAATCCACATGGAAGAGGCCCA 1920  
QY 641 GtThrTyrlleProSerArgAlaValSerLeuPheAsnTrpIysGlnIupheArg 660  
Db 1921 GAAACCTACATTTCCACGACGGGCTGATCTTTGTTCTTAACCTGGAAGCAGAAATTCACG 1980  
QY 661 ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrlleu 680  
Db 1981 ACTCTGAGAGGTACACATCCGGGATTTTCACCAAGTTGAATACCAAGATATCATATCTCG 2040  
QY 681 GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVal 700  
Db 2041 GGGAAAATATTTCAGCTCTGCCCAAGCCCTCAGCTGCAAAATGAAGAGATGCTCGTGTCG 2100  
QY 701 AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleLysSerLeuMetValGlu 720  
Db 2101 GCTGGAGGCTCAGTTTGGTCTCTCAGCCCTGTAAAGACATTTATCTCTCATGGGGAA 2160  
QY 721 AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr 740  
Db 2161 GGCAGTCCCTCCACCATGAAGATGAGAGGCAATCACAATCTGTAAACAACCTGAAAAAC 2220  
QY 741 LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly 760  
Db 2221 TTGAGTATTTCATGACCTACAGAAATCAAGCGCTCCGGGTGCTGACTACAGCTTGGGT 2280  
QY 761 AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGlnLysAla 780  
Db 2281 AACCTTGAAAGAACCTTACAAAGCTCATAAATGATTAACATTAAGATGAATGAAGAAGTGT 2340  
QY 781 IleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis 800  
Db 2341 ATAAACATAGCTGAGAGGCTGAAAAACCTGAAAGATGTGTTATTTTCATTGACCCAC 2400  
QY 801 LeuSerAspIleGlyGlnGlyMetAspTyrIleValLysSerLeuSerGlnProCys 820  
Db 2401 TTGTCTGACATTGGAGAGGGAATGATTAACATAGTCAAGTCTCTGCAAGTGAACCTGT 2460  
QY 821 AspLeuGlnGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu 840  
Db 2461 GACCTTGAAAGAAATCATATGCTCTGCTGCTGCTGCTGCAAAATGACGTGAAATCCGA 2520  
QY 841 AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGlnAsnTyrLeu 860  
Db 2521 GCTCAGAAATCTTCACAAATTTGGTCAAACTGACATCTTTGATTTATCAGAAATTAACCTG 2580  
QY 861 GtLysAspGlyAsnGlnAlaLeuHisGluLeuIleAspArgMetAsnValLeuGlnGln 880  
Db 2581 GAAAAAGATGGAAATGAAGCTCTTCATGAACATGATCGACAGCATGAAGCTCTTACAGAC 2640  
QY 881 LeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeu 900  
Db 2641 CTCACCGCATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2700  
QY 901 LysHisLeuGlnGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThr 920  
Db 2701 AAACATTTGGAGAGGTCCCAACTCGTCAAGCTTGGGTTGAAAACTGAGACTCACA 2760  
QY 921 AspThrGluIleArgIleLeuGlnLysAlaPhePheGlyLysAsnProLeuLysAsnPheGln 940  
Db 2761 GATTAAGAGATTGAATTTTGTAGTCAATTTTGTGAAGAACCCCTGTGAAAAACTTCCAG 2820  
QY 941 GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetCysAla 960  
Db 2821 CAGTTGAAATTTGGCGGGAATCGTGTGACAGCATGTGATGCTGCTTCTCATGGGTGA 2880  
QY 961 PheGlnAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGlnPheLeuProAsp 980  
Db 2881 TTTCGAGATCTTAACCAATTTAGTGTGTTTGTGACTTACACTAAAGAAATTTCTACTCAT 2940  
QY 981 ProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnAla 1000  
Db 2941 CCAGCATTTAGTCGAAAACTTAAGCCAAAGTGTATTCCAAGTTTAACCTTTCTCGAAGAACCT 3000

QY 1001 ArgLeuValGlyTrpGlnPheAspAspAspSerValIleThrGlyAlaPheLys 1020  
Db 3001 AGCTTTGTTGGGTGGCAATTTGATGATGATGATCTCAGTGTTATTTACAGGCTTTTAAA 3060  
QY 1021 LeuValThrAla 1024  
Db 3061 CTAGTAACGTCT 3072

RESULT 3  
US-09-841-739-3  
; Sequence 3, Application US/09841739  
; GENERAL INFORMATION:  
; APPLICANT: Berlin, Jovel  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES TH  
; FILE REFERENCE: 07334-329001  
; CURRENT APPLICATION NUMBER: US/09/841,739  
; PRIOR FILING DATE: 2001-08-29  
; PRIOR APPLICATION NUMBER: US 09/697,089  
; PRIOR FILING DATE: 2000-10-26  
; PRIOR APPLICATION NUMBER: US 60/161,822  
; PRIOR FILING DATE: 1999-10-27  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 3072  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-841-739-3

Alignment Scores:  
Pred. No.: 0 Length: 3072  
Score: 5459.00 Matches: 1024  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
DB: 32

US-09-697-089-2 (1-1024) x US-09-841-739-3 (1-3072)

QY 1 MetAsnPheIleLysAspAsnSerArgAlaLeuIleGlnArgMetCylMetThrValIle 20  
Db 1 ATGAATTTTCATTAAGACATAGCCGAGCCCTTATTTCAAAAGAAATGGAATGACTGTATA 60  
QY 21 LysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluGluValAsnIle 40  
Db 61 AAGCAAAATCACAGATGACCTTATTTGTATGGAATGTTCTGAATCGCGAAGAACTAAACATC 120  
QY 41 IleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60  
Db 121 ATTTCCTCGAAGAACGTGAGAGCATGCTGCTAGAGGATCATTCACATGATTTTGAANA 180  
QY 61 LysGlySerGlnSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeu 80  
Db 181 AAGGTTTCAGACTCTCTGTAACCTCTTCTTAATCCCTTAAGAGATGGAACATATCTCTTA 240  
QY 81 PheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluLysAspLeuAspAsp 100  
Db 241 TTTCAGACTGGAATGGAACAAAGCTTTTTCATTCAGACATCAGAAAGGAGACTTGGACAT 300  
QY 101 LeuAlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTyrProLeu 120  
Db 301 TTGGCTCAGGAATTTAAAGACTGTGTACCATACCCCATCTTTTCTGAACTTTTATCCCTT 360  
QY 121 GlyGluAspIleAspIleIlePheAsnLeuLysSerThrPheThrGluProValLeuTrp 140  
Db 361 GGTGAAGATATTGACATATTATTGTAACCTTGAAACACCTTCACAGAACTGTCTGTGG 420  
QY 141 ArgLysAspGlnHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAla 160  
Db 421 AGGAAGGCAACACCATCACCGCGGTGAGAGCACTGACCTGTGAATGGCTCTCTGAGGCT 480  
QY 161 LeuGlnSerProCysIleIleGluGlyLysSerGlyLysSerThrLeuLeuGln 180



Dd	481	CTTCAGACCCCTGCATCATTTGAAGGGAGATTGGCAAGGCAAGCTCCACTCTGCTGAG	540
Qy	181	ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal	200
Dd	541	CGCATGTGCATGCTCTGGGGCTCCGGAAAGTGCAGAGCTCTCACCAAGTCAAAATTCGTC	600
Qy	201	PhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGluThrLeuCysAspGlnLeu	220
Dd	601	TTCTTCCTCCCTCTCACAGAGGGCCAGGGGTGGACTTTTGAAAACCCCTGTGATCAACTC	660
Qy	221	LeuAspIleProGluThrIleArgLysGlnThrPheMetAlaMetLeuLysLeuArg	240
Dd	661	CTGGATATACCTGGCACAAATCAGAAAGCAACATTATGCGCATCTGCTGAAGCTGGG	720
Qy	241	GlnArgValLeuPheLeuLeuAspGlyLysGlnPheLysProGlnAsnProGlu	260
Dd	721	CAGAGGGTCTTTTCCTTCTTGATGGGTCAATGATTCACACCCCAAGACCTGCCCAAA	780
Qy	261	IleGluAlaLeuLleLysGlnAsnHisArgPheLysAsnMetValIleValThrThrThr	280
Dd	781	ATCGAAGCCCTGATAAAGAAACCAACCCCTTCAAAACATGTGATGTCACCACTACC	840
Qy	281	ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet	300
Dd	841	ACTGATGCTCCGAGGCAATACGGCAATGGTGGCTTACGCTCAGAGTGGGGATATG	900
Qy	301	ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuLleLysGluMetAlaGluLys	320
Dd	901	ACAGAAGACAGCCGCCAGGCTCTCATCCGAAAGTCTGATACAGAGCTTCTCTAAGGC	960
Qy	321	LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe	340
Dd	961	TTGTGTCTCCAAATTTCAGAAATCCAGATGCTTGAGAACTCATGATCAAGACCCCTCTTTT	1020
Qy	341	ValValIleThrCysAlaIleGlnMetGlyGluSerGlnPheHisSerHisThrGlnThr	360
Dd	1021	GGGTGCATCACTTGTGGAAATCCAGATGGGGAAGAGATTCACACTCCACACAAACA	1080
Qy	361	ThrLeuPheHisThrPheTyrAspLeuLysIleGlnLysAsnLysHisLysHisLysGly	380
Dd	1081	ACCGCTTCCATACCTCTATGATCTGTGATACAAAAACAAACAAACATATAAGT	1140
Qy	381	ValAlaAlaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGlnLys	400
Dd	1141	GTGGCTGCAAGTCACTTCATTCGGAGGCTGGACCACTGTGGAGACCTACTGTGAGGGT	1200
Qy	401	ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal	420
Dd	1201	GGTGTCTCCCAAGATTGATTTCGAACCTCAGAGATGTCTCCAGCGTGAATAGCATGTC	1260
Qy	421	LeuLeuThrThrGluLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys	440
Dd	1261	CTGCTGACAACTGGGGCTCTCTGTAAATATACAGCTCAAGGTTCAAGCCAAAGATATAA	1320
Qy	441	PhePheHisLysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerSerLeuLeuThr	460
Dd	1321	TTCTTTCACAAGTCACTTCCAGAGATACACAGCAGACGAAAGCTACGAGTTATTGACG	1380
Qy	461	SerHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle	480
Dd	1381	TCTCATGACCCAGAGAGAGGTGACCAGAGGGAATGGTTACTTCACAGAAATGGTTCCATT	1440
Qy	481	SerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu	500
Dd	1441	TTCGACATTAATCACTCTTATAGACGCTGCTCCGGTATCACTGTGGGTCACTGTGGAA	1500
Qy	501	AlaThrArgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuLeuGly	520
Dd	1501	GCCACAGAGGCTGTATTGAAACACTCCGACGAGTATTCAACACAGGCTGCCCTTCCGA	1560
Qy	521	LeuSerIleAlaLysArgProLeuThrParGlnGluSerLeuGlnSerValLysAsnThr	540

Db	1561	CTTCCATCCGCAAGAGCGCTCTCTCGACACAGATCTTTGGCAAAAGTGTAAAAACACC	1520
Qy	541	ThrgInglngIuIeUlySaIaIleasnIleasnSerPheValGluCysGlyIleHis	560
Db	1621	ACTGAGCAAGAAATTCTGAAGCCATAAACATCAATTCTCTTGTGTAGATGGCATCAT	1680
Qy	561	LeuTyTngIngluSerThrSerLysSerAlaLeuSerGlnIupheGluAlaPhepheGln	580
Db	1681	TTATATCAAGAGATACATCAATCAATAGCCCTGAGCAGAATTTTGAAGCTTTCTTCAA	1740
Qy	581	GlyLysSerLeuTyTleIleasnSerGlyAsnIleProaspTyTleuPheaspPheGlu	600
Db	1741	GGTAAAGCTTATATATCAATCAATGAGGAAACATCCCGATTAATTGTGACTTCTTTGAA	1800
Qy	601	HisLeuProasnCysAlaSerAlaLeuaspPheIleLysLeuaspPheTyTglyAla	620
Db	1801	CATTGGCCCAATTGTGCAGTGTCTGTGACTTCATTAAACTGACTTTATGGGGAGCT	1860
Qy	621	MetalaserTrpGluLysAlaAlaGluaspThrGlyGlyIleHisMetGluAlaPro	640
Db	1861	ATGGCTTCATGGGAAAAGCGCTGCAGAAAGACACAGGTGCATCCATGGAAGAGCCCA	1920
Qy	641	GluThrTyTleProSerArgAlaValSerleuPheasnTrpLysGlnIupheArg	660
Db	1921	GAACCTACATTTCCACACAGGCTGTATCTTGTCTTCACTGAGAACAGAAATTACG	1980
Qy	661	ThrLeuGluValThrLeuAlaGaspPheSerLysLeuAsnLysGlnAspIleThrTyTleu	680
Db	1981	ACTCGAGAGTCACACCTCGGGATTTTCAGCAAGTTGAATAAACAGATATCACATATCTG	2040
Qy	681	GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVal	700
Db	2041	GGGAAAATATTCACCTCTGCCACAAACCTCAGGCTCAATTAAGATGTGCTGTGTG	2100
Qy	701	AlaGlySerLeuSerLeuValIleuSerThrCysLysAsnIleTySerLeuMetValGlu	720
Db	2101	GCTGGAAACCTCACTGTGGTCTCGACACTGTAAACATTATTCCTCATGTGTGGA	2160
Qy	721	AlaSerProLeuThrIleGluaspGluArgHisIleThrSerValThrAsnLeuLysThr	740
Db	2161	GGCAATCCCCCACCACATAGAAGATGAGAGGCACATCACAATCTGTAAACAACCTGAAACC	2220
Qy	741	LeuSerIleHisaspLeuGlnasnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly	760
Db	2221	TTGACTATTCATGACCTACAGAAATCAACGGCTGCGGGGTGCTGACGACAGCTTGGT	2280
Qy	761	AsnLeuLysAsnLeuThrTyTleuIleMetAspAsnIleLysMetAsnGluAlaPala	780
Db	2281	AACTTGAAGAACCTTTACAAAGCTCATTAATGATTAACATTAACATGAAGAAGATGCT	2340
Qy	781	IleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis	800
Db	2341	ATAAACTAGCTGAGGCTCGAAAACCTCGAAGAGAGTGTGTTATTTTCATTATACCCAC	2400
Qy	801	LeuSerAspIleGlyGluGlyMetaspTyTleValLysSerLeuSerSerGluProCys	820
Db	2401	TTGTCTGACATTTGAGAGGGAATGATTAATCATATGCTCAAGTCTGTCAAGTGAACCTGT	2460
Qy	821	AspLeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu	840
Db	2461	GACCTTGAAGAAATTCATTATATGCTCTGCTGTGCTGTGCAAAAGCATGAAAAATCTTA	2520
Qy	841	AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAspTyTleu	860
Db	2521	GCTCAGAACTTTCACAATTTGGTCAAACTGAGATTCTTGATTATTCAGAAAATTTACCTG	2580
Qy	861	GluLysaspGlyAsnGluAlaLeuHisGlyLeuIleAspArgMetAsnValLeuGlnGln	880
Db	2581	GAAAAAGATGGAATGAAAGCTTTTCATGAATCATGTGACAGAGATGAAGCTGTAAACAG	2640
Qy	881	LeuThrAlaLeuMetLeuProTrpGlyCysaspValGlnGlySerLeuSerSerLeuLeu	900
Db	2641	CTCACCGCATGATGTGCGCTGGGGCTGTGACGTGTCAAGGAGCGCTGACAGCTGTGTG	2700

QY 901 LYSNLSLEUGLNUVALPROGLNLEUVALYSLEUGLYLEUYSANTRPARGLEUTHR 920  
| | | | |  
DB 2701 AAMCATTTGGAGAGAGTCCACACACTGCTACACTGGTTGAAACCTGGAGACTACAC 2760  
QY 921 ASPTHRGLULIENRGLILEUGLYALAPHEPHEGLYLSASNPROLEUYSASNPHGLN 940  
| | | | |  
DB 2761 GATACAGAGATTAGAAATTTAGTGATTTTGGAAAGAACCTCTGAAACCTCCAG 2820  
QY 941 GINLEASNLEUALAELYSNARGVALSERSEASPGLYTRPLEUALAPHEMETGLYVAL 960  
| | | | |  
DB 2821 CAATTAAATTTGGCGGGAATCTCTGACACAGATGATGCGCTTCCTTCATAGGGTGTA 2880  
QY 961 PHEGLASNLEUYSGLNLEUVALPHEPHEASPHESETHRYSGLUPHELEUPROASP 980  
| | | | |  
DB 2881 TTTGACAACTTACAGCAATTAAGTGTGTTTGGACTTACACTTAAGAAATTTTACCTGAT 2940  
QY 981 PROALALEUVALARGYLSLEUSERGINVALLEUSERYLSLEUTHRPHLEUGINGLUALA 1000  
| | | | |  
DB 2941 CCAGCATFTAGTCAGAAACTTACCAAGTGTATCCAAAGTTACTTTCTGCAAGAAGCT 3000  
QY 1001 ARGLEUVALGLYTRPGINPHEASPAASPASPSEUSeVALLETHRGLYALAPHELYS 1020  
| | | | |  
DB 3001 AGCGTTGGTGGGGCAATTTGATGATGATGATCTCAGTGTATACAGTCTTTTAA 3060  
QY 1021 LEUVALTHRALA 1024  
| | | | |  
DB 3061 CTGATACCTGCT 3072

RESULT 4  
PCT-US00-29643-1  
; Sequence 1, Application PC/TUS0029643  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
; FILE REFERENCE: 07334-136W01  
; CURRENT APPLICATION NUMBER: PCT/US00/29643  
; CURRENT FILING DATE: 2000-10-26  
; PRIOR APPLICATION NUMBER: US 60/161,822  
; PRIOR FILING DATE: 1999-10-27  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 3133  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (36)...(3107)  
PCT-US00-29643-1

Alignment Scores:  
Pred. No.: 0 Length: 3133  
Score: 5459.00 Matches: 1024  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 1 Gaps: 0

US-09-697-089-2 (1-1024) x PCT-US00-29643-1 (1-3133)

QY 1 MetAsnPheILeLYsAspAsnSerArgAlaLeuILeGLIARMeTcJLmEThrValILle 20  
| | | | |  
DB 36 ATGAATTTTATTAAGACAAATAGCCGACCTTATTCCAAAGATGGGAATGACTGTTATA 95  
QY 21 LysGlnILeThrAspAspLeuPheValITrPasnValLeuAsnArgGLInLUValAsnILe 40  
| | | | |  
DB 96 AAGCAATATCAGAGATGACCTATTGTATGGAATGTTCTGAATCGCAAGAACGTAACATC 155  
QY 41 ILeCysCyGlnULysValGLInAspAlaIaIaArgGLYILeILeHISMeTILeULys 60  
| | | | |  
DB 156 ATTGCTCGAGAGAGTGGAGCAGATGCTGCTAGAGGATCATTCACATGATTTTGAA 215

QY 61 LysGLYSerCIuSerCysAsnLeuPheLeuLYsSerLeuLYsGLInTrPasnITrProLeu 80  
| | | | |  
DB 216 AAGGATTCAGAGTCCTGTATACCTCTTTCTTAATCCCTTAAGAGTGAAGACTATCCCTTA 275  
QY 81 PheGLIAspLeuAsnGLInSerLeuPheHISGLInThrSerGLInLUAspLeuAspASP 100  
| | | | |  
DB 276 TTTCAAGACTTGAATGAGCAAACTCTTTTTCATCAGACATCAGAAAGAGACTTGGAGAT 335  
QY 101 LeuAlAGlnAspLeuLYsAspLeuYrHISThrProSerPheLeuAsnPhETrProLeu 120  
| | | | |  
DB 336 TTGGCTCAGGATTTAAAGCACTTGATCAATACCCCACTTTTCTGAACTTTATCCCTT 395  
QY 121 GLYGLnAspILeAspILeIlePheAsnLeuLYsSerThrPheHrGLInUPROVALLeuTrp 140  
| | | | |  
DB 396 GGTGAAGATATATACATATATTTTAACTTGAAAGCACTTCAAGAACTGCTGCTGG 455  
QY 141 ArgLYsAspGLInHISHisArgValGLInLeuThrLeuAsnGLYLeuLeuGLnAla 160  
| | | | |  
DB 456 AGGAAGGACCAACACATACCGCGTGGAGCACTGACCTGAATGGCTCCTGCAAGCT 515  
QY 161 LeuGLnSerTrOCysILeILeGLInGLYGLnSerGLYLYsSerThrLeuLeuGLn 180  
| | | | |  
DB 516 CTTCAGAGCCCTGCATCATTTGAAGGGGAATCTGGCAAAAGGCCAAGTCCACTGCTGCAG 575  
QY 181 ArgILeAlaMeILeuthrPGIYSerGLYsCysLYsAlaLeuThrLYsPheLYsPheVal 200  
| | | | |  
DB 576 CGCATTCGCACTGCTGGGGCTCCGAAAGTGCAGAGCTGTGACCAAGTTCAATTCGTC 635  
QY 201 PhePheLeuArgLeuSerArgAlaGLInGLYLeuPheGLInThrLeuCysAspGLInLeu 220  
| | | | |  
DB 636 TTTCTTCCTCGTCTCAGAGGGCCAGGGGTGACTTTTGAACCTCTGTGATCAACTC 695  
QY 221 LeuAspILeProGLYThrILeArgLYsGLInThrPheMeAlaMeLeuLeuLYsLeuArg 240  
| | | | |  
DB 696 CTGGATATACCTGGCAATCAGAGAGCAGACATTCATGCGCCATGCTGTGAAGCTGCGG 755  
QY 241 GlnArgValLeuPheLeuLeuAspGLYTrAsnGLInPheLYsProGLInAsnCyProGLIn 260  
| | | | |  
DB 756 CAGAGGGTCTTTTCTTCTTGATGGCTACATGAATTAAGCCCAAGAACTCCAGAA 815  
QY 261 ILeGLnAlaLeuILeLYsGLnAsnHISArgPheLYsAsnMeValILeValThrThrThr 280  
| | | | |  
DB 816 ATCGAAGCCCTGATTAAGGAAACCAACCGCTTCAAGACATGGTGCATCGCACCACTACC 875  
QY 281 ThrGLnCYsLeuArgHISILeArgGLInPheGLYAlaLeuThrAlaLUValGLYAspMet 300  
| | | | |  
DB 876 ACTGAGTGCCTGAGCAGATACGCGAGTTGCTGCTGACCTGACGTGAGTGGCGGATATG 935  
QY 301 ThrGLAspSerAlaGLInAlaLeuILeArgGLnValLeuILeLYsGLInLeuAlaGLInGLY 320  
| | | | |  
DB 936 ACAGAAAGACAGCCCGACGCTCTCATCCGAAAGTCTGATCAAGAGCTTGTGAAAGC 995  
QY 321 LeuLeuLeuGLnILeGLInLYsSerArgCysLeuArgAsnLeuMeLYsThrProLeuPhe 340  
| | | | |  
DB 996 TTGTTCTCCCAATTCAGAAATCCAGGTGCTTGAGAAATCTCATGAAGACCCCTCTCTT 1055  
QY 341 ValValILeThrCYsAlaILeGLInMeTGLYGLnSerGLInPheHISerHISThrGLInThr 360  
| | | | |  
DB 1056 GTGGTATCATCTGTGCATCCAGATGGGTGAAGGATTTCCACTCCACACACAAACA 1115  
QY 361 ThrLeuPheHISThrPheTrAspLeuLeuILeGLInLYsAsnLYsHISLYsGLY 380  
| | | | |  
DB 1116 AGCGCTTTCATACCTCTTCTATGATCTGTTGATACAGAAAACCAACACCAATTAAGGT 1175  
QY 381 ValAlaAlaSerAspPheILeArgSerLeuAspHISCYsGLYAspLeuAlaLeuGLInGLY 400  
| | | | |  
DB 1176 GTGGCTGCAAGTCACTTATCTGAGACCTGAGCACTGTGGAGACTTACCTGTGGAGGT 1235  
QY 401 ValPheSerHISLYsPheAspPheGLInLeuGLnAspValSerSerYAlaSnGLInAspVal 420  
| | | | |  
DB 1236 GTGTTCTCCACAAAGTTTGAATTCGAACTGAGGATGTCTCAGCGCTGAATGAGATGTC 1295

OY	421	LeuLeuThrThrGlyLeuLeuCysLysTYrThrAlaGlnArgPheLeuProLysTYrLys	440
Db	1296	CTGGTGCACAACTGGGGCTCCCTCTAAATATACAGCTCAAGGTTCAAGCCAAAGATATAA	1355
OY	441	PhePheHisLysSerPheGlnGlnTYrThrAlaGlyArgArgLeuSerSerLeuLeuThr	460
Db	1356	TTCTTTCACAAGTCATTCACGAGGTACACGACGACGACGAAGCTCAGCAGTTATTATGCG	1415
OY	461	SerHisGluProGlnGlnValThrLysGlyAsnGlyTYrLeuGlnLysMetValSerIle	480
Db	1416	TCTCATGAGCCAGAGGAGGTGACCAAGGGGAATGCTTACTTCACAAAATGGTTTCCATT	1475
OY	481	SerAspIleThrSerThrTYrSerSerLeuLeuArgTYrThrCysGlySerSerValGlu	500
Db	1476	TCGGACATTTACATCCACTTTTACACCTGCTCCGTATCACCTGGGGCATCTGTGGAA	1535
OY	501	AlaThrArgAlaValMetLysHisLeuAlaAlaValTYrGlnHisGlyCysLeuLeuGly	520
Db	1536	GCCACCAAGGGCTGTATGAAGCACCTCCGACAGTGTATCAACACGGCTGCCCTTCCGA	1595
OY	521	LeuSerIleAlaLysArgProLeuThrParGlnGlnSerLeuGlnSerValLysAsnThr	540
Db	1596	CTTTCATCCGCAAGAGGCTCTCTGGAGACAGATCTTTGCCAAAGTGTAAACACCC	1655
OY	541	ThrGlnGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGlnCysGlyIleHis	560
Db	1656	ACTGACGAAGAAATTCGAAAGCCATTAACATCAATCTCTGTGTAGAGTGTGCATCAT	1715
OY	561	LeuTYrGlnGlnSerThrSerLysSerAlaLeuSerGlnGlnPheGlnAlaPheGln	580
Db	1716	TTATATCAAGAGATACATCCAAATCCAGCCCTGACCAAGAAATTGAAAGCTTCTTTAA	1775
OY	581	GlyLysSerLeuTYrIleAsnSerGlyAsnIleProAspTYrLeuPheAspPheGln	600
Db	1776	GGTAAAGCTTAATATATCACTCAGGGAACATCCCGATTACTTATTGACTCTTTGAA	1835
OY	601	HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTYrGlyAla	620
Db	1836	CATTTCGCCAATTGTGGCAAGTGCCTCTGCACTCATTAACCTGCACTTTATGGGGAGCT	1895
OY	621	MetIaSerTrpGluLysAlaIleGluAspThrGlyGlyIleHisMetGlnGlnAlaPro	640
Db	1896	ATGGCTTCATGGGAAAGGCTGCCAGAGACACAGGGGATCCACTGGGAAGAGGCCCA	1955
OY	641	GluThrTYrIleProSerArgAlaValSerLeuPhePheAsnTrpLysGlnGluPheArg	660
Db	1956	GAACCTACATCCCAACAGGGCTGATCTTTGTTCTTCACTCGAAGCAGGAATTCAGG	2015
OY	661	ThrLeuGlnValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTYrLeu	680
Db	2016	ACTCTGGAGGTCAACCTCCGGGATTTTCAGCAAGTTGAATACAGAGATATCCATATCTG	2075
OY	681	GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgGlyAlaGlyAla	700
Db	2076	GGGAAATATTTCACCTCTGCCACAGGCTCAGGCTCAATTAAGAGATGTCGTGCTG	2135
OY	701	AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTYrSerLeuMetValGlu	720
Db	2136	GCTGGAGGCTCACTTGGTCCCTCAGACCTGTAAACAATTTATCTCTCATGGTGGAA	2195
OY	721	AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr	740
Db	2196	GCCAGTCCCTCCACCATTAAGAAGATGAGAGGCACATCACTCTGTAAACAACTGTAAACC	2255
OY	741	LeuSerIleHisAspLeuGlnHisGlnArgLeuProGlyGlyLeuThrAspSerLeuGly	760
Db	2256	TTTAGTATCATGCACTACAGAAATCAACGGCTGCCGGGGTGTGACTACAGCTTTGGGT	2315
OY	761	AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGlnLysPheAla	780
Db	2316	AACTTGAAGAACTTACAAAGCTCATTAATGATTAACATTAAGATGAATGAAGAATGCT	2375
OY	781	IleLysLeuAlaGlnGlyLeuLysAsnLeuLysMetCysLeuPheHisLeuThrHis	800

Db	2376	ATPAAACTAGCTGAAGGCCCTGAAAAACCTGAGAGAGATGTGTTATTTCATTTCAGCCAC	2435
Qy	801	LeuSerAspIleGlyIugIyMeLaspYrIleValLysSerLeuSerSerGluProCys	820
Db	2436	TTTGCTGCACATTGGAGAGGGAATGATTCATACATAGTCAAGTCTGTCTCAAGGAACCGTGT	2495
Qy	821	AspLeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu	840
Db	2496	GACCTTGAGAAATTCATTAGTCTCTGCTGCTGTGTCTGCAAAAGCAGTGAATACTCTA	2555
Qy	841	AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeu	860
Db	2556	GCTAGAACTCTTCACAAATTTGGTCAACACGAGCATCTTGATTATTCAGAAAATTACCTG	2615
Qy	861	GluLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGln	880
Db	2616	GAATAAGTGAATGAAATGAACTCTTCATGAACATGATGACAGATGACGCTGTACAAAG	2675
Qy	881	LeuThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerLeuSerSerLeuLeu	900
Db	2676	CTCACCGCAGTACGATGTCCTCGGCGGTGAGCTGCAAGCAGCAGCCTGAGCCTGTGG	2735
Qy	901	LysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrArgLeuThr	920
Db	2736	AAACATTTGGAGGAGGTCGCCAACACGTCACACTTGGGTTAAAAAATGGGAGACTCACA	2795
Qy	921	AspThrGluIleArgIleLeuGlyAlaIlePheGlyLysAsnProLeuLysAsnPhenGln	940
Db	2796	GATACACAGATTAGACATTTTAGCTGCATTTTGGAAAAACCCCTCTGAAAAACTCTCAG	2855
Qy	941	GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrLeuAlaPheMetGlyVal	960
Db	2856	CAGTTGAATTTGGCGGGAATCGNGAGACAGATGATGATGAGCTTGCTCATGGGTGTA	2915
Qy	961	PheGluAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuProasp	980
Db	2916	TTTGGAATCTTAAAGCAATTAGTGTGTTTGGACTTTAGTACAAAGAAATTTCTTACCTGAT	2975
Qy	981	ProAlaLeuValAlaGlyLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGluAla	1000
Db	2976	CCAGCATTTAGTCAGAAAACTTAGCCCAAGTATTCACAACTTACTTTCTCGACAGAGCT	3035
Qy	1001	ArgLeuValGlyTyrGlnPheAspAspAspAspLeuSerValIleThrGlyAlaPheLys	1020
Db	3036	AGGCTGTGGTGCGCAATTGATGATGATGATCAGTGTATTATACAGGTGCTTTTAAA	3095
Qy	1021	LeuValThrAla 1024	
Db	3096	CTAGTAACCTGCT 3107	
RESULT 5			
US-09-697-089-1			
Sequence 1, Application US/09697089			
GENERAL INFORMATION:			
APPLICANT: Berlin, John			
APPLICANT: Robison, Keith E.			
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED			
TITLE OR INVENTION: PROTEIN FAMILY AND USES THEREOF			
FILE REFERENCE: 07334-136001			
CURRENT APPLICATION NUMBER: US/09/697,089			
CURRENT FILING DATE: 2000-10-26			
PRIOR APPLICATION NUMBER: US 60/161,822			
PRIOR FILING DATE: 1999-10-27			
NUMBER OF SEQ. ID NOS: 12			
SOFTWARE: FastSeq for Windows Version 4.0			
SEQ ID NO 1			
LENGTH: 3133			
TYPE: DNA			
ORGANISM: Homo sapiens			
FEATURE:			
NAME/KEY: CDS			
LOCATION: (36)...(3107)			

## US-09-697-089-1

## Alignment Scores:

Pred. No.:	0	Length:	3133
Score:	5459.00	Matches:	1024
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	27	Gaps:	0

US-09-697-089-2 (1-1024) x US-09-697-089-1 (1-3133)

Qy 1 Methanpheielysaspasnserrarglaleuileglnarqmetglywethervalile 20  
Db ATGAATTCATAAAGACAAATAGCCGAGCCCTTATTCAAAGAAATGGAAATGACTGTANA 95  
Qy 21 lysglnliethrpsaspheuphevaltrpnsvalileuasnarqgluclvalanslle 40  
Db AAGCAAAATCACAGATGACCTATTGTATGCAATGTTCTGAATCGCAAGAACTAAACATC 155  
Qy 41 ilecyscysglulysvalgluglnaspalaiaargglyllelhismetlleulelys 60  
Db ATTCTCTCGAGAAAGTGGAGCAGATGCTGCTAGAGGGATATTCACTATGATTTTGANA 215  
Qy 61 lysglsyserglusercysasnleupheuleylserserleuylsglutrpasntyrproleu 80  
Db AAGGTTTCAGAGTCCGTATACCTCTTTCTTAAATCCCTTAAAGAGTGGAACTATCTCA 275  
Qy 81 pheglnaspheuasnglylinserserleuphehisglnthrsergluglylaspheuaspsp 100  
Db TTTCGGAGCTTGAAATGGAAGCAAGTCTTTTTCATCAGACATCAGAGAGGAGACTTGAGCAT 335  
Qy 101 leuallaglnaspheuleylaspheulthrshthrproserpheleuasnpheulthrproleu 120  
Db TTGGCTCAGGATTTAAAGACTTGTACATACCCATCTTTTCTTAACTTTATCCCTT 395  
Qy 121 glylunaspileasepiellepheuasnleuylserserthrphethrgluprovalleuutr 140  
Db GGTGAAGATATTGACATATATTTTAACTTGAAAGCACCTTCACAGAACTCTGCTGG 455  
Qy 141 arglyasarpghlnhisshisargvalgluglnleuthrleuasnglyleuleucnlaia 160  
Db AGGAAGGACCAACACACATCCGCTGAGACAGCTGACCTGMAAGGCTCTCTGACGCT 515  
Qy 161 leuglnserprocysillelelgluglulyserserlylsglylvserserthreuleugln 180  
Db CTTGAGACCCCTGCATATGTAAGGGAATCTGGCAAGGCAAGTCCACTGTGCTGAG 575  
Qy 181 argilealametleuutrpilyserserlylscyslvsalaleuthrlyspheulspheval 200  
Db CGCATGCGCATGCTCTGGGGCTCCGGAAAGTGCAAGGCTGTGACCAAGTTCAAATTCGT 635  
Qy 201 phepheleuasngleserarglalnlglyleupheugluthrleucysaspqlnleu 220  
Db TTCTTCCCTCCCTCAGAGGGCCAGGGGTGACTTTTGAAGCCCTGTGATCAACTC 695  
Qy 221 leuaspiileploglythrilearglysglnthrphemetlaleuthleuleuylsleuarg 240  
Db CTGATATACCTGGCACATGCGAAGGACAGACATTCATGGCCATCTGTGAAGTGGGG 755  
Qy 241 glinarvalleupheuleuaspslytyrasnglupheylsproglnasncysproglu 260  
Db CAGAGGGTCTTTTCTCTTGTATGCGTACAAATGAATCAAGCCCAAGACCTGCCAGAA 815  
Qy 261 lleglualaleuileylsglunasnhisarqphelysasmetvalillevalthrthrthr 280  
Db ATCGAAGCCCTGATAAAGAAACCAACCGCTTCAAGAACATGTCATGCTGCACCACTACC 875  
Qy 281 thrglucysleuarghnlislarqglinphesglualaleuthralaglivalglyspmet 300  
Db ACTGATGCTCTGAGGCAATACGGCAGATTTGGTGGCTGTACTGCTGAGGTTGGGGATATNG 935  
Qy 301 thrgluaspserralaglnalaleuilearqgluvalleuileylsgluleuualaglucl 320

Db 936 ACAGAAAGACAGGCGCCAGGCTCTCATCCGAAAGTGTCTATCAGAGGCTCTGAGGCC 995  
Qy 321 leuleuleuglnlileglnlyserrargcysleuargasnleumellythrproleuphe 340  
Db TTTTGTGCTCCAAATTCAGAAATCCAGGTCTTGAGGAATCTCATGAAGACCCCTCTT 1055  
Qy 341 valvaliilethrasyalalelelmetgluglusergluphehisserhistrghlnthr 360  
Db GTGGTCATCTTGTGCAATCCAGATGGGTGAAAGTGAATTCACCTCTCACACAAACA 1115  
Qy 361 thrleuphehisthrphetyraspheuleuileglnlysasnlyshislysgly 380  
Db ACGTGTTCATACCTTGTATGATCTGTGATACAGAAACAAACAAACATTAAGGT 1175  
Qy 381 valalaialaseraspheulleargserleuasprhisqysglylaspheualaileuclugly 400  
Db GTGGTGCAGAGTGTCTTCGAGGCTTGAGCCACACCTGTGAGACCTTACTCTGGAGGCT 1235  
Qy 401 valpheSerHislyspheasphegluleuglnaspvaliserSerValasnqluaspa 420  
Db GTGTTCTCCACAAAGTTTATTTGCACTGCGAGATGTCTCAGGCTGATAGCATGTC 1295  
Qy 421 leuleuthrthrghlyleuleucyslystytrhralaglnarqphelysbrolysstylys 440  
Db CTGCTGACAACTGGGCTCCTGTGAAATATACAGCTCAAAAGTTCAGGCCAAAGTATAA 1355  
Qy 441 phephehislysserphesingluuylthrallaglylharqgluSerSerleuuthr 460  
Db TTCTTTCACAAATGATTCACAGAGTACACAGACAGCAAGCACTGACAGTTATTTGAGC 1415  
Qy 461 serhisgluprogluglulvalthrlysglylansglytyrleuglnlysmetvaliserile 480  
Db TTTCTATGAGCCAGAGAGGTGACCAAGGGGAATGCTTACTTCAGAAATGCTTCCATT 1475  
Qy 481 seraspilierhserthrtyrserSerleuuarqytrthrCysglyserSerValglu 500  
Db TCGGACATTAACATCCACTATAGACGCTGCTCGGTACACCTGGGGTCATCTGGANA 1535  
Qy 501 alathrarglialailemetlyshisleuilaialvaltylghlnhisglysleuleugly 520  
Db GCCACAGGGCTGTATATGAAGCACCTCGAGAGGTATCAACACGGCTCTTCGGGA 1595  
Qy 521 leuserllealalyasrproleuthrparqngluserleuglnserValiylasanthr 540  
Db CTTTCCATCCGCAAGAGGCTCTCTGGAGACAGAAATCTTTCANAGTGTGAAAAACACC 1655  
Qy 541 thrghluginluilleuleylsalalleasnilleasnserphevalglucysglyllehis 560  
Db ACTGAGCAAGAAATCTGAAAGCCATAAACATCAATTCCTTGTAGAGTGTGCATCCAT 1715  
Qy 561 leutyrgluginluserthrserlysserlaleuSerGlnlupheglualaphhegln 580  
Db TTTTATCAAGAGATACATCCAAATCAGCCCTGAGCCAAAGAAATTTGAACCTTCTTTCA 1775  
Qy 581 glylysserleuthrilleasnsergluasnlleproaspyrleupheasphephecgu 600  
Db GGTAAAGCTTATATATCACTCAGGAGACATCCCGATTAATTATTGACTTCTTTGAA 1835  
Qy 601 hisleuproasnqysalaserlaleuasppheilleylsleuasppheutrglylalyala 620  
Db CATTGGCCCAATGTGCAAGTGTCTGTGACTTCATTAACGTGACTTTATGAGGGAGGT 1895  
Qy 621 metlasertrpglulysalialaaglsapnrhrglylilehismetglulualapro 640  
Db ATGGCTTCATGGGAAAGGCTGCAGAAAGACACAGGTGCAATCACAATGGAAGAGCCCCA 1955  
Qy 641 giuthrtyrileproserarglavalserleupheaspheasrtrpdyglinluphearg 660  
Db GAAACCTACATTCACAGCAGGGCTGTATCTTGTCTTCACTGGAAGCAGGAATTCAGG 2015  
Qy 661 thrleuglulvalthrleuargaspheSerlyslasnllyglinspiilethrtyrleu 680

Dh 2016 ACTCTGGAGGTACACACTCCGGGATTTTCAGCAAGTTGAATAAGCAATATCATATCTGTG 2075  
Qy 681 G1YLSIIEPHESESERAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVal 700  
Dh 2076 GGGAAATATTCAGCTCTGCCACAAAGCTCAGGCTGCAGAAATAAGAGATGTGGTGTG 2135  
Qy 701 AlAglSerLeuSerLeuValLeuSerThrCysLysAsnIleLysSerLeuMetValGlu 720  
Dh 2136 GCTGGAAGCCTCAGTTGGTCTCCAGCACCTGTAAAGACATTTATTCATGGTGGAA 2195  
Qy 721 AlAserProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr 740  
Dh 2196 GCCAGTCCCTCCACCATAGAAGATGAGAGCCACATCATCTGTGAACAACTGAAAAAC 2255  
Qy 741 LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly 760  
Dh 2256 TTGAGTATCTAGACCTACAGAAATCAACGCGCTGCCGGTGGTCTGACACGACCTGGGT 2315  
Qy 761 AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluAspAla 780  
Dh 2316 AACTTGAAGAACCTTACAAACCTCATATATGATTAACATTAAGATGAAGAAAGATGCT 2375  
Qy 781 IleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis 800  
Dh 2376 ATAAACTAGCTGAAGGCGCTGAAAAACCTGAAGAGATGTATTATTCATTTGACCCAC 2435  
Qy 801 LeuSerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCys 820  
Dh 2436 TTGTCTGACATTTGAGAGAGGAAATGATTAATGATCAAGTCTGTCTCAAGTGAACCCGT 2495  
Qy 821 AspLeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu 840  
Dh 2496 GACCTTGAAGAAATTCATTAATGATCTCCGCTGCTGTCTGCAAAATGACAGTGAATCCTA 2555  
Qy 841 AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeu 860  
Dh 2556 GCTCAGATCTTCACAAATTTGGTCAAACTGAGCACTTCTTGATTTATCGAAAAATTAACCTG 2615  
Qy 861 GluLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGln 880  
Dh 2616 GAAAAAGATGGAATGAAGCCTTCATGAATGATCGACAGATGAAGAGTCTGTGAACAG 2675  
Qy 881 LeuThrAlaLeuMetLeuProTyrPglyCysAspValGlnGlySerLeuSerSerLeuLeu 900  
Dh 2676 CTCACCCGACATGATGCTGCCCTGGGGCTGTGACGTGCAAGGACAGCTGACAGCTCTTG 2735  
Qy 901 LysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrArgLeuThr 920  
Dh 2736 AAACATTTGGAGAGGCTCCCAACACTGCTCAAGCTTGGGTGAAAAAACTGAGACTCACA 2795  
Qy 921 AspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln 940  
Dh 2796 GATACAGAGATTAAGAAATTTAGTGTCATTTTGGAAAGAACCTCTGAAAAAAGCTCCAG 2855  
Qy 941 GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrPleuAlaPheMetGlyVal 960  
Dh 2856 CAGTTGAATTTGGGGGAAAACTGTGTGAGCATGTGATGATGCTTGGCTTCATGGGTGTA 2915  
Qy 961 PheGlnAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGlnPheLeuProAsp 980  
Dh 2916 TTTAGAAATCTTAAGCAATTAATGTCTTTTGTACTTTTACTTAAGAAATTTCTACCTGAT 2975  
Qy 981 ProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGluAla 1000  
Dh 2976 CCACCATTAAGCAAAAACTTAAGCAAGTGTATTCACCAAGTTAACTTTCTCCAGAAAGCT 3035  
Qy 1001 ArgLeuValGlyTyrPglInPheAspAspAspAspLeuSerValIleThrGlyAlaPheLys 1020  
Dh 3036 AGGCTTCTTGGGTGCAATTTGATGATGATGATCATCTGATTATTACAGGTCTTTTAA 3095  
Qy 1021 LeuValThrAla 1024  
Dh 3096 CTAGTAAGTCT 3107

RESULT 6  
US-09-841-739-1  
: Sequence 1, Application US/09841739  
: GENERAL INFORMATION:  
: APPLICANT: Bertin, John  
: TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES TH  
: FILE REFERENCE: 07334-32901  
: CURRENT APPLICATION NUMBER: US 09/841,739  
: PRIORITY FILING DATE: 2001-08-29  
: PRIOR APPLICATION NUMBER: US 09/697,089  
: PRIOR FILING DATE: 2000-10-26  
: PRIOR APPLICATION NUMBER: US 60/161,822  
: PRIOR FILING DATE: 1999-10-27  
: NUMBER OF SEQ ID NOS: 16  
: SOFTWARE: FastSeq for Windows Version 4.0  
: SEQ ID NO 1  
: LENGTH: 3133  
: TYPE: DNA  
: ORGANISM: Homo sapiens  
: FEATURE:  
: NAME/KEY: CDS  
: LOCATION: (36)..(3107)  
US-09-841-739-1  
Alignment Scores:  
Pred. No.: 0 Length: 3133  
Score: 5459.00 Matches: 1024  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
US-09-697-089-2 (1-1024) x US-09-841-739-1 (1-3133)  
Qy 1 MetAsnPheIleLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20  
Dh 36 ATGATTTTCATAAAGAGCAATAGCCGAGCCCTTATTCAAAAGAAAGGGAATGACTGTATA 95  
Qy 21 LysGlnIleThrAspAspLeuPheValIrrAsnValLeuAsnArgGluGluValAsnIle 40  
Dh 96 AAGCAATACAGATGACCTATTTGTATGAGATGTCTGAATCCGGAAGAAATGAACATC 155  
Qy 41 IleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60  
Dh 156 ATTTGCTCGAGGAAGGTGAGCAGAGATGCTGCTAGAGGAGATCATCATGATTTTGAA 215  
Qy 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTyrPAsnTyrProLeu 80  
Dh 216 AAGGTTTCAGAGTCTCCTGTAACCTCTTCTTAAATCCCTTAAGAGAGTGAATATCTCTA 275  
Qy 81 PheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAspAsp 100  
Dh 276 TTTCAAGACTTGAATGACAAAGCTCTTTTCATAGACATAGAAAGAGACTTGAGACAT 335  
Qy 101 LeuAlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTyrProLeu 120  
Dh 336 TTGGCTCAGATTTAAAGACTTGTACCATACCCCATCTTTCTGAACTTTATCCCTT 395  
Qy 121 GlyLysAspIleAspIleIlePheAsnLeuLysSerThrPheThrGluProValLeuThr 140  
Dh 396 GGTGAAGATTTGACATTAATTTTAACCTGAAAAAGCACTTCACAGAACCTGTCTGTG 455  
Qy 141 ArgLysAspGlnHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAla 160  
Dh 456 AGGAAGGACCAACACCATACCGGCTGAGAGCACTGCACTGAAATGGCTCTCAGAGCT 515  
Qy 161 LeuGlnSerProCysIleIleGluGlyGluSerGlyLysGlyLysSerThrLeuLeuGln 180  
Dh 516 CTTCAGAGCCCTGCATCATTTGAAGGGGAATCTGGCAAAAGCAAGTCCACTCTGCTGAG 575  
Qy 181 ArgIleAlaMetLeuTyrPglySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 200

Dh 576 CGCATGGCATGCTCTGGGGCTCCGGAAAGTCGAAGGCTCTGACCAGTTCAAAATTCGTC 635  
Qy PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuCysAspGlnLeu 220  
Dh TTTCTTCCTCCCTCAGCAGGGGCCAGGGTACTTTTGAAACCTCTGTGATCAACTC 695  
Qy 221 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 240  
Dh CTGATATACCTGGGCAAAATCAGGAAGCAGACATTCATGGCCATGCTCTGAAGCTGGGG 755  
Qy 241 GlnArgValIleuPheLeuLeuAspGlyTyrrasnGluPheLysProGlnAsnProGlu 260  
Dh 756 CAGAGGGTCTTTCTCTGTGATGGCTACATGATTCAGGCCCAACCTGGCCCAAGAA 815  
Qy 261 IleGluAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValThrThrThr 280  
Dh 816 ATCGAAGCCCTGATTAAGAAACACCGCTTCAGAAACATGATGTCATGCCACTACC 875  
Qy 281 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 300  
Dh 876 ACTGAGTCCCTGAGGCACATACGGCAGTTGTGTCCTGACTGCTGAGAGTGGGGATATG 935  
Qy 301 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 320  
Dh 936 ACAGAAACAGCGCCAGCGCTCTCATCCGAGAAGCTGTATCAAGACCTGTCTGAAGGC 995  
Qy 321 LeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe 340  
Dh 996 TTGTGTCCCAAAATTCAGAAATCCAGGTGCTGAGGAATCTCATGAACACCCCTCTCTTT 1055  
Qy 341 ValValIleThrCysAlaIleGlnMetGlyLysSerGluPheHisSerHisThrGlnThr 360  
Dh 1056 GTGGTCATCACTTGTCGCAATCCAGATGGGTGAAGTGAAGTTCCTCCTCACACCAAA 1115  
Qy 361 ThrLeuPheHisThrPheTyrrAspLeuLeuIleGlnLysAsnLysHisLysHisLysGly 380  
Dh 1116 ACGGTGTCCATACCTCTATGATCTGTTGATACGAAACAAACACAAACATTAAGGT 1175  
Qy 381 ValAlaAlaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGlnGly 400  
Dh 1176 GTGGCTCAAGTCACTTCAATTCGGAGCCTGGAACCACTGTGAGACCTGTGAGAGGT 1235  
Qy 401 ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal 420  
Dh 1236 GTGTTCTCCCAAGTTGATTGCGAATGCGAAGATGTCTCAGCGTAAATGAGGATGTC 1295  
Qy 421 LeuLeuThrThrGlyLeuLeuCysLysTyrrThrAlaGlnArgPheLysProLysTyrrLys 440  
Dh 1296 CTGGTGAACAAGTGGCTCTCTGTAATATATACAGCTCAAAAGTTCAAGCCAAAGTATAA 1355  
Qy 441 PhePheHisLysSerPheGlnGluTyrrThrAlaGlyArgLeuSerSerLeuLeuThr 460  
Dh 1356 TTTCTTTTCAAAAGTCAATTCAGAGATACACAGACAGCAACACTCAGAGTTTATTTGACG 1415  
Qy 461 SerHisGluProGlnGluValThrLysGlnLysAsnGlyTyrrLeuGlnLysMetValSerIle 480  
Dh 1416 TCTCATGAGCCAGAGAGGATACCAAGGGGATGTTACTTGCGAAGAAATGGTTCCATT 1475  
Qy 481 SerAspIleThrSerThrTyrrSerSerLeuLeuArgTyrrThrCysGlySerSerValGlu 500  
Dh 1476 TCGGACATTTACATCCATTAAGCAGCTGCTCGGTACACTGTGGGTCAATCGTGGAA 1535  
Qy 501 AlaThrArgAlaValMetLysHisLeuAlaAlaValTyrrGlnHisGlyCysLeuLeuGly 520  
Dh 1536 GCCACACAGGGCTGTATTAACACCTCGCACAGATGTAACAACGGGTGCTTCGGA 1595  
Qy 521 LeuSerIleAlaLysArgProLeuTyrrArgGlnLysSerLeuGlnSerValLysAsnThr 540  
Dh 1596 CTTTCATCGCCCAAGAGGCCCTCTCGGAGACAGGAATTTTGCAAAAGTGAATAAACACC 1655  
Qy 541 ThrGlnGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHis 560  
Dh 1656 ACTGAGCAAGAAATTTCTGAAGCCATTAACATCAATTCCTTTGTAGAGTGGCATTCAT 1715

Qy 561 LeuTyrrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePheGln 580  
Dh 1716 TTATATCAAGAGATACATCCAAATCACCCTGAGCCAAAGATTTGAAAGCTTTCTTTAA 1775  
Qy 581 GlyLysSerLeuTyrrIleAsnSerGlyAsnIleProAspTyrrLeuPheAspPheGlu 600  
Dh 1776 GGTAAAGACTTATATATCACTACAGGAACATCCCCGATTTACTTATTTGACTTCTTTGAA 1835  
Qy 601 HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrrGlyAla 620  
Dh 1836 CATTTGGCCCAATTTGCAAGTCTCTGACATTAACATGCACTTATATAGGGGAGCT 1895  
Qy 621 MetalSerTrpGluLysAlaAlaGluAspThrGlyGlyIleHisMetGlnGluLapro 640  
Dh 1896 ATGGCTTATGGGAAAGGCTCCAGAAACACAGCTGCAATCCATGCAATGCAAGAGCCCA 1955  
Qy 641 GluThrTyrrIleProSerArgAlaValSerLeuPheAsnTrpLysGlnGluPheArg 660  
Dh 1956 GAAACCTACATTTCCAGCAGGCGCTATCTTTGTTCTTCAACTGGAAGAGGAATTCAGG 2015  
Qy 661 ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrrLeu 680  
Dh 2016 ACTGTGAGAGTCCACACTCCGGGATTTCAAGTGAATTAAGCAAGATATCATATCTCG 2075  
Qy 681 GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVal 700  
Dh 2076 GGGAAATATTTACGCTGTGCCCAAGCTCAGGCTGCAAAATTAAGATATGCTGTGTGTG 2135  
Qy 701 AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrrSerLeuMetValGlu 720  
Dh 2136 GCTGGAACCTCATGTTGTGCTCTCGACACCTGTAAAGCATTTATTTCTCATGTGGAA 2195  
Qy 721 AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr 740  
Dh 2196 GCCAGTCCCTCACCATGTGAAGATGAGAGCACATCATCTGTGAACAACTGAAACCC 2255  
Qy 741 LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly 760  
Dh 2256 TTGATATTTCAAGACTTCACAGATTCACGCGTCCGGGTGTGTACGTACACGCTTGGGT 2315  
Qy 761 AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAla 780  
Dh 2316 AACTTGAAGAACCTTACCAAGCTCATATGATATACATTAAGATGAATGAAGAAATGCT 2375  
Qy 781 IleLysLeuAlaGlnGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis 800  
Dh 2376 ATAAACTAAGCTGAAGGCGCTGAAAAACCTGAAGAAGATGTGTTATTTCAATTTGACCCAC 2435  
Qy 801 LeuSerAspIleGlyGluGlyMetAspTyrrIleValLysSerLeuSerSerGluProCys 820  
Dh 2436 TTGCTGTCAATTTGGAGAGGATGATTAATAGTCAAGATGCTCTGTCAAGTGAACCCCTGT 2495  
Qy 821 AspLeuGlnGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu 840  
Dh 2496 GACCTTGAAGAAATTCATTTAGTCTCTGCTGCTGTGTGCAAAATGCGTGAATAATCTTA 2555  
Qy 841 AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrrLeu 860  
Dh 2556 GCTCGAATCTTCAACAATTTGGTCAAACTGAAGCATTTCTGATTTATCGAAATAATACCTG 2615  
Qy 861 GluLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGlnGln 880  
Dh 2616 GAAAAAAGTGAAGAAATGAAGCTTTCATATACGTACGACAGATGAAGAGTCTGAAACAG 2675  
Qy 881 LeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeu 900  
Dh 2676 CTCACCGACATGATGCTCCCTGGGGCTGTGACGCGCAAGCAGCCTGACAGCCTGTGTG 2735  
Qy 901 LysHisLeuGlnGluValProGlnLeuValLysLeuGlnLysLeuLysAsnTrpArgLeuThr 920  
Dh 2736 AAACATTTGAGAGAGGTCCCAACACTGTCGTAAGCTTGTTGTAATAAATGTGAGACTCA 2795



Oy	921	AshtRGtGLEatgLEleuGlyValApehPheGlyLVasAspProLeuLysAspNheGln	940
Db	2796	GATACAGAGATTAGCAATTTTAGTGCAATTTTTGGAAAGAACCCCTGTGAANAACCTTCAG	2855
Oy	941	GlnLeuAsnLeuAlaGlyAsaAspValSerSerAspGlyTrpLeuAlaPheMetGlyVal	960
Db	2856	CAGTTGAAATTTGGGGGGAATTCGTGTGACAGAGATGATGAGCTGCCCTTCATGGGTGA	2915
Oy	961	PheGlnAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGlnPheLeuProAsp	980
Db	2916	TTTGAGATCTTAAGCAATTAGTGCTTTTGGACTTAGTACTTAAGCAATTTTCACTGAT	2975
Oy	981	ProAlaLeuValAArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnAla	1000
Db	2976	CCACGATTAGCACAAAACTTACGCCAAGTGTATCCAACTTAACCTTTCTGCAGAAACACT	3035
Oy	1001	ArgLeuValGlyTrpGlnPheAspAspAspLeuSerValIleThrGlyAlaPheLys	1020
Db	3036	AGGCTGTGGTGCGCAATTTGATGATGATGATGATCTCAGCTTATTACAGAGCTCTTTAA	3095
Oy	1021	LeuValThrAla	1024
Db	3096	CTAGTAACCTGCT	3107



Qy	461	SeHisgluProGluValThrLySGlyasnGlyTyrLeuGlnLysMetValSerLe	480
Db	1381	TCTATAGGCAAGGAGGGGACCAAGGGGAATGGTTACTTGCACAAAATGGTTCCATT	1440
Qy	481	SerAspLleHisSerThrTyrSerSerLeuAsnArgTyrThrCysGlySerSerValGlu	500
Db	1441	TGCGAACATTACATCCACTTATACAGCCCTGCTCCGGTACACCTGTGGGTCAATCTGTGGA	1500
Qy	501	AlaThrArgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuLeuGly	520
Db	1501	GCCACACGAGGCGCTGTATGAAGCACCTCGCAGCAGTGATATCAACACAGCGCTGCTCGGA	1560
Qy	521	LeuSerLleAlaLysArgProLeuThrPargGlnGlnSerLeuGlnSerValLysAsnThr	540
Db	1561	CTTTTCCATCCCAAGAGCGCTCTGTGAAACAGAGATCTTTGCAAAAGTGAATAAACACC	1620
Qy	541	ThrGlnGlnLleLleuLysAlaIleAsnIleAsnSerPheValGlyCysGlyIleHis	560
Db	1621	ACTGACGAAGAAATTCGAAGAGCCATTAACATCATCTCTTGTGTAGATGTGGCATCAT	1680
Qy	561	LeuTyrGlnGlnSerThrSerLysSerAlaLeuSerGlnGluPheGlnAlaPheGln	580
Db	1681	TTTATATCAAGAGTACATCCAAATCAGCCCTGACGCAAGAAATTTGAAGCTTTCTTCAA	1740
Qy	581	GlyLysSerLeuTyrLleAsnSerGlyAsnIleProAspTyrLeuPheAspPheGlu	600
Db	1741	GGTAAAGCTTATATATCACTAGGAAACATCCCGATACTTATTTGTGACTCTCTTGAA	1800
Qy	601	HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyIleAla	620
Db	1801	CATTGGCCCAATTGTGCAAGTGCCTCGGACTCATTTAAACCTGACTTTATGTGGGGAGCT	1860
Qy	621	MetLaserTrpPoliLysAlaAlaGluAspThrGlyGlyIleHisMetGlnAlaPro	640
Db	1861	ATGGCTTCATGGAAGAAAGCGTGCAGAGACACAGGTGAATCCACATGGAAGAGCCCA	1920
Qy	641	GluThrTyrLleProSerArgAlaValSerLeuPheAsnTrpLysGlnGluPheArg	660
Db	1921	GAACCTACATCCCGACAGCGGCTGTATCTTTGTTCTTCACTGGAACAGAAATTCAG	1980
Qy	661	ThrLeuGlnValThrLeuArgAspPheSerLysLeuAsnLysGlnAspLleThrTyrLeu	680
Db	1981	ACCTGTGAGGTACACTCCGGGATTCACCAAGTTGAATACCAAGATACAGATATCTGTG	2040
Qy	681	GlyLysLlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVal	700
Db	2041	GCGAAATATTCAGCTCTGCCACAAACCCTCAGCTGCAAATTAAGAGATGTGCTGTGTG	2100
Qy	701	AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnLleTyrSerLeuMetValGlu	720
Db	2101	GCTGGAGGCTCAGTTGGTCCCTCAGACACTGTAGAACAATTTATCTCATGTGTGAA	2160
Qy	721	AlaSerProLeuThrLleGluAspGluArgHisIleIleIleIleIleIleIleIleIleIle	740
Db	2161	GCGAGTCCCTCCACCTAGAAATGAGAGGCGACATCTGTATACAAACCTGAANAACC	2220
Qy	741	LeuSerLleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly	760
Db	2221	TTTGAGTATTCATGACTACAGAAATCAACGCGTCCGGGGGTCGTACTGACAGCTTGAGT	2280
Qy	761	AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGlnGluAspAla	780
Db	2281	AACCTGGAAGAACTTACAAAGGCTCATTAATGATTAACATTAAGATTAATGAAGAAAGTCT	2340
Qy	781	IleLysLeuAlaGlnGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis	800
Db	2341	ATAAACTAGCTGAAGCGCTGAAAAACCTCGAAGAGATGTGTTATTCATTGACCCAC	2400
Qy	801	LeuSerAspLleGlyGlnGlyMetAspTyrIleValLysSerLeuSerSerGluProCys	820
Db	2401	TTTGCTGTACATTTGGAAGGAATGAGATTTCATATGTCAGGTCTGTGTCAATGAAGACCTGT	2460

QY	821	AspLeuGIUGluIUGInLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu	840
Db	2461	GACCTTGAAGAAATTCATTAGCTCCCTGCTGCTTGTGCAAAAGCAGTGAATATCCTA	2520
QY	841	AlaGInAsnLeuHISAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeu	860
Db	2521	GCTCGAATCTTTCACAAATTGGTCCAAACTGAGCATTTCTTGATTATCAGAAAATTACCTG	2580
QY	861	GluLysAspGlyAsnGluAlaLeuHISGluIleLeuAspArgMetAsnValLeuGluGln	880
Db	2581	GA AAAAGATGGAATTAAGAGCTCTTCATGAACCTGATGCAGAGATGAAGCTGTAGAACAG	2640
QY	881	LeuThrAlaLeuMetLeuProTrrpGlyCysAspValGlnGlySerLeuSerSerLeuLeu	900
Db	2641	CTCACCGCATCGATGCGCCCTGGGGCTGTGAGCTGCAAGCAGCCTGAGCAGCCTGTGG	2700
QY	901	LysHISLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTrrpArgLeuThr	920
Db	2701	AAACCTTTGGAGGAGGTCACCAACTGCTACACTGGGTTGAAAACTGGAGACTACA	2760
QY	921	AspTrrpGluLeuArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln	940
Db	2761	GATACAGAGATTAAATTTAGTGCATTTTGGAAAGAACCCCTGTA AAAACTTCAG	2820
QY	941	GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrrpLeuAlaPheMetGlyVal	960
Db	2821	CAGTTGAATTTGGCGGGAATTCGTGAGCAGATGATGAGCTTGCCCTCATGGGTGA	2880
QY	961	PheGluAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuProAsp	980
Db	2881	TTTGGAACTCTTAAGCAATTAGTGTTTTGGACTTTAGTACAAAGAAATTTCTACCTGAT	2940
QY	981	ProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGluAla	1000
Db	2941	CCAGATTAGTCACAAAACTTAGCCACAGTGTATTCACATTAACTTTCTCGACAAAGCT	3000
QY	1001	ArgLeuValGlyTrrpGlnPheAspAspAspAspLeuSerValIleThrGlyAlaPheLys	1020
Db	3001	AGGCTTGTGGGTGGCAATTGTGATGATGATCTCAGTGTATTATACAGGTGCTTTTAA	3060
QY	1021	LeuValTrrpAla 1024	
Db	3061	CTAGTAAGTCT 3072	
RESULT 8			
US-10-156-733-14			
; Sequence 14, Application US/10156733			
; GENERAL INFORMATION:			
; APPLICANT: Alnemrl, Emad S.			
; TITLE OF INVENTION: IPAF, AN ICE-PROTEASE ACTIVATING			
; FILE REFERENCE: 480140.477			
; CURRENT APPLICATION NUMBER: US/10/156,733			
; CURRENT FILING DATE: 2002-05-24			
; NUMBER OF SEQ ID NOS: 14			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 14			
; LENGTH: 3219			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-156-733-14			
Alignment Scores:			
Pred. No.: 0			
Score: 5453.00			
Percent Similarity: 99.908			
Best Local Similarity: 99.908			
Query Match: 99.89%			
DB: 41			
Length: 3219			
Matches: 1023			
Conservative: 0			
Mismatches: 1			
Indels: 0			
Gaps: 0			
US-09-697-089-2 (1-1024) x US-10-156-733-14 (1-3219)			
QY	1	MetAsnPhelIeLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle	20

Db 145 ATGAATTTCAATAAGGACAAATAGCCGAGCCCTTATTTCAAAAGATGGAGATGACTGTATTA 204  
 Qy 21 LysGlnIleThrAspAspLeuPheValIrrAsnValIleAsnArgGluGluValAsnIle 40  
 Db 205 AAGCAAAATCAGATGAGACTTATTTCTATGATGTCTTGAAATCGCGAAGAAAGTAACATC 264  
 Qy 41 IleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60  
 Db 265 ATTTGCTCCGGAAGGTGAGACAGCATCTGTAGAGGAGCATTCACATGATTTTGAAA 324  
 Qy 61 LysGlySerGlySerCysAsnLeuPheLeuLysSerLeuLysGluIrrAsnIrrProLeu 80  
 Db 325 AAGGTTAGAGTCTCTGTAACCTCTTCTTAATCCCTTAAGAGATGGAACTATCTCTTA 384  
 Qy 81 PheGlnAspLeuAsnGluGlnSerLeuPheHisGlnThrSerGluGluAspLeuAspAsp 100  
 Db 385 TTTCAGAGACTTGAAATGAGCAAAAGTCTTTTCATGACATCAGAGAGAGACTGGACAT 444  
 Qy 101 LeuAlaGlnAspLeuLysAspLeuTyrrHisThrProSerPheLeuAsnPheTyrrProLeu 120  
 Db 445 TTGGCTCAGAGATTAAAGACTTTCATCCATCCCATCTTTCTGAACTTTATCCCTT 504  
 Qy 121 GlyGluAspIleAspIleIlePheAsnLeuLysSerThrPheThrGluProValLeuThr 140  
 Db 505 GGTGAAGATTTGACATTTATTTTACTTGAAGACCTTCACAGAACTGTCTCTGTTGG 564  
 Qy 141 ArgLysAspGlnHisHisHisArgValGluGlnLeuThrLeuAsnGluLeuGlnAla 160  
 Db 565 AGGAAGAGCAACAACCATCACCGGTGAGCAGCATGCCCGAATGGCTCTCTGACAGCT 624  
 Qy 161 LeuGlnSerProCysIleIleGluGluGlnSerGlyLysSerThrLeuGln 180  
 Db 625 CTTGAGAGCCCTGATCATTTGAAGGGGAATCTGGCAAGCAATGCCACTCTGCTGAG 684  
 Qy 181 ArgIleAlaMetLeuThrGlySerGlyLysCysLysAlaLeuThrLysPheLysPheAl 200  
 Db 685 CGAATGGCAATGCTCTGGGGCTCCGGAAGGTGCAAGGCTGACCAATTCATAATTCCTC 744  
 Qy 201 PhePheLeuArgLeuSerArgAlaGlnGlyLysLeuPheGluThrLeuCysAspGlnLeu 220  
 Db 745 TTCTTCCTCCGCTCAGCAGAGGCCAGGCTGGACTTTTGAACCCCTGTGATCAACTC 804  
 Qy 221 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLysLeuArg 240  
 Db 805 CTGGATATACCTGGCAATCAGCAAGCAATCATTCATGGCCATCTGCTGAGCTGGCG 864  
 Qy 241 GlnArgValIleuPheLeuLeuAspGlyTyrrAsnGluIrrPheLysProGlnAsnProGlu 260  
 Db 865 CAGAGGGTTCTTTCTCTGATGGCTACAAATGAATTCAGCCCAAGAACTGCCCAAGAA 924  
 Qy 261 IleGlnAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValIrrThrThr 280  
 Db 925 ATCGAAGCCCTGATTAAGAAACACCGCTTCAGAAACATGTGATGTCAACCTACC 984  
 Qy 281 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 300  
 Db 985 ACTGAGTCTCGAGGACATACGCGAGTTGTGGCTGACTGCTGAGAGTGGGGATATG 1044  
 Qy 301 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 320  
 Db 1045 ACAGAAAGCAGCGCCAGCGCTCATCGAAGAGTGTGATCAAGAGAACTGTCTGAAGGC 1104  
 Qy 321 LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe 340  
 Db 1105 TTGTGCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAACCCCTCTCTTT 1164  
 Qy 341 ValValIleThrCysAlaIleGlnMetGlyLysSerGluPheHisSerHisThrGlnThr 360  
 Db 1165 GTGTGATCACTGTGCAATCAGATGGGTGAAGTGAATTCACATCTGCACACAAACA 1224  
 Qy 361 ThrLeuPheHisThrPheTyrrAspLeuLeuIleGlnLysAsnLysHisLysGly 380

Db 1225 ACGCTGTTCCATACCTCTATGATCTGTGATACAGAAAAACAAACAAATTAAGCT 1284  
 Qy 381 ValAlaAlaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGly 400  
 Db 1285 GTGGCTGCAAGTGAATTCATTCGAGGCTGGACACCTGTGAGACATTAAGCTGTGAGAGGT 1344  
 Qy 401 ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal 420  
 Db 1345 GTGTCTCCCAAGATTGATTTGAACTGCAGAGATGTCTCACCGTGAAGAGATGTC 1404  
 Qy 421 LeuLeuThrThrGlyLeuLeuCysLysTyrrThrAlaGlnArgPheLysProLysTyrrLys 440  
 Db 1405 CTGCTGACAACTGGGCTCTCTGTAAATATACAGCTCAAGGTTCAACCCAAATTAATA 1464  
 Qy 441 PhePheHisLysSerPheGlnGluTyrrThrAlaGlyArgLeuSerSerLeuLeuThr 460  
 Db 1465 TTCTTTCACAAAGTATTCACAGAGATACACAGACAGAGCAAGACAGAGTTATTTGACG 1524  
 Qy 461 SerHisGluProGluGluValThrLysGlyAsnGlyTyrrLeuGlnLysMetValSerIle 480  
 Db 1525 TCTCATGAGCCAGAGAGGATGACCAAGGGGAATGTTACTTGCAAAAATGGTTCATT 1584  
 Qy 481 SerAspIleThrSerThrTyrrSerSerLeuLeuArgTyrrThrCysGlySerSerValGlu 500  
 Db 1585 TCGGACATTAATCATCTTAACAGCTCTCCGATACACTGTGGTCACTGTGTGGA 1644  
 Qy 501 AlaThrArgAlaValMetLysHisLeuAlaAlaValTyrrGlnHisGlyCysLeuGluGly 520  
 Db 1645 GCCACCAAGGCTGTTATGAAACACCTCGCAGCAGATGATCAACAGGCTGCTCTCGGA 1704  
 Qy 521 LeuSerIleAlaLysArgProLeuThrArgGlnGlnSerLeuGlnSerValLysAsnThr 540  
 Db 1705 CTTTCATCGCCCAAGAGGCTCTCTGAGACAGAAATCTTTCGAAAGTGTAAACAAACC 1764  
 Qy 541 ThrGluGlnGluIleLeuLysAlaIleAsnLysSerPheValGluCysGlyIleHis 560  
 Db 1765 ACTGAGCAGAAATTCGAAAGCCATTAACATCAATCTCTTTGTAAGTGTGGATTCAT 1824  
 Qy 561 LeuTyrrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePheGln 580  
 Db 1825 TTATATCAAGAGATGACATTCAAATTCAGCCCTGAGCCAAAGAAATTTGAAGCTTTTCA 1884  
 Qy 581 GlyLysSerLeuTyrrIleAsnSerGlyAsnIleProAspTyrrLeuPheAspPheGlu 600  
 Db 1885 GGTAAAGCTTATATCACTCAAGGCAATCCCGATCTCTTAATTTGACTCTTTGAA 1944  
 Qy 601 HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrrGlyVal 620  
 Db 1945 CATTGCCCCAATGTGCAAGTGCCTGGACTTCATTAACGTGACTTTTATGAGGGAGCT 2004  
 Qy 621 MetaLaserTyrrGluLysAlaGluAspThrGlyGlyIleHisMetGluGluAlaPro 640  
 Db 2005 ATGGCTTATGGAAGAAAGCTGCGAAGACACAGGTGGAATCCCATGGAAGAGGCCCA 2064  
 Qy 641 GluThrTyrrIleProSerArgAlaValSerLeuPheAsnTyrrLysGlnGluPheArg 660  
 Db 2065 GAAACCTCATCTCCAGCAGAGGCTGTATCTTTGTTCTTCACTGGAAGACAGAAATTCAGG 2124  
 Qy 661 ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrrLeu 680  
 Db 2125 ACTGTGAGGTCACACTCCGGGATTTTCAGCAAGTTGAATTAAGCAAGATATGATATCTG 2184  
 Qy 681 GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVal 700  
 Db 2185 GGGAAATATTCAGCTCTGCCACAAAGCTCAGGCTGCAAAATTAAGATGTGCTGGTGTG 2244  
 Qy 701 AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrrSerLeuMetValGlu 720  
 Db 2245 GCTGGAACCTCAGATTGCTCTCAGCAGCACTGTAAAGAAATTTATCTCATGTGTGGA 2304  
 Qy 721 AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr 740  
 Db 2305 GCCAGTCCCTCACCATAGAAAGATGAGAGGCATCATCTGTAAACAAACCTGAAACCC 2364

QY 741 LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly 760  
|||||  
Db 2365 TTGAGTATTCATGACCTACAGAAATCAACGGCTGGCTGCTGACAGCAGCTTGAGT 2424  
QY 761 AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAspGluGlnAspIle 780  
|||||  
Db 2425 AACTTGAAGAACCTTACAAAGCTCTAATGCTAATACATTAAGATTAATGAAGAGATGCT 2484  
QY 781 IleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis 800  
|||||  
Db 2485 ATAAACTAGCTGAAGGCTGAAAAAAGCTGAAGAGATGCTGTTATTCATTGACCCAC 2544  
QY 801 LeuSerAspIleGlyGlyGlyMetAspTyrIleValLysSerLeuSerSerGluProCys 820  
|||||  
Db 2545 TTGCTGACATTGGAGAGGAGATGATTACATAGTCAAGTCTCTGCAAGTGAACCTGCT 2604  
QY 821 AspLeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu 840  
|||||  
Db 2605 GACCTGAAGAAATTCATTAGTCTCCCTGCTGCTGCTGCTGCAAAATGCAAGTGAACCTG 2664  
QY 841 AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeu 860  
|||||  
Db 2665 GCTCAGAAATCTTCAACAATTTGGTCAAACTGAGACATTTGATTTATCAGAAAAATTAACCTG 2724  
QY 861 GluLysAspGlyAsnGlnAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGln 880  
|||||  
Db 2725 GAAAAAGATGAAATGAAGCTTCTCATACATGATGAGATGAGATGAACGCTGTAAACAG 2784  
QY 881 LeuThrAlaLeuMetLeuProTyrPglCysAspValGlnGlySerLeuSerSerLeuLeu 900  
|||||  
Db 2785 CTCACCGACATGATGCTCCCTGGGGCTGTGACGTGCAAGCAGCAGCTGAGCAGCTGTG 2844  
QY 901 LysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrPargLeuThr 920  
|||||  
Db 2845 AAACATTTGGAGAGGCTCCCACTGCTCAAGCTTGGGTTGAAAAAACTGGAGACTCACA 2904  
QY 921 AspThrGluIleArgIleLeuGlnValAlaPhePheGlyLysAsnProLeuLysAsnPheGln 940  
|||||  
Db 2905 GATCAGAGATTAACATTTTGGTGTCATTTTGGAAAGAACCTCTGAAAAAACTTCCAG 2964  
QY 941 GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrLeuAlaPheMetGlyVal 960  
|||||  
Db 2965 CAGTTGATTTGGCGGGAATCGTGAGCAGTGTGATGATGCTTGCCTTCATGGGTGTA 3024  
QY 961 PheGluAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuProAsp 980  
|||||  
Db 3025 TTTGGAATCTTAAGCAATTAAGTGTGTTTTGACTTACTTAAGAAATTTCTACCTGAT 3084  
QY 981 ProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGluAla 1000  
|||||  
Db 3085 CCAGCATTAAGCAGAAAACTTAACCAAGTGTATTCAGATTAACCTTCTGCAAGAACT 3144  
QY 1001 ArgLeuValGlyTyrPglNpheAspAspAspAspLeuSerValIleThrGlyAlaPheLys 1020  
|||||  
Db 3145 AGGCTTGTGGGTGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3204  
QY 1021 LeuValThrAla 1024  
|||||  
Db 3205 CTAGTAACCTGCT 3216

## RESULT 9

PCT-US01-07143-23  
Sequence 23, Application PC/TUS0107143  
GENERAL INFORMATION:  
APPLICANT: SMITHKLINE BEECHAM CORPORATION  
APPLICANT: SMITHKLINE BEECHAM P.L.C.  
TITLE OF INVENTION: NOVEL COMPOUNDS  
FILE REFERENCE: GP50016  
CURRENT APPLICATION NUMBER: PCT/US01/07143  
CURRENT FILING DATE: 2001-03-08  
PRIOR APPLICATION NUMBER: 60/187,107  
PRIOR FILING DATE: 2000-03-06

;; PRIOR APPLICATION NUMBER: 60/236,874  
;; PRIOR FILING DATE: 2000-10-03  
;; PRIOR APPLICATION NUMBER: 60/188,916  
;; PRIOR FILING DATE: 2000-03-13  
;; PRIOR APPLICATION NUMBER: 60/237,846  
;; PRIOR FILING DATE: 2000-10-03  
;; NUMBER OF SEQ ID NOS: 52  
;; SOFTWARE: FASTSeq for Windows Version 3.0  
;; SEQ ID NO 23  
;; LENGTH: 3213  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
PCT-US01-07143-23  
  
Alignment Scores:  
Pred. No.: 0 Length: 3213  
Score: 5448.00 Matches: 1022  
Percent Similarity: 99.90% Conservative: 1  
Best Local Similarity: 99.80% Mismatches: 1  
Query Match: 99.80% Indels: 0  
Gaps: 0  
  
US-09-697-089-2 (1-1024) x PCT-US01-07143-23 (1-3213)  
  
QY 1 MetAsnPheIleLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20  
:::|||||  
Db 139 TTGAATTCATTAAGAACAAATAGCCGAGCCCTTATTCAAAAGATGGAAATGACGTGTATA 198  
QY 21 LysGlnIleThrAspAspLeuPheValTyrAsnValLeuAsnArgGluValAsnIle 40  
|||||  
Db 199 AAGCAATACACAGATGACCTTATTTGTATGAAATGTTCGATTCGGAGAAAGTAAACATC 258  
QY 41 IleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60  
|||||  
Db 259 ATTGCTCTCGAAGAGCTGACAGCATGCTGTAGAGGAGCATTCACATGATTTTGAAA 318  
QY 61 LysGlySerGlySerCysAsnLeuPheLeuLysSerLeuLysGluTyrPargLeuThr 80  
|||||  
Db 319 AAGGTTAGAGTCTCTGTAACCTCTTCTTAAATCCCTTAAGAGTGGAGATATCTCTTA 378  
QY 81 PheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAspAsp 100  
|||||  
Db 379 TTTCAGAGCTTGAATGACAAAGTCTTTTCATCAGACATCAGAAAGAGACTTGGAGAT 438  
QY 101 LeuAlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTyrProLeu 120  
|||||  
Db 439 TTGGCTCAGGATTTAAAGACTTGTACCATCCCATCTTTCGAACTTTATCCCTT 498  
QY 121 GlyGluAspIleAspIleIlePheAsnLeuLysSerThrPheThrGluProValLeuThr 140  
|||||  
Db 499 GGTGAAGATATTGACATTTATTTTAACTTGAAGAACCTTCAACAGAACTGTCTGTGG 558  
QY 141 ArgLysAspGlnHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAla 160  
|||||  
Db 559 AGGAAGACCAACACCATCACCGGTGAGCAGTGAACCTTGAAATGGCTCTGAGAGCT 618  
QY 161 LeuGlnSerProCysIleIleGluGlyLysSerGlyLysGlyLysSerThrLeuLeuGln 180  
|||||  
Db 619 CTTCAAGACCCCTGCATCATTAAGAGGGAATCTGGCAAGGCAAGTCCACTCTCTGAG 678  
QY 181 ArgIleAlaMetLeuTyrPglSerGlyLysCysLysAlaLeuThrLysPheLysPheVal 200  
|||||  
Db 679 CGAATTTGCATGCTCTGGGGCTCCGGAAAGTGCAGAGGCTTGACCAAGTTAAATTGCTC 738  
QY 201 PhePheLeuArgLeuSerArgAlaGlnGlyLysLeuPheGluThrLeuCysAspGlnLeu 220  
|||||  
Db 739 TTCTTCCCTCCGTCACAGAGGCCACAGGCTGACTTTTGAACCTCTGATCAACTC 798  
QY 221 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 240  
|||||  
Db 799 CTGATATTAACCTGCACAAATCAGAGACGACATTAAGCCATGCGCATGTAACCTCGG 858  
QY 241 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 260

|||||  
Db 859 CAGAGGGTCTTTTCTTCTTGATGGCTACAAAGAAATTCAGGCCCAAGAACTCCCAAGAA 918  
OY 261 ILEGLALALEUILLEYSGLIUAASNHISARGPHELYASNMETVALILEVALTHRTHT 280  
Db 919 ATGGAAACCCCTGATMAAGAAAAACACCCGCTTCAAGACATGGTCAATCGTACACAGCTACC 978  
OY 281 ThrGluCysLeuArghHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 300  
Db 979 ACTGAGTGCTGAGGACACATACGGCAGTTGTGGCCCTGACTGCTGAGGGGGGATATG 1038  
OY 301 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 320  
Db 1039 ACAGAAACAGCGCCCAAGGCTCATCCGAGAACTGCTGATCAAGAGAGCTTGGCTGAAGGC 1098  
OY 321 LeuLeuLeuGlnIleGlnLysSerArgCysLeuArghAsnLeuMetLysThrProLeuPhe 340  
Db 1099 TTGTGGTCCCAAAATTCAGAAATCCAGGTGCTTGAGGAAATCTCATGAAGACCCCTCTTT 1158  
OY 341 ValValIleThrCysAlaIleGlnMetGlyLusSerGluPheHisSerHisThrGlnThr 360  
Db 1159 GTGGTATCATCTGTGCATTCAGATGGGTGAAGATGATGCTCCACTCCACACACAACA 1218  
OY 361 ThrLeuPheHisThrPheTyrrAspLeuLeuIleGlnLysAsnLysHisLysGly 380  
Db 1219 ACGCTGTTCATACCTTCTATGATCTGTGATACAGAAAAACAACAACATMAAGGT 1278  
OY 381 ValAlaIleAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGly 400  
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OY 421 LeuLeuThrThrGlyLeuLeuCysLysTyrrThrAlaGlnArghLysProLysTyrrLys 440  
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OY 521 LeuSerIleAlaLysArgProLeuThrArgGlnGluSerLeuGlnSerValLysAsnThr 540  
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OY 621 MetAlaSerTrpGluLysAlaIleGluAspThrGlyGlyIleHisMetLugluAlaPro 640  
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OY 741 LeuSerIleHisAspLeuGlnAsnGlnArghLeuProGlyGlyLeuThrAspSerLeuGly 760  
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OY 761 AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluAspAla 780  
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OY 861 GluLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGln 880  
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OY	481	Serasp1leThrSerThrYrSerSerLeuLeuAArgYrThrCysG1YSerSerValGlu	500
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OY	501	AlaThrArgAlaValMetLysHisLeuAla1Ala1Val1YrGlnHisG1YSerLeueng1Y	520
Db	1639	GCCACACAGGCTGTATGAGAGCACCTCGCAGCAGTGAATCAACACGGCTGCTTCGGA	1698
OY	521	LeuSer1leAla1YsArgProLeuTrpArgG1ng1UserLeuG1nSerValLysAsnThr	540
Db	1699	CTTTCATCCGCGCAAGAGCGCTCTCTGGACAGAGAACTTTTGCAAAGTGATGAAAAACAC	1758
OY	541	ThrlG1ng1U1leLeuLysAla1leAsn1leAsnSerPheValG1UcysG1Y1leHis	560
Db	1759	ACTAGACAGAAATTCGAAAGCCATTAACATAACTTCCTTGTATAGAGTGCGATCCAT	1818
OY	561	LeuYrG1ng1UserThrSerLysSerAlaLeuSerG1ng1UphG1n1AphPheGln	580
Db	1819	TTATATCAAGAGAGTACATCCAAATACGCCCTGAGCCAAAGATTTAAACCTTTCTTCA	1878
OY	581	G1Y1YsSerLeuYr1leAsnSerG1YAsn1leProAspYrLeuPheAspPheG1n	600
Db	1879	GGTAAAGCTTATATATCAACTCAGGAGAACATCCCGATTACTTATTTAGACTTCTTGA	1938
OY	601	HisLeuProAsnCysAlaSerAlaLeuAspPheG1leLysLeuAspPheYrG1YAla1	620
Db	1939	CATTTCGCCAATTGTGCAGAGTCCCTTGACATTTATTAACGTGACCTTTATGGGGAGCT	1998
OY	621	MetaSerTrpG1U1YsAla1AlaG1UAspTrhG1Y1leHisMetG1ng1UAlaPro	640
Db	1999	ATGGCTCATATGGGAAAGCGCTGCAGAGACACAGTGCGAATCCACATGGAGAGGCCCA	2058
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OY	681	G1Y1Ys1lePheSerSerAla1ThrSerLeuArgLeng1n1leYsArgCysAlaG1YAl	700
Db	2179	GGGAAATATTCACCTCTGCACAGGCTCAGGCTGCAATAAAGAGATGCTGCTGTG	2238
OY	701	AlaG1SerLeuSerLeuValLeuSerThrCysLysAsn1leYrSerLeuMetValGlu	720
Db	2239	GCTGGAACCTCATTTTGTCCTCAGCAGCCTGTAAAGACATTTATCTCTCATGGTGA	2298
OY	721	AlaSerProLeuThr1leG1UAspG1UArgHis1leThrSerVal1ThrAsnLeuYsThr	740
Db	2299	GCCAGTCCCTCACACATAGAGAGAGGACACATCACTGTATCAACAAACCTGAAAC	2358
OY	741	LeuSer1leHisAspLeuG1nAsnG1nArgLeuProG1YG1YleuThrAspSerLeuG1Y	760
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Db	2599	GACCTTGAGGAANTTCATATTAGTCTCTGCTGCTTGTCTGCAGAAATGCAAGTGAATAATCTGA	2658
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Db	2659	GCTCAGATCTTCACATTTGGTCTCAACACGACGACATCTTGATTTATCAGAAATTAACCTG	2718
QY	861	GluLysAspGlyAsnGluAlaLeuHisGluIleAspArgMetAsnValLeuGluGln	880
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QY	881	LeuThrAlaLeuMetLeuPheProTyrGlyCysAspValGlnGlySerLeuSerSerLeuLeu	900
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QY	901	LysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLeuAsnTyrArgLeuThr	920
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES			
FILE REFERENCE: 21272-103			
CURRENT APPLICATION NUMBER: PCT/US01/14826			
CURRENT FILING DATE: 2001-05-16			
PRIOR APPLICATION NUMBER: 09/577,408			
PRIOR FILING DATE: 2000-05-18			
PRIOR APPLICATION NUMBER: 09/677,298<151>			2000-09-22
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NAME/KEY: CDS			
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Score:	5441.00	Matches:	1020
Percent Similarity:	99.80%	Conservative:	2



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Db 2795 CTCACCCGACATGATGCTCCCTGGGGCTGTGACGTGCAAGCAGCCTGAGCAGCCTGTGG 2854  
QY 901 LysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrArgLeuThr 920  
|||||  
Db 2855 AAAACATTTGGAGAGGCTCCCAACCTGCTCAAGCTTGGGTGAAAACTGGAGACTCACA 2914  
QY 921 AspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln 940  
|||||  
Db 2915 GATACAGAGATTAGAAATTTAGTGCATTTTGGAAAGAACCTCGAAAAACCTTCAG 2974  
QY 941 GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrPheAlaPheMetGlyAla 960  
|||||  
Db 2975 CAGTTGAATTTGGGGGAAATCGTGTGAGCAGTGTGATGGCTTGCCTTCATGGGTCTA 3034  
QY 961 PheGlnAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGlnPheLeuProAsp 980  
|||||  
Db 3035 TTTGAGAAATCTTAACCAATTTAGTGTTTTGAACCTTAACCTTAACCAATTTCTACCTAT 3094  
QY 981 ProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGluAla 1000  
|||||  
Db 3095 CCAGATTAAGTCAGAAACCTTAAGCAAGTGTATCCAGTTAACTTTCTCGCAAAACACT 3154  
QY 1001 ArgLeuValGlyTyrPheAspAspAspAspLeuSerValIleThrGlyAlaPheLys 1020  
|||||  
Db 3155 AGGCTTGTGGGTGGCATTTGATGATGATGATCATCTGTTATTACAGGTCTTTTAAA 3214  
QY 1021 LeuValThrAla 1024  
|||||  
Db 3215 CTAGTAACCTGCT 3226

RESULT 12  
US-09-667-298-66  
; Sequence 66, Application US/09667298  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom

APPLICANT: Liu, Chenghua  
APPLICANT: Zhou, Ping  
APPLICANT: Asundi, Vinod  
APPLICANT: Ren, Feiyan  
APPLICANT: Zhao, Qing A.  
APPLICANT: Zhang, Jie  
APPLICANT: Xue, Aidong J.  
APPLICANT: Wang, Jidan-Rui  
APPLICANT: Chen, Rui-hong  
APPLICANT: Dramac, Radje T.  
TITLE OF INVENTION: Novel Nucleic Acids and  
FILE REFERENCE: Polypeptides  
CURRENT APPLICATION NUMBER: US/09/667,298  
CURRENT FILING DATE: 2000-09-22  
PRIOR APPLICATION NUMBER: 09/577,408  
PRIOR FILING DATE: 2000-05-18  
NUMBER OF SEQ ID NOS: 178  
SOFTWARE: pt\_fl\_genes Version 2.0  
SEQ ID NO 66  
LENGTH: 3260  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (29)..(3229)  
US-09-667-298-66  
Alignment Scores:  
Pred. No.: 0 Length: 3260  
Score: 5441.00 Matches: 1020  
Percent Similarity: 99.80% Conservative: 2  
Best local Similarity: 99.61% Mismatches: 2  
Query Match: 99.67% Indels: 0  
Gaps: 0  
US-09-697-089-2 (1-1024) x US-09-667-298-66 (1-3260)  
QY 1 MetaSnPheIleLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20  
:::|||||  
Db 155 TTGATTTTCATTAAGAGCAATAGCCGAGCCCTTATTCAAAGATGGGATACATATATA 214  
QY 21 LysGlnIleThrAspAspLeuPheValTyrAsnValLeuAsnArgGluGluValAsnIle 40  
|||||  
Db 215 AAGCAAAATCACAGATGACCTATTTGTATGGAATGTTCTGAATCCCGAAAGATGAACATC 274  
QY 41 IleCysGlyLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLys 60  
|||||  
Db 275 ATTTGCTCGAAGAGGTGAGCAGAGATGCTGTAGGGGATCATTCACATGATTTTGAA 334  
QY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTyrPasnTyrProLeu 80  
|||||  
Db 335 AAGGTTAGAGTCTCTGTAACCTCTTTCTTAATCCCTTAAGAGTGGAACTATCCCTGA 394  
QY 81 PheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAspAsp 100  
|||||  
Db 395 TTTCAGAGCTTGAATGACAAAGCTTTTTCATCAGACATCAGAAAGAGACTTGGAGAT 454  
QY 101 LeuAlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTyrProLeu 120  
|||||  
Db 455 TTGGCTCAGGATTTAAAGACTTGTACCATACCCCATCTTTTCGAACTTTTATCCCTT 514  
QY 121 GlyGlnAspIleAspIleIlePheAsnLeuLysSerThrPheThrGluProValLeuTyr 140  
|||||  
Db 515 GGTGAAGATTTGACATATTTTAACTTGAAGAACACCTTCACAGAACCTGTCTGGG 574  
QY 141 ArgLysAspGlnHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAla 160  
|||||  
Db 575 AGGAAGAGCAACACCATCACCGGTGAGCAGCTGACCTCGAATGGCTCTGAGAGCT 634  
QY 161 LeuGlnSerProCysIleIleGluGlyLysSerGlyLysGlyLysSerThrLeuLeuGln 180  
|||||  
Db 635 CTCAGAGCCCTGCTCATCATGTAAGGGGAAATCTGCAAGCAAGTCACACTCTGCTGAG 694

QY	181	ArgLIaLeaMeLeuThrPgiSerGlyLysCysLysAlaLeuThrLysPheLysPheVal	200
Db	695	CGAATTGCCATGCTCTGGGGCTCCGGAAAGTGCAAAGGCTCTGACCAAGTCAAAATTCGTC	754
QY	201	PhePheLeuArgLysSerArgAlaGlnGlyLysLeuPheGluThrLeuCysAspGlnLeu	220
Db	755	TTCTCTCCGCTCCACACAGGGGCCAGGGGTGACCTTTTGAACCCCTGTGATCAATC	814
QY	221	LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMeLeuLeuLysSerArg	240
Db	815	CTGGATTAACCTGGCAACAATCAGGAAGCAGACATTATGCGCATCTGCTGAACTGGCG	874
QY	241	GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu	260
Db	875	CAGAGGGTCTCTTCTCTCTTGGATGGCTCAATGAATTCACCCCAACACTGCCCAAGA	934
QY	261	IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThr	280
Db	935	ATCCAAAGCCCTGATAAAGAAACCAACCGCTTCAMAAATGTCATGCTACCACTAC	994
QY	281	ThrGlnCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet	300
Db	995	ACTGAGTGCCCTGAGGACATACGACGAGTTGGTGGCCCTGACTGCTGAGGTGGGATATG	1054
QY	301	ThrGlnAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGlu	320
Db	1055	ACAAAGAAGACGGCCAGGGCTCTCATCCGAAAGTCTGATCAAGAGACTTGCTGAAGC	1114
QY	321	LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe	340
Db	1115	TTGTGGCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCATGATGAACCCCTCTCTT	1174
QY	341	ValValIleThrCysAlaIleGlnMetGlyLysGluPheHisSerHisThrGlnThr	360
Db	1175	GTGGTCACTACCTTGTCGAATCCAGAGGGGTGAAGAGATTCCTCACTCCACACAACA	1234
QY	361	ThrLeuPheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysHisLysGly	380
Db	1235	ACGGTGTTCATACCTCTCTATGATCTGTTGATRCAGAAAACAAACAAACATRAAGT	1294
QY	381	ValAlaAlaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGlu	400
Db	1295	GTGGCTCTCAAGTACTTTCATTCGAGACCTCGAGCCACTGTGGAGACCTTGCTGAGAGGT	1354
QY	401	ValPheSerHisLysPheAspPheGluLeuGlnAsnValSerValAsnGluAspAla	420
Db	1335	GTGTTCCTCCCAAGTTTGATTCGAAAGTCGAGAGATGTCTCAGGCTGAAGAGATGTC	1414
QY	421	LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys	440
Db	1415	CTGTGCACAACCTGGGCTCCTCTGTAATATATACAGCTCAAGGTTCAAGCCAAAGATATAA	1474
QY	441	PhePheHisLysSerPheGlnGluTyrThrAlaGlyArgLeuSerSerLeuLeuThr	460
Db	1475	TTCTTTCACAAAGTCATTCACAGGAGTACACAGAGACGAAAGCACTCAGAGTTTATGACG	1534
QY	461	SerHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle	480
Db	1535	TTCATGACGACGAGGAGGGGTGACCAAGGGGAATGGTTACTTGSCAATAAATGTTCCATT	1594
QY	481	SerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu	500
Db	1595	TTCGACATTCATCCACTATACACCCGTCGCGTCAACCTGTGGGTCACTGTGGAA	1654
QY	501	AlaThrArgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuLeuGly	520
Db	1655	GCACACAGGGCTGTATGAAGACACTCCGAGACAGTATCAACACGGCTGCTCTCGGA	1714
QY	521	LeuSerIleAlaLysArgProLeuThrParGlnGluSerLeuGlnSerValLysAsnThr	540
Db	1715	CTTTCCTACCCCAAGAGGCTCTCTCTGAGACAGGAATCTTTCAAAGCTGTAACAAACCC	1774

QY	541	ThrGluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHis	560
Db	1775	ACTGGCAAGAAATTCGTGAAAGCCATTAACATCAATTCCTTGATAGAGTGGCATCCAT	1834
QY	561	LeuTrpGlnIleuSerThrSerLysSerAlaLeuSerGlnGluPheGlnAlaPheGln	580
Db	1835	TTATATCAAGAGAGACTCCAAATCCAAATCAGCCCTTAGCCAAAGAAATTCAACTTCCTTTCAA	1894
QY	581	GlyLysSerLeuTrpIleAsnSerGlyAsnIleProAspTyrLeuPheAspPheGlu	600
Db	1895	GGTAAACCTTATATATCAACTCACTGAGGAAACATCCCGATTACTTATTTACTCTTTGAA	1954
QY	601	HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyAla	620
Db	1955	CATTGGCCCAATGTGCAAGTGGCCCTGGACTTCATTAACTGGGCTTTTATGGGGACT	2014
QY	621	MetAlaSerTrpGlyLysAlaIleGluAspThrGlyGlyIleHisMetGluAlaPro	640
Db	2015	ATGGCTTATATGGGAAAGAGCGCGCAAGACACAGGGGATCCACATGGAAAGGCCCA	2074
QY	641	GluTrpTyrIleProSerArgAlaValSerLeuPheAsnTrpLysGlnLysPheArg	660
Db	2075	GAACCTCACTATCCACAGAGGCGCTGATCTCTTTTCTTCACTCGAAGCAGCAATTCAG	2134
QY	661	ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeu	680
Db	2135	ACTCGAGAGTCAACACTCGGGAATTCAGCAAGTTGAATACCAAGATATACAGATCTG	2194
QY	681	GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyAla	700
Db	2195	GGGAAATATTCACACTCTGGCACAGGCTCAGGCTCCAAATAAAGATGTCTGGTGTG	2254
QY	701	AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGlu	720
Db	2255	GCTGGAAACCTCACTAGTTGGTGCCTCAGCACCCTGAAACAATTTATTCCTCATGGTGAA	2314
QY	721	AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr	740
Db	2315	GCCAGTCCCTCACCATTAAGAAAGATGAGAGCACATCATCTGTAAACAACCTGAAAC	2374
QY	741	LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly	760
Db	2375	TTGACTATTTCATGACACACAGAAATCAACGGCTCCCGGGTGGTCTACACAGCTTGGCT	2434
QY	761	AsnLeuLysAsnLeuThrTrpLysLeuIleMetAspAsnIleLysMetAsnGluAla	780
Db	2435	AACTTGAAGAACCTTACAAAGCTCATTAATGATTAATAAAGTGAATGAAGACAGATCT	2494
QY	781	IleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis	800
Db	2495	ATTAACACAGCTGAAGGCGTGAATAACGTAACAAATCATGTGTTATTTTCATTGTGACCAC	2554
QY	801	LeuSerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerGluProCys	820
Db	2555	TTGTCTGCATTTGAGAGGGGAATGGATTAATGTCAACTCTCTGTCAAGTGAACCCGT	2614
QY	821	AspLeuGlnGluIleGlnLeuValSerCysCysLeuSerSerAlaAsnAlaValLysIleLeu	840
Db	2615	GACCTTGAAGAAATTCATTAATGCTCTGCTGCTTCTTCGCAAAATGCACTGAAATTCCTA	2674
QY	841	AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeu	860
Db	2675	GCTGAGATCTTCACAAATTTGGTCAAACTGACATTCCTTGATTTATCAAGAAATTAACCTG	2734
QY	861	GluLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGln	880
Db	2735	GAATAAGATGAATTAAGACTCTTCATGAACGTATGACAGGATTAACGCTGTGAACAG	2794
QY	881	LeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeu	900
Db	2795	CTCACCCGACACTGACTGCGCTTGGGGCTGTGAGGTGCANAGGACCTTAGACGCTTGTG	2854
QY	901	LysHisLeuGlnGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThr	920



Db 1357 ACGCTGTTCCATACCTCTGATGATCTGTTGATACAGAAAAACAAACAAACATAAGGT 1416  
Qy 381 VALAIAIAASerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaIleuGluGly 400  
Db 1417 GTGGCTGCAGAGCTTATTCTGGAGCTCGACACCGGTGGAGACCTAGCTCTGGAGGCT 1476  
Qy 401 ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal 420  
Db 1477 GTGTTCTCCCAAGCTTGTATTCGAACTGCAGAGATGTCTCCAGCTGATGATGAGATGTC 1536  
Qy 421 LeuLeuThrThrGlyLeuLeuGlnLysTyrThrAlaGlnArgPheLysProLysTyrLys 440  
Db 1537 CTGCTGACAACTGGGCTCCTCTGTAATATATACAGCTCAAGGTCAAGGCCAAAGATATAA 1596  
Qy 441 PhePheHisLysSerPheGlnGluTyrThrAlaGlyArgGluSerSerLeuLeuThr 460  
Db 1597 TTCCTTCCAAAGTCTATTCAGAGATACAGAGAGCAGACAGACTGAGCATTTATTTGACG 1656  
Qy 461 SerHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGluLysMetValSerIle 480  
Db 1657 TCTCATGAGCCAGAGAGAGGTACCAAGGGGAATGCTTACTTCAGAAAAATGCTTCATTT 1716  
Qy 481 SerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu 500  
Db 1717 TCGGACATTACATCCACTTATAGCAGCTGCTCCGCTACACTGTGGGTCACTGTGGA 1776  
Qy 501 AlaThrArgAlaValMetLysHisLeuAlaValAlaValTyrGlnHisGlyCysLeuGlu 520  
Db 1777 GCCACCAAGGCTGTATATAGACACTGCAGACGTGTATCAACACAGGCTTCCTCGA 1836  
Qy 521 LeuSerIleAlaLysArgProLeuTyrArgGlnGlnSerLeuGlnSerValLysAsnThr 540  
Db 1837 CTTTCATCGCCAGAGAGGCTCTGTGAGACAGAGATCTTTGCAAAAGTGTGAAAAACAC 1896  
Qy 541 ThrGlnGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHis 560  
Db 1897 ACTGAGCAAGAAATTTCTAAAGCCCTAAACATCAATCTCTTGTGTAGATGTGGCATCAT 1956  
Qy 561 LeuTyrGlnGlnSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePheGln 580  
Db 1957 TTATATCAAGAGATACATCCAAATCAGCCCTGAGCCAAAGATTTGAAAGCTTCTTTCA 2016  
Qy 581 GlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPhePheGlu 600  
Db 2017 GGTAACAACTATATATCACTCAAGGAAACATCCCCGATTACTTTTGACTCTTTGAA 2076  
Qy 601 HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyAla 620  
Db 2077 CATTTGCCCAATTTGCAAGTGCCTGCACTTCAATTAACAGACTTTTATGGGGAGCT 2136  
Qy 621 MetAlaSerTPGulLysAlaAlaGlnAspThrGlyGlyIleHisMetGluGluAlaPro 640  
Db 2137 ATGGCTTATGGGAAAGGCTGCAAGAACAGAGGTGAATCCAAATGAAGAGGCCCA 2196  
Qy 641 GluThrTyrIleProSerArgAlaValSerLeuPheAsnTyrLysGlnGluPheArg 660  
Db 2197 GAAACCTCATATCCAGAGAGGCTGTATCTTGTCTTCACTGCAACAGAGAAATTCAGG 2256  
Qy 661 ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeu 680  
Db 2257 ACTGTGAGGTCTACACTCCGGGATTTTCAGCAAGTTGAATTAAGCAAGATATCAGATATCTG 2316  
Qy 681 GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyAla 700  
Db 2317 GGGAAAAATATTCAGCTCTGCCACAGCCTCAGGCTGCAAAATTAAGATGTGCTGTGTG 2376  
Qy 701 AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGlu 720  
Db 2377 GCTGGAACCTCAGTGTGCTCTCAGCACCTGTAAAGAACATTATTTCTCATGTGTGAA 2436  
Qy 721 AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr 740  
Db 2437 GCCAGTCCCTCACCACATAGAGATGAGAGCACATCATCTGTAAACAACTGAAAC 2496

Qy 741 LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly 760  
Db 2497 TTGAGTATTTCAGACCTCAGACATACAGGCTGGCGGGGTGTCTACTGACAGCTTGGGT 2556  
Qy 761 AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAla 780  
Db 2557 AACTTGAAACACCTTATCAAAAGCTCATATGATGATTAACATTAAGATGATATCAAGAAATGCT 2616  
Qy 781 IleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis 800  
Db 2617 ATAAACATGCTGAAGGCTGAAAAACCTGAAGAGATGTGTATTTCATTGACCCAC 2676  
Qy 801 LeuSerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerLysProCys 820  
Db 2677 TTGCTGACATTGGAGAGGGAATGATTAACATATGCAATCTCTGTCAAGTGAACCTGT 2736  
Qy 821 AspLeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu 840  
Db 2737 GACCTTGAAGAAATTCATTAATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2796  
Qy 841 AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeu 860  
Db 2797 GCTCAGAAATCTTCACAAATTTGCTCAAACTGACAGCATTTGTGATTCAGAAAAATTACCTG 2856  
Qy 861 GluLysAspArgLysAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGln 880  
Db 2857 GAAAAAGATGAAATGAAGCTTTCATGAACATGATCGACAGAGATACAGTGTGTAAACAG 2916  
Qy 881 LeuThrAlaLeuMetLeuProTyrPheLysCysAspValGlnGlySerLeuSerSerLeuLeu 900  
Db 2917 CTCACCGCAGCTGATCTGCTCCCTGGGCTGTGTACAGTCAAGCAGGCTGAGCAGCCTGTGTT 2976  
Qy 901 LysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrArgLeuThr 920  
Db 2977 AAACATTTGGAGAGAGCTCCACCACTGTCAAAGCTTGGGTGAAAAACGTGAGACTCACA 3036  
Qy 921 AspThrGluIleArgIleLeuGluAlaPhePheGlyLysAsnProLeuLysAsnPheGln 940  
Db 3037 GATACAGAGATTGATGATTTAGTGCATTTTGTGAAAAAGAACCTCTGAAAAACTTCCAG 3096  
Qy 941 GlnLeuAsnLeuValAlaGlnAsnArgValSerSerAspGlyTyrLeuAlaPheMetGlyAla 960  
Db 3097 CAGTTGAATTTGGCGGGAATGTGTGAGCACTGATGATGGCTGCTCATGGGTGTA 3156  
Qy 961 PheGluAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuProAsp 980  
Db 3157 TTTGAGAAATCTTAACCAATTAGTGTTTTGTGACTTACTTAAGAAATTTCTACTGAT 3216  
Qy 981 ProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGluAla 1000  
Db 3217 CCAGCATTAAGTCAGAAACTTAAGCCCAAGTGTATCCAAAGTTAACTTCTCTGCAAGACCT 3276  
Qy 1001 ArgLeuValGlyTyrGlnPheAspAspAspAspLeuSerValIleThrGlyAlaPheLys 1020  
Db 3277 AGCGTTGTGGGTGGCAATTTGATGATGATATCTCAAGTGTATTAACAGGTGCTTTTAA 3336  
Qy 1021 LeuValThrAla 1024  
Db 3337 CTAGTAACCTGCT 3348

RESULT 14  
US-09-491-404-1319  
; Sequence 1319, Application US/09491404  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Yuanhua T.  
; APPLICANT: Tillinghast, John  
; APPLICANT: Sinku, Ankura  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Dimanac, Radoje T.  
; TITLE OF INVENTION: Novel Contigs Obtained  
; TITLE OF INVENTION: From Various Libraries  
; FILE REFERENCE: 785

CURRENT APPLICATION NUMBER: US/09/491,404  
CURRENT FILING DATE: 2000-01-27  
NUMBER OF SEQ ID NOS: 3796  
SOFTWARE: PC\_SP\_genes Version 1.0  
SEQ ID NO 1319  
LENGTH: 3545  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: (781)...(916)  
OTHER INFORMATION: this location contains the signal peptide sequence,  
OTHER INFORMATION: MIMSGCKALTKRFVFLNLSRAQGGFLFLCDLIDIFETIK, Run with SignalP  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (679)...(3279)  
OTHER INFORMATION: similar to g13688110 in the genepept database release 114,  
OTHER INFORMATION: Run with FASTX 3.3t00, default parameters  
US-09-491-404-1319

## Alignment Scores:

Pred. No.:	0	Length:	3545
Score:	5438.00	Matches:	1021
Percent Similarity:	99.71%	Conservative:	0
Best Local Similarity:	99.71%	Mismatches:	3
Query Match:	99.62%	Indels:	0
DB:	18	Gaps:	0

US-09-697-089-2 (1-1024) x US-09-491-404-1319 (1-3545)

QY 1 MetAsnPhelIeLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20  
DB 232 ATGAATTTCATAAAGACAATAGCCGAGCCCTATTCAAAGATGGGAATGACTGTATA 291  
QY 21 LysGlnIleThrAspAspLeuPheValTyrAsnValLeuAsnArgGluGluValAsnIle 40  
DB 292 AAGCAAAATCACAGATGACCTATTGTATGCAATGTTCGAATCCGGAAGAGTAAACATC 351  
QY 41 IleCysGylLysValGluGlnAspAlaIleArgIleIleIleHsMetIleLeuLys 60  
DB 352 ATTTGCGCGGAGGAAGGTGAGACAGATGCTCTAGAGGAGCATTCACATATTTTGAA 411  
QY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTyrPasnTyrProleu 80  
DB 412 AAGGTTCCAGAGTCTGTAACCTCTTTCTTAATCCCTTAAGGAGTGAACATATCTCTA 471  
QY 81 PheGlnAspLeuAsnGlyLysSerLeuPheHisGlnThrSerGluGlyAspLeuAsnAsp 100  
DB 472 TTTCAGGACTTGAAATGACAAAGTCTTTTTCATCAGACATCAGAAAGGAGACTTGACGAT 531  
QY 101 LeuAlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTyrProleu 120  
DB 532 TTGGCTCGAGATTAAAGGACTTGACCATACCCCATCTTTTCGAACTTTATACCCCTT 591  
QY 121 GlyLysAspIleAspIleIlePheAsnLeuLysSerThrPheThrGluProValLeuTyr 140  
DB 592 GGTAAAGATATGACATTAATTTTAACCTTGAAAGACCTTCACAGAACCTGCTCTGGG 651  
QY 141 ArgLysAspGlnHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAla 160  
DB 652 AGGAAGACACACACATCACCGGTGGAGCAGTGAACCTGGAATGGGCTCTCGAGGCT 711  
QY 161 LeuGlnSerProCysIleIleGluGlyLysSerGlyLysSerThrLeuLeuGln 180  
DB 712 CTTCAGAGCCCTGCATCATATTGAAGGGGAATCTGGCAAGGCAAGTCCACCTGCTGAG 771  
QY 181 ArgIleAlaMetLeuTyrPglySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 200  
DB 772 CGCAATTCAGATGCTCTGGGGCTCCGGAAGAGTCAAGGCTCTGACCAAGTTCAAAATTCGTC 831  
QY 201 PhePheLeuArgLeuSerArgAlaGlnGlyLysLeuPheGluThrLeuLysAspGlnLeu 220  
DB 832 TTCTTCTCTCCGCTCAGCAGGGGCCAGGGTGACTTTTGAAGACCTCTGTGATCAACTC 891

QY 221 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLysLeuArg 240  
DB 892 CTGATATACCTGGCACAAATCAGAGACAGACATTAATGGCCATGCTGTAACCTCGG 951  
QY 241 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 260  
DB 952 CAGAGGGTCTCTTCCCTCTTGATGGGTACAAATTAATCAAGCCCAAGTCCAGAA 1011  
QY 261 IleGlnAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThrThr 280  
DB 1012 ATCGAAGCCCTGATTAAGAAAGAACCCACCGCTTCAGAAACATGTCATCTCACCACATC 1071  
QY 281 ThrGluLysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 300  
DB 1072 ACTAGATGCTCGAGGACACATTCGCGCAGATTGGTCCCTGACTGCTGAGGTGGGGATATG 1131  
QY 301 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 320  
DB 1132 ACAGAAAGACAGCCGCCAGGCTCTCATCCGAAAGTGTGATCAAGAGACTTGCTGAAGGC 1191  
QY 321 LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe 340  
DB 1192 TTGTTCCTCCAAATTCAGAAATCCAGGTGCTGAGGAATTCATGAAGACCCCTCTCTT 1251  
QY 341 ValValIleThrCysAlaIleGlnMetGlyLysSerGluPheHisSerHisThrGlnThr 360  
DB 1252 GTGGTCATCACTTGTGCATTCACATCGGATGGAAGTGAATGATTCACATCCACACAAACA 1311  
QY 361 ThrLeuPheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysGly 380  
DB 1312 ACGCTGTTCATACCTTCTATGATCTGTGTATACAGAAACAAACCAATCAATAAAGT 1371  
QY 381 ValAlaIleSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGly 400  
DB 1372 GTGGCTGAAATGACTTCATTCAGAGCTGGAGCCAGCTGTGATACCTTGTGAGAGGT 1431  
QY 401 ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal 420  
DB 1432 GTGTTCCTCCCAAGATTGATTTGAACTGCAGATGCTGCACGCAATGAAGATGTC 1491  
QY 421 LeuLeuThrThrGlyLeuLeuLysCysLysTyrThrAlaGlnArgPheLysProLysTyrLys 440  
DB 1492 CTGCTGACAACTGGCTCTCTGTAATATACACTCAAAAGTTCAAAGCCCAATATAAA 1551  
QY 441 PhePheHisLysSerPheGlnGluTyrThrAlaGlyArgLeuSerSerLeuLeuThr 460  
DB 1552 TTCTTTTCAAGATCATTCACAGAGTACACAGCAGAGCAAGACTCAGCAGTTTATGACG 1611  
QY 461 SerHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle 480  
DB 1612 TCTCATGAGCCAGAGGAGGTGACCAAGGGGAATGTTACTTCGAAATGTTTCATTT 1671  
QY 481 SerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu 500  
DB 1672 TCGGACATTTACATCCACTTAATAGCAGCTGCTCGGTAACACTGTGGGTCAATCTGTGAA 1731  
QY 501 AlaThrArgAlaValMetLysHisLeuAlaValTyrGlnHisGlyCysLeuLeuGly 520  
DB 1732 GCCACCGAGGCTGTATATGAACACCTCGCAGCAGATGATCAACACGGCTGCTCTCGGA 1791  
QY 521 LeuSerIleAlaLysArgProLeuTyrArgGlnLysSerLeuGlnSerValLysAsnThr 540  
DB 1792 CTTCATTCAGCCAGAGAGGCTCTCTGAGACAGAAATCTTTGCAAAAGTGAATAAACACC 1851  
QY 541 ThrGluGlnGluIleLeuLysAlaIleAsnLysSerPheValGluCysGlyIleHis 560  
DB 1852 ACTGAGCAAGAAATTCGAAGGCCATTAACATCAATCTTTGTAGAGTGGGATCATCAT 1911  
QY 561 LeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePheGln 580  
DB 1912 TTATATCAAGAGATACATCCAAATTCAGCCCTGAGCCAAAGATTTGAAGCTTTCTTTCAA 1971

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QY 581 GlySerLeuTyrIleAsnSerGlyAsnIleProAspTyrIleuPheAspPhePheGlu 600
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Db 1972 GGTAAACCTATATATACACTCAGGGAACAATCCCGATTCTTTGACTTCTTTGAA 2031
QY 601 HisLeuProAsnCysAlaSerAlaLeuAspPheIleYsLeuAspPheTyrGlyAla 620
    |||
Db 2032 CATTTGCCCAATTTGGCAAGGCTCTGCACTTCAATTAACGCGCTTTTATGCGGAGACT 2091
QY 621 MetAlaSerTPGluValAlaGluAspThrGlyIleHisMetGluGluValPro 640
    |||
Db 2092 ATGGCTTCATGGAAAGAGGCTGCGACAGACACAGGTGGATCCACATGGAAAGAGGCCCA 2151
QY 641 GluThrTyrIleProSerArgAlaValSerLeuPheAsnTPYsGluGluPheArg 660
    |||
Db 2152 GAAACCTCATTTCCAGCAGGAGGCTGATCTTTGTTCTTCACTGGAACGAGGAATTCAGG 2211
QY 661 ThrLeuGluValIleThrLeuArgAspPheSerTyrLeuAsnIlyGluAspIleThrTyrLeu 680
    |||
Db 2212 ACTCTGGAGGTCCACACCTCCGGGATTTTCAGCAAGTTGAATTAAGCAAGATATCAGATATCTG 2271
QY 681 GlyIlyIlePheSerSerAlaThrSerLeuArgLeuGluIleYsArgCysAlaGlyVal 700
    |||
Db 2272 GGGAAATATTCAGCTGCTGCCACAAAGCTCAGGCTGCATAAATAAGAGATGCTGCTGTG 2331
QY 701 AlaGlySerLeuSerLeuValLeuSerThrCysIlyAsnIleTyrSerLeuMetValGlu 720
    |||
Db 2332 GCTGGAACCTCATGCTTGTGCTCCTCAGCAGCTGTAAAGCAATTTATCTCTCATGCTGAG 2391
QY 721 AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuIlyThr 740
    |||
Db 2392 GCCAGTCCCTCCACCAATGAAGATGAGAGGACATCATCTGTAAACAACTGAAACCC 2451
QY 741 LeuSerIleHisAspLeuGluAsnGluArgLeuProGlyIleuThrAspSerLeuGly 760
    |||
Db 2452 TTGACTATTCATGACCTCAACAATCAACGCGCTCCGCTGCTGACTGACAGACTTGGCT 2511
QY 761 AsnLeuIlyAsnLeuThrIlyLeuIleMetAspAsnIleYsMetAsnGluGluAspAla 780
    |||
Db 2512 AACTTGAAGAACCTTACAAACCTCATATGATGAATGAATGAAGAAAGATGCT 2571
QY 781 IleYsLeuAlaGluGlyLeuIlyAsnLeuIlySlyMetCysLeuPheHisLeuThrHis 800
    |||
Db 2572 ATAAACCTAGCTGAAGGCTCAAAAACCTGAAGAGATGTTTATTTCAATTTGACCCAC 2631
QY 801 LeuSerAspIleGlyGluGlyMetAspTyrIleValIlySerLeuSerSerGluProCys 820
    |||
Db 2632 TTGCTGACATTTGAGAGGAGGATGATTAATAGTCAAGTCTCTCTCAAGGAACCTGCT 2691
QY 821 AspLeuGluGluIleGluLeuValSerCysCysLeuSerAlaAsnAlaValIlySerLeu 840
    |||
Db 2692 GACCTTGAAGAAATTCATTTAGTCTCTGCTGCTGCTTGTCTGCAAAATGCAAGTAAATCTTA 2751
QY 841 AlaGluAsnLeuHisAsnLeuValIlySerIleLeuAspLeuSerGluAsnTyrLeu 860
    |||
Db 2752 GCTCAGAAATCTTCACAATTTGTCAAAACCTGAGCATTTCTTGAATTAATCAGAAAATTA 2811
QY 861 GluIlyAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGln 880
    |||
Db 2812 GAAAAAGATGGAATGAAGGCTTTCATGAACTGATCGACAGAGATGAACGCTCTGAAACAG 2871
QY 881 LeuThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerLeuSerSerLeuLeu 900
    |||
Db 2872 CTCACCGACATGATGCTCCCTCGGCGCTGATGCTGCAAGCAGCAGCTTGAAGCCTGTG 2931
QY 901 LysHisLeuGluGluValProGluLeuValIlySerLeuGlyLeuIlyAsnTyrArgLeuThr 920
    |||
Db 2932 AAAATTTGAGAGAGGCTCCCACTGCAAGCTTGGGTTGAAAAAATGAGAGACTGACA 2991
QY 921 AspThrGluIleArgIleLeuGlyAlaPhePheGlyIlyAsnProLeuIlyAsnPheGln 940
    |||
Db 2992 GATCAGAGGATTAAGAAATTTTGGTGCATTTTGGAAAGAACCTCTGAAAAACCTTCCAG 3051
QY 941 GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrPheAlaPheMetGlyVal 960

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Db 3052 CAGTTGAATTTGGCGGAAATCGTGTGAGCAGTGTGATGGCTGCTCATGGGTGA 3111
QY 961 PheGluAsnLeuIlyGlnLeuValPhePheAspPheSerThrIlyGluPheLeuProAsp 980
    |||
Db 3112 TTGGAATCTTAAACCAATTAATGTTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGT 3171
QY 981 ProAlaLeuValArgIlyLeuSerGlnValLeuSerIlySerLeuThrPheLeuGluGluAla 1000
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Db 3172 CCAGCATTTAGTCAGAAAACCTTAAGCCAAAGTGTATTCAAAGTTACTTTCTGCAAGAACT 3231
QY 1001 ArgLeuValIlyTyrPGLnPheAspAspAspLeuSerValIleThrGlyAlaPheIly 1020
    |||
Db 3232 AGGCTTGTGGGTGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3291
QY 1021 LeuValThrAla 1024
    |||
Db 3292 CTAGTAACTGCT 3303

RESULT 15
US-09-922-279-1319
: Sequence 1319, Application US/09922279
: GENERAL INFORMATION:
: APPLICANT: Tang, Yuanhua T.
: APPLICANT: Tillinghast, John
: APPLICANT: Slinku, Ankura
: APPLICANT: Liu, Chenghua
: APPLICANT: Drmanac, Radote J.
: TITLE OF INVENTION: Novel Contigs Obtained
: TITLE OF INVENTION: From Various Libraries
: FILE REFERENCE: 785
: CURRENT APPLICATION NUMBER: US/09/922, 279
: PRIOR FILING DATE: 2001-08-03
: PRIOR APPLICATION NUMBER: 09/491,404
: PRIOR FILING DATE: 2001-01-25
: NUMBER OF SEQ ID NOS: 3796
: SOFTWARE: PL_sp_genes Version 1.0
: SEQ ID NO 1319
: LENGTH: 3545
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: sig_peptide
: LOCATION: (781)..(916)
: OTHER INFORMATION: this location contains the signal peptide sequence,
: OTHER INFORMATION: MIMSGCKALKKFFFLRSRAGGGLFLLCDQLDIPETIR, Run with Signal
: NAME/KEY: misc_feature
: LOCATION: (679)..(3279)
: OTHER INFORMATION: similar to g13688110 in the genepept database release 114,
: OTHER INFORMATION: Run with FASTX 3.3000, default parameters
US-09-922-279-1319

Alignment Scores:
Pred. No.: 0
Score: 5438.00
Percent Similarity: 99.71%
Best Local Similarity: 99.71%
Query Match: 99.62%
DB: 34
Length: 3545
Matches: 1021
Conservative: 0
Mismatch: 3
Indels: 0
Gaps: 0

US-09-697-089-2 (1-1024) x US-09-922-279-1319 (1-3545)
QY 1 MetAsnPheIleYsAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20
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Db 232 ATGATTTTCATTAAGAGACAAATAGCCGACCTTATTTCAAAAGATGGGATGACTGTATA 291
QY 21 LysGlnIleThrAspAspLeuPheValIleThrAsnValLeuAsnArgGluGluValAsnIle 40
    |||
Db 292 AAGCAATACACAGATGACCTATTTGTATGAGATGCTTGAATCCGGAAGATTAACATC 351
QY 41 IleCysCysGluIlyValGluGlnAspAlaIlaArgGlyIleIleHisMetIleLeuIly 60
    |||
Db 352 ATTTGCTCGGAAGAGGTGAGACAGAGATGCTCTGAGAGGAGATTCACATGATTTTGAA 411

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OY	61	LysGIserGIserCySaInLeuPheLeuLYSSerLeuLYSGluTrpAsnTrpProLeu	80
Db	412	AAGGTTACAGAGTCTGTAACTCTTCTTAATATCCCTTAAGAGTGAATATCTCTTA	471
OY	81	PheGIAsnLeuAsnGLYInserLeuPheHisGIInThrSerGIuLYSLeuAspSP	100
Db	472	TTTCAGACTTGAAATGGACAAAGCTTTTTCATCAACATCCAGAAAGAACTTGGACGAT	531
OY	101	LeuAlaInAsnLeuLYSAspLeuTrpHisThrProSerPheLeuAsnPheTrpProLeu	120
Db	532	TTGGCTCAGATATTAAGAGACTTGATACCATACCACATCTTTCTGAACTTATCCCTT	591
OY	121	GIuLYSAsnPIleAsnPIleIlePheAsnLeuLYSserThrPheTrGIuProValLeuTrp	140
Db	592	GGTGAAGTATATGGACATATATTTTAACTTGAAGAAAGCACTTCACAAACACTTCCTGTGG	651
OY	141	ArgLYSAspGIInHisHisArgValGIuGIInLeuThrLeuAsnGLYLeuGIInAla	160
Db	652	AGGAAGAGCAACACCATCAACCCGTGGAGACTGACCTCGAATGGCTCTTGCAGGCT	711
OY	161	LeuGIInSerProCYSLIleIleGIuGLYserGIuLYSGLYLYSserThrLeuGIIn	180
Db	712	CTTCAGAGCCCTTCATCATTTGAAGGGGAAATCTGGCAAGGCAAGCCACTCTGCTGAG	771
OY	181	ArgIleAlaMetLeuTrpGLYserGIuLYSGLYValAlaLeuThrIlyPheIlyPheVal	200
Db	772	CGCATTCGCATGCTCTGTGGGCTCGGGAABATGGAAAGCTCTGACCAAGTCAAAATCTGTG	831
OY	201	PhePheLeuArgLeuSerArgAlaGIInGLYIleuPheGIInThrLeuCYSAspIInLeu	220
Db	832	TTTCTCCCTCCCTCACACAGGGCCAGAGGGGACTTTTGAACCCCTGTGATCAACTC	891
OY	221	LeuAspIleProGLYTrpIleArgLYSGLInThrPheMetAlaMetLeuIlyserLeuArg	240
Db	892	CTGGATATACCTGGCAAAATCAGGAACCAACATTCATGGCCATGGCTGTGAAGCTGGGG	951
OY	241	GIInArgValLeuPheLeuLeuAspGLYTrpAsnGLIuPheLYSProGIInAsnCYSProGIu	260
Db	952	CAGAGGGTTCTTTTCTTCTTGTGAATGGCTCAATGAATTCAGGCCCAAGCCCAAGTCCACAGA	1011
OY	261	IleGIuAlaLeuIleLYSGLIuAsnHisArgPheLYSAsnMetValIleValInThrThr	280
Db	1012	ATCGAAGCCCTCGATTAAGGAAGAAACCAACCGCTTCAAGACATGGTCACTCCACTACC	1071
OY	281	ThrGIuCYSLeuArgHisIleArgGIInPheGIuAlaLeuThrAlaGIuValGIuAspMet	300
Db	1072	ACTGATGCTCGAGAGCAACATACGGCAGTTTGGTCCCTGATCGTGAAGTGGGGGATATGG	1131
OY	301	ThrGIuAspSerAlaGIInAlaLeuIleArgGIuValLeuIleLYSGluLeuAlaGLY	320
Db	1132	ACAGAAACACAGCCGCCAGGCTCTCATCCGGAAGTCTGATCAAGGACTTCTCTAAGGC	1191
OY	321	LeuLeuLeuGIInIleGIInLYSserArgCYSLeuArgAsnLeuMetLYSTrpProLeuPhe	340
Db	1192	TTGTGTCCTCCAAATTCGAAATCCAGGTGCTTAGGAATCTCATGAAGACCCCTCTCTTT	1251
OY	341	ValValIleThrCYSLaIleGIInMetGLYIuSerGIuPheHisSerHisThrGIInThr	360
Db	1252	GTGGTCATCACTTGTGCATACCGAATGGGGAAGTGAAGTTCACCTCTCACACACAAACA	1311
OY	361	ThrLeuPheHisThrPheTrpAspLeuLeuIleGIInLYSAsnIlyHisIlyHisGLY	380
Db	1312	ACGGCTGTCCATTACCTTCTATGATCTGTGTATACAAAAAACAACAAACAAATATAAAGT	1371
OY	381	ValAlaIlaIleSerAspPheIleIleArgSerLeuAspHisCYSGIAspLeuAlaLeuIly	400
Db	1372	GTGGCTGGAAGTGACTTCATTCGGAGGCTGGACACATGTGGATACCTAGCTTGGAGGCT	1431
OY	401	ValPheSerHisLYSLeuAspPheGIuLeuGIInAspValIleSerValAsnGIuAspVal	420
Db	1432	GTGTTCCTCCCAAGTTTGATTTTCGAATCGAAGATGTGTCCAGCTGTGAATAGGATGTG	1491

QY	421	LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys	440
Db	1492	CTGGGACAACTGGGCTCCCTGTAATAATATACAGCTCAAAAGGTTCAAGCCAAAGATATAA	1551
QY	441	PhePheHisLysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerLeuLeuThr	460
Db	1552	TTCTTTCAAGATCATTCACAGAGTACACAGCAGGACGAAAGCTACAGATTATTTAGCG	1611
QY	461	SerHisGluProGlnGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerLeu	480
Db	1612	TGCTATGAGCCACAGAGGAGGAGACCAAGGGGAATGGTTACTTGACAGAAATGGTTCCATT	1671
QY	481	SerAspIleIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu	500
Db	1672	TGCGCAATTACATCCACTTTATACAGCTGGCTCCGGTCAACCTGTGGGTCACTGTGGAA	1731
QY	501	AlaThrArgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuLeuGly	520
Db	1732	GCCACACAGGGCTGTTATGAAGACCTTCGACAGCTGATATCAACAGCGGCTTCGGA	1791
QY	521	LeuSerIleAlaLysArgProLeuTyrParGlnGlnSerLeuGlnSerValLysAsnThr	540
Db	1792	CTTTCACATCGCCACAGAGCGCTCTCTGGAGACAGAGATCTTTGCCAAAGTGTAAAAACAC	1851
QY	541	ThrGlnGlnGluIleLeuLysAlaAlaLeuAsnIleAsnSerPheValGluCysGlyIleHis	560
Db	1852	ACTGACGAGAAATTCGAAAGCCATTAACATCAATTCCTTGTTAGAGTGTGGCATCAT	1911
QY	561	LeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGlnAlaPheGln	580
Db	1912	TTATATCAAGAGATACATCCAAATCGCCCTGAGCCAAAGAAATTTGAAGCTTCTTTAA	1971
QY	581	GlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrIleuPheAspPheGln	600
Db	1972	GGTAAAGCTTATATATCACTACAGGGAACATCCCGGATTTACTTATTTGACTCTTTGAA	2031
QY	601	HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyAla	620
Db	2032	CATTTGCCCAATTTGCAAGTGGCTCGGACTTCATTTAACTGGGCTTTTATAGGGGAGCT	2091
QY	621	MetAlaSerTrpGluLysAlaAlaGluAspThrGlyGlyIleHisMetGlnGluAlaPro	640
Db	2092	ATGGCTTCATGGGAAAAGGCTGCCAGAGACACAGGTGGGATCCACATGGAGAGGCCCA	2151
QY	641	GluThrTyrIleProSerArgAlaValSerLeuPheAsnTrpLysGlnGluPheArg	660
Db	2152	GAAACCTACATTCACACAGAGGGCTGATCTTTGTTCTCACTGAGAGAGGAATTCAGG	2211
QY	661	ThrLeuGlnValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeu	680
Db	2212	ACTCTGGAGGTCAACCTCCGGGATTCAGCAAGTTGAATAACAGATATACGATATCTCG	2271
QY	681	GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVal	700
Db	2272	GGGAAATATTCACCTCTGCGACAGAGCTCAAGCTCCAAATTAAGATAGTGCTGGTGTG	2331
QY	701	AlaGlySerLeuSerLeuValIleuSerThrCysLysAsnIleTyrSerLeuMetValGlu	720
Db	2332	GCTGGAAGCCCTCATTTGGTCCCTACAGACCTGTAAACAACATTTATCTCTCATGTGTGAA	2391
QY	721	AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr	740
Db	2392	GCCAGTCCCTCACCATAGAAAGATGAGAGCAGCATCACTGTGTAAACAACCTGAAAC	2451
QY	741	LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGly	760
Db	2452	TTTGATATCTATGACCTTAACAGAAATCAACGGCTCCCGGGTGGTCACTACACAGCTTGGGT	2511
QY	761	AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAla	780
Db	2512	AACTTGGAAGAACCTTACAAAGGCTCATATATGATTAACATTAAGATGAATGAAGACATCT	2571
QY	781	IleLysLeuAlaGlnGluIleLysAsnLeuLysMetCysLeuPheHisIleuThrHis	800



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Db 2572 ATAAACTAGCTGAAGCCCTGAAAAAAGAGATGTGTTATTCATTGACCCAC 2631
OY LeuSerAspIleGlyGluGlyMetAspTyrIleValIysSerLeuSerSerGluProCys 820
Db 2632 TTGTCGACATTGGAGAGGAAATGATACATAGCAAGTCTCTGCAAGTGAAACCTGT 2691
OY AspleuGIuGIleGIleuValSerCysCysLeuSerAlaAsnAlaValIysIleLeu 840
Db 2692 GACCTTGAAAGAAATTCATTAGTCTCCCTGCTGCTGTGTCGAAATGCAGTAAAAATCCTA 2751
OY AlaGlnAsnLeuHisAsnLeuValIysLeuSerIleLeuAspLeuSerGluAsnTyrLeu 860
Db 2752 GCTCAGAACTTCAACAATTTGGTCAAACTGAGACATTTTGATTTATCAGAAAAATTACCTG 2811
OY GluIysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGln 880
Db 2812 GAAAAAGATGAAATGAAAGCTTTCATGAACTGATCGACAGATGAACTGCTGAAACAG 2871
OY LeuThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerLeuSerSerLeu 900
Db 2872 CTCACCGACATGATGCTCCCTGGGGCTGTGACGTGCAAGCGACCTGAGCAGCCTGTG 2931
OY LysHisLeuGIuGIuValProGlnLeuValIysLeuGIuLeuLysAsnTyrArgLeuThr 920
Db 2932 AAACATTGGAGAGAGTCCCACTGCTCAAGCTTGCGTTGAAAAACTGGAGACTCACA 2991
OY AspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln 940
Db 2992 GATACAGAGATTAGAAATTTAGTGCAATTTTGGAAAGAACCCCTGAAAAACTTCCAG 3051
OY GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrPheValAlaPheMetGlyAla 960
Db 3052 CAGTTGAATTTGGCGGGAATCGTGTGACAGTATGATGATGCTTGCTTCATGGGTGA 3111
OY PheGlnAsnLeuLysGlnLeuValPhePheAspPheSerThrIysGluPheLeuProAsp 980
Db 3112 TTGAGAAATCTTAAGCAATTAGTGTGTTTGTACTTAAGTAAGAAATTTCTACTGAT 3171
OY ProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGluAla 1000
Db 3172 CCACCATTAGTCAGAAAAAAGTCCAGGTATCCAAAGTTAACTTTCTGCAAGAAAGCT 3231
OY ArgLeuValGlyTyrGlnPheAspAspAspAspLeuSerValIleThrGlyAlaPheLys 1020
Db 3232 AGGCTTGTTGGGTGGCAATTTGATGATGATGATCTCAGTGTATATACAGGTGCTTTAA 3291
OY LeuValThrAla 1024
Db 3292 CTAGTAACTGCT 3303
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Search completed: January 31, 2003, 13:16:41  
Job time : 5276 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 31, 2003, 08:55:41 : Search time 310 Seconds

(without alignments)  
4026.925 Million cell updates/sec

Title: US-09-697-089-2

Perfect score: 5459

Sequence: 1 MNFIKDSRALIQMGMTVI.....MQPDDDLSTVITGAFKLVTA 1024

Scoring table:

PAM120	4.0 ,	Xgapext 12.0
Xgapop	4.0 ,	Ygapext 12.0
Fgapop	6.0 ,	Fgapext 7.0
Delop	6.0 ,	Delext 7.0

Searched: 2500250 seqs, 609544256 residues

Total number of hits satisfying chosen parameters: 5000500

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB-pending_Patents_NA_New-QFMT-fastap -SUFFIX=p2n.rnpa -MINMATCH=0.1
-LOOPCL-0 -LOOPEXT=0 -UNITS-bits -START=1 -END=1 -MATRIX-pam120
-TRANS-human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09697089 -ECGN_1_1_114 -etunat_29012003.092506.19212
-NCPU=6 -ICPU=3 -NO_XLPHY -NO_MMAP -LARGQUERY -NEG_SCORES=0 -WAIT -LONGLOG
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=4 -XGAPEXT=12 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=4 -YGAPEXT=12 -DELOP=6 -DELEXT=7

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Database :

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3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5453	99.9	3075	1	PCT-US02-21946A-1
2	5453	99.9	3219	1	PCT-US02-21946A-14
3	5438	99.6	3545	6	US-10-276-781-111
4	435	8.0	421	6	US-10-203-138A-4307
5	391	7.2	220	6	US-10-203-138A-9429
6	279	5.1	5984	6	US-10-285-408-2
7	279	5.1	6133	5	US-09-949-002-84
8	279	5.1	6133	5	US-09-949-002-125
9	279	5.1	60194	5	US-09-949-002-656
10	279	5.1	60195	5	US-09-949-002-697
11	270	4.9	3210	5	US-09-724-676-6819

12	270	4.9	3210	5	US-09-724-676A-6819	Sequence 6819, Ap
13	270	4.9	3597	5	US-09-724-676-6801	Sequence 6801, Ap
14	270	4.9	3597	5	US-09-724-676A-6801	Sequence 6801, Ap
15	270	4.9	4143	5	US-09-724-676-6810	Sequence 6810, Ap
16	270	4.9	4143	5	US-09-724-676A-6810	Sequence 6810, Ap
17	270	4.9	4259	5	US-09-724-676-6816	Sequence 6816, Ap
18	270	4.9	4259	5	US-09-724-676A-6816	Sequence 6816, Ap
19	270	4.9	4268	5	US-09-724-676-6824	Sequence 6824, Ap
20	270	4.9	4268	5	US-09-724-676A-6824	Sequence 6824, Ap
21	270	4.9	4280	5	US-09-724-676-6818	Sequence 6818, Ap
22	270	4.9	4280	5	US-09-724-676A-6818	Sequence 6818, Ap
23	270	4.9	4646	5	US-09-724-676-6798	Sequence 6798, Ap
24	270	4.9	4646	5	US-09-724-676A-6798	Sequence 6798, Ap
25	270	4.9	4667	5	US-09-724-676-6800	Sequence 6800, Ap
26	270	4.9	4667	5	US-09-724-676A-6800	Sequence 6800, Ap
27	270	4.9	5189	5	US-09-724-676-6815	Sequence 6815, Ap
28	270	4.9	5189	5	US-09-724-676A-6815	Sequence 6815, Ap
29	270	4.9	5192	5	US-09-724-676-6807	Sequence 6807, Ap
30	270	4.9	5192	5	US-09-724-676A-6807	Sequence 6807, Ap
31	270	4.9	5210	5	US-09-724-676-6817	Sequence 6817, Ap
32	270	4.9	5210	5	US-09-724-676A-6817	Sequence 6817, Ap
33	270	4.9	5213	5	US-09-724-676-6809	Sequence 6809, Ap
34	270	4.9	5213	5	US-09-724-676A-6809	Sequence 6809, Ap
35	270	4.9	5576	5	US-09-724-676-6797	Sequence 6797, Ap
36	270	4.9	5576	5	US-09-724-676A-6797	Sequence 6797, Ap
37	270	4.9	5597	5	US-09-724-676-6799	Sequence 6799, Ap
38	270	4.9	5597	5	US-09-724-676A-6799	Sequence 6799, Ap
39	270	4.9	6122	5	US-09-724-676-6806	Sequence 6806, Ap
40	270	4.9	6122	5	US-09-724-676A-6806	Sequence 6806, Ap
41	270	4.9	6143	5	US-09-724-676-6808	Sequence 6808, Ap
42	270	4.9	6143	5	US-09-724-676A-6808	Sequence 6808, Ap
43	96	1.8	601	5	US-09-949-002-3101	Sequence 3101, Ap
44	96	1.8	601	5	US-09-949-002-3981	Sequence 3981, Ap
45	94	1.7	916	5	US-09-724-676-19376	Sequence 19376, A

# ALIGNMENTS

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RESULT 1
PCT-US02-21946A-1
: Sequence 1, Application PC/TUS0221946A
: GENERAL INFORMATION:
: APPLICANT: Thomas Jefferson University
: APPLICANT: Alomari, Emed S.
: TITLE OF INVENTION: IPAF, AN ICE-PROTEASE ACTIVATING
: TITLE OF INVENTION: FACTOR
: FILE REFERENCE: 480140.477PC
: CURRENT APPLICATION NUMBER: PCT/US02/21946A
: CURRENT FILING DATE: 2002-05-24
: NUMBER OF SEQ ID NOS: 14
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1
: LENGTH: 3075
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(3075)
: PCT-US02-21946A-1

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Alignment Scores:

Pred. No.:	0	Length:	3075
Score:	5453.00	Matches:	1023
Percent Similarity:	99.90%	Conservative:	0
Best Local Similarity:	99.90%	Mismatches:	1
Query Match:	99.89%	Indels:	0
DB:	1	Gaps:	0

US-09-697-089-2 (1-1024) x PCT-US02-21946A-1 (1-3075)

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Db 1 ATGATTTCATTAAGGACAAATAGCCGAGCCCTTATTCAAGAATGGATGACTGTATA 60

QY	21	LysGlnLleThrAspAspLeuPheValTTPAsnValLeuAsnArgGluGluValAsnIle	40
Db	61	AAGCAATTCACAGATGACCTATTGTATGGAATGTTCTGAATCGCGAAGAAGTAAACATC	120
QY	41	IleCysCysGluLysValAGluGlnAspAlaIleArgGlyIleIleHisMetIleLeuLys	60
Db	121	ATTGTCTCGCGAAGGATGGAGACAGAGATGCTGGTACGAGGAGATCAATTCACATGATGTTTTGAA	180
QY	61	LysGlySerGlnSerCysAsnLeuPheLeuLysSerLeuLysGluTTPAsnTyrProLeu	80
Db	181	AAGGTTTCAGAGTCTCTTAACCTCTTTCTTAAATCCCTTAAGAGATGGAATCTCTCTA	240
QY	81	PheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAspAsp	100
Db	241	TTTCAGACGCTGATGAGCAAACTCTTTTTCATCAGACATCAGAGAAGAGACTTGAGCAT	300
QY	101	LeuAlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTyrProLeu	120
Db	301	TTGGCTCAGGATTTAAAGGACTGTACCAATCCCACTTTTCTCAACTTTATATCCCTT	360
QY	121	GlyGluAspIleAspIleIlePheAsnLeuLysSerThrPheThrGluProValLeuTyr	140
Db	361	GGTGAAGATATTCATATATTTTAACTTGAAGAACCTTTCACAGAACTGTCTGTGG	420
QY	141	ArgLysAspGlnHisHisAsnArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAla	160
Db	421	AGGAAGGACCAACACCATCCCGCGTGGAGAGCTGACCTCAATGGGCTCTGGAGGCT	480
QY	161	LeuGlnSerProCysIleIleGluGlyGlnSerGlyLysGlyLysSerThrLeuLeuGln	180
Db	481	CTTCAGAGCCCTGCATCATTTGAAGGGGAAATCTGGCAAAAGCAATCCACTCTGCTGAG	540
QY	181	ArgIleAlaMetLeuTTPGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal	200
Db	541	CGAATTGCATGCTCTGTGGGCTCCGGAAAGTCAGAGGCTCTGACCAAGTTCAATGTCTC	600
QY	201	PhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGluThrLeuCysAspGlnLeu	220
Db	601	TTTCTTCCTCGCTCAGACAGGGCCAGGGGGGACTTTTGAAAACCTCTGTGATCAACTC	660
QY	221	LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg	240
Db	661	CTGGATATACCTGGCACAAATCAGGAAGACAGACTTCATGGCATGCTGCTGAAGCTCGCG	720
QY	241	GlnArgValLeuPheLeuLeuAsnAspGlyTyrAsnGlnPheLysProGlnAsnSerProGlu	260
Db	721	CAGAGGGTCTTTTCTCTTGTGATGGCTCAAAAGAAATTTAAACCCCGAAGACTGGCCAA	780
QY	261	IleGluAlaLeuIleLysGluAsnHisAsnArgPheLysAsnMetValIleValThrThr	280
Db	781	ATCAGAGCCCTGATAAAGAAACCAACCCGTTCAAGACATGTGTATGTGTCACCACTTCC	840
QY	281	ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet	300
Db	841	ACTGATGTCCTCGAGGSCACATACGGGAGTTGGTGGCCCTGACTGTCGAGGTGGGGATATG	900
QY	301	ThrGluAspSerAlaGlnAlaLeuIleIleArgGluValLeuIleLysGluLeuAlaGluLys	320
Db	901	ACAGAGACACAGCCCGGCTGTCAATCCGGAAGTCTCATCAAGAGACTTGTCTGAAGCC	960
QY	321	LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe	340
Db	961	TTGTGTCTCCAAATTCAGAAATCCAGGTGCTTGAGGAATCTCATGAAGACCCCTCTCTTT	1020
QY	341	ValValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnThr	360
Db	1021	GTGGTCATCACTTGTCGAATCAGATGGGGGAAAGTGAATTCCTCACTGCACACAAACA	1080
QY	361	ThrLeuPheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysLysGly	380
Db	1081	ACGGTGTTCATACCTCTTGATCTGTGATTCACAAAAACAAACACAAACATTAAGT	1140

QY	381	VAL	ALA	SER	ASP	PH	ELL	EAR	SER	LEU	ASP	PH	S	CYS	GLY	ASP	LEU	ALA	LEU	GLU	GLY	400	
DB	1141	GTGGCTGCA	AACTG	CTT	CACTT	CGG	AGC	CTG	GA	CCACT	GTG	GA	CCACT	GTG	GA	CCACT	GTG	GA	CCACT	GTG	GA	1200	
QY	401	VAL	PH	SER	TH	S	LYS	PH	ASP	PH	GLU	ASP	PH	GLU	ASP	PH	GLU	ASP	PH	GLU	ASP	420	
DB	1201	GTG	TTCTCC	CA	CAAG	TTG	TA	TTTC	GA	AACTG	CA	AGATG	TC	TC	CA	AGATG	TC	TC	CA	AGATG	TC	1260	
QY	421	LEU	LEU	TH	R	TH	GLY	LEU	LEU	CYS	LYS	TYR	TH	ALA	GLN	ARG	PH	LEU	PRO	LYS	TYR	440	
DB	1261	CTG	CG	ACA	ACT	GG	CT	CC	T	CTG	T	AA	TAT	T	AC	AG	CT	CA	AA	GGT	TC	CA	1320
QY	441	PHE	PH	E	TH	S	LYS	SER	PH	E	GLN	LYR	TH	R	ALA	GLY	ARG	LEU	SER	LEU	LEU	THR	460
DB	1321	TTCTT	TC	CA	AG	T	CA	T	AT	CC	AG	GT	AC	AG	CT	CA	AG	CT	CA	AG	CT	CA	1380
QY	461	SER	TH	S	GLU	PRO	GLU	GLU	VAL	TH	R	LYS	GLY	ASN	GLY	TYR	LEU	GLN	LYS	MET	VAL	SER	480
DB	1381	TC	CA	TG	CA	CG	CA	AG	G	GG	GG	GG	GG	GG	GG	GG	GG	GG	GG	GG	GG	GG	1440
QY	481	SER	ASP	LEU	THR	SER	TH	R	TYR	SER	SER	LEU	LEU	ARG	TYR	TH	CYS	GLY	SER	SER	VAL	GLU	500
DB	1441	TGC	GA	CA	T	TA	CT	CA	CT	T	T	AG	CA	GC	CT	CT	CG	GT	TA	CA	CT	GT	560
QY	501	ALA	THR	ARG	ALA	VAL	MET	LYS	SH	S	LEU	ALA	ALA	VAL	TYR	GLN	SH	GLY	CYS	LEU	LEU	GLY	520
DB	1501	GCC	AC	CA	CA	GG	CG	CT	GT	T	TA	GA	AG	CA	CT	CG	CA	GG	CT	GT	TA	GA	1560
QY	521	LEU	SER	TH	LEU	ALA	LYS	ARG	PRO	LEU	THR	PAR	GLN	SER	LEU	GLN	SER	VAL	LYS	PRO	THR	540	
DB	1561	CTT	TC	CA	TG	CA	AG	CA	AG	CG	CT	CT	CG	CA	AG	CA	AG	CA	AG	CA	AG	CA	1620
QY	541	THR	GLU	GLN	GLU	LEU	LYS	ALA	LEU	ASN	LEU	ASN	SER	PHE	VAL	GLU	CYS	GLY	LEU	SH	LEU	560	
DB	1621	ACT	GA	CA	GA	AA	GA	AA	TT	CT	GA	AA	CC	ATA	CA	AT	CT	CT	TT	GT	TA	AG	1680
QY	561	LEU	TYR	GLN	GLU	SER	TH	R	SER	LYS	SER	ALA	LEU	SER	GLN	GLU	PH	E	GLU	ALA	PH	E	580
DB	1681	TTA	T	AT	TC	CA	AG	AG	ACT	AT	CA	TC	CA	AA	T	CA	AG	CG	CT	TA	GA	CG	1740
QY	581	GLY	LYS	SER	LEU	TYR	LEU	ASN	SER	GLY	ASN	LEU	PRO	ASP	TYR	LEU	PH	E	ASP	PH	E	HEU	600
DB	1741	GGT	AA	AA	CTT	AT	T	AT	CA	CT	CA	CT	CA	GG	AA	AT	CC	CG	AT	T	CT	TT	1800
QY	601	HIS	LEU	PRO	ASN	CYS	VAL	SER	ALA	LEU	ASP	PH	E	LEU	LYS	LEU	ASP	PH	E	TYR	GLY	VAL	620
DB	1801	CAT	TT	G	CC	CA	AA	TT	GT	GA	AG	T	GC	CT	GT	GA	CT	CT	TA	T	TA	AG	1860
QY	621	MET	ALA	SER	TRP	GLU	LYS	ALA	ALA	GLU	ASP	THR	GLY	LEU	SH	GLU	GLU	GLU	ALA	PRO	640		
DB	1861	ATG	CG	T	CA	T	AT	G	GA	AA	G	CG	T	GC	GA	AA	CA	CA	CG	TA	GA	1920	
QY	641	GLU	THR	TYR	LEU		PRO	SER	ARG	ALA	VAL	SER	LEU	PH	E	ASN	TRP	LYS	GLN	UPH	EAR	660	
DB	1921	GAA	AA	CT	CA	AT	T	CC	AC	AG	CG	CT	GT	AT	CT	T	TT	CA	CT	GA	CA	AA	1980
QY	661	THR	LEU	GLU	VAL	THR	LEU	ARG	ASP	PH	SER	LYS	LEU	ASN	LYS	GLN	ASP	LEU	THR	TYR	LEU	680	
DB	1981	ACT	CG	AG	GT	CA	ACT	CC	CG	GA	T	TC	CA	CA	AG	TT	GA	TA	TA	CA	CA	AA	2040
QY	681	GLY	LYS	LEP	SER	SER	ALA	THR	SER	LEU	ARG	LEU	GLN	LEU	LYS	ARG	CYS	ALA	GLY	VAL	700		
DB	2041	GGG	AAA	AA	T	T	C	ACT	CT	G	GC	CA	CA	AG	CT	C	CA	AA	T	AA	GA	TA	2100
QY	701	ALA	GLY	SER	LEU	SER	LEU	VAL	LEU	SER	TH	R	CYS	LYS	ASN	LEU	TYR	SER	LEU	MET	VAL	GLU	720
DB	2101	GCT	GA	AA	CC	CT	CA	GT	T	GG	T	CT	C	AG	CA	CT	GT	TA	AA	AA	CA	ATT	740
QY	721	ALA	SER	PRO	LEU	TH	R	LEU	GLU	ASN	GLY	ASN	GLY	SH	LEU	SER	VAL	THR	ASN	LEU	LYS	THR	760
DB	2161	GCG	AG	T	CC	CT	CA	CT	TA	GA	AA	GA	TA	GA	AG	CG	CA	AT	CA	CT	GT	TA	2220
QY	741	LEU	SER	LEU	SH	ASP	LEU	GLN	ASN	GLN	ARG	LEU	PRO	GLY	GLY	LEU	TH	R	ASP	SER	LEU	GLY	760

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Db 2221 TTGAGTATCTGACCTACACAAATACACGGCTCCGGCTGGCTGACTGACAGCTTGGCT 2280
Qy 761 AsnLeuYsAsnLeuThrLysLeuLleMetAspAsnLleYsMetAsnGluLysAla 780
Db 2281 AACTTGAAGACCTTACAAACCTCATATGATGATTAACATTAAGATGAATGAAGAAGATGCT 2340
Qy 781 IleYsLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis 800
Db 2341 ATAAACTAGCTGAAGGCTGAAAAACCTGAAGAAGATGTTTATTCATTTGACCCAC 2400
Qy 801 LeuSerAspLleGlyGluGlyMetAspTyrLleValLysSerLysSerSerGluProCys 820
Db 2401 TTGCTCAGCATTTGAGAGAGGAAATGATTAATGATCAAGCTCTCTGCAAGTGAACCTTGT 2460
Qy 821 AspleuGluGluLleGluLeuValSerCysLeuSerAlaAsnAlaValLysLleLeu 840
Db 2461 GACCTTGAAGAAATTCATATGCTCCCTGCTGCTGCTGCAAAATGCAATGAATCCCTA 2520
Qy 841 AlaGlnAsnLeuHisAsnLeuValLysLeuSerLleLeuAspLeuSerGluAsnTyrLeu 860
Db 2521 GCTCAGATCTTCACAAATTTGGTCAACCTGACATCTTGTATTAATCAGAAATTAACCTG 2580
Qy 861 GluYsAspGlyAsnGluAlaLeuHisGluLeuLleAspArgMetAsnValLeuGluGln 880
Db 2581 GAAAAAGATGGAATGAAGCTCTTCATGACTGATCGACAGATGAAGCTGCTAGACAG 2640
Qy 881 LeuThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerLeuSerSerLeuLeu 900
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Qy 921 AspThrGluLleArgLleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln 940
Db 2761 GATACAGAGATTGAATTTTGTGTCATTTTGTGAAAGAACCTCTGAAAAACTCCAG 2820
Qy 941 GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrPheAlaPheMetGlyAla 960
Db 2821 CAGTTGATTTGGGGGGAATCGTGTGAGCATGTGATGATGGCTTGGCTTATGGGTGTA 2880
Qy 961 PheGluAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuProAsp 980
Db 2881 TTTAGATATCTTAAGCAATTAAGTGTTTTGTACCTTAAGTAAGAAATTTCTACCTGAT 2940
Qy 981 ProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGluAla 1000
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Qy 1001 ArgLeuValGlyTyrGlnPheAspAspAspLeuSerValIleThrGlyAlaPheLys 1020
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Qy 1021 LeuValThrAla 1024
Db 3061 CTAGTAACCTGCT 3072

RESULT 2
PCT-US02-21946A-14
; Sequence 14, Application PC/TUS0221946A
; GENERAL INFORMATION:
; APPLICANT: Thomas Jefferson University
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: IPAF, AN ICE-PROTEASE ACTIVATING
; TITLE OF INVENTION: FACTOR
; FILE REFERENCE: 480140.477PC
; CURRENT APPLICATION NUMBER: PCT/US02/21946A
; CURRENT FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
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; LENGTH: 3219
; TYPE: DNA
; ORGANISM: Homo sapiens
; PCT-US02-21946A-14

Alignment Scores:
Pred. No.: 0
Score: 5453.00
Percent Similarity: 99.90%
Best Local Similarity: 99.90%
Query Match: 99.89%
DB: 1
gaps: 0

US-09-697-089-2 (1-1024) x PCT-US02-21946A-14 (1-3219)

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Qy 21 LysGlnIleThrAspAspLeuPheValIleTrpAsnValLeuAsnArgGluGluValAsnIle 40
Db 205 AAGCAATCACAGATGACCTATTGTATGATGATGTTCTGAATCGCGAAGATGAACATC 264
Qy 41 IleCysCysGluYsValGluGlnAspAlaIleArgGlyIleIleHisMetLleLeuLys 60
Db 265 ATTGCTCGAGAAAGGTGAGCAGAGATCTCTAGAGGATCATTCATCATATTTTGAAA 324
Qy 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTyrPasnTyrProLeu 80
Db 325 AAGGTTCAAGATCCTGTAACTCTTCTTAATCCCTTAAGAGATGAGATATTCCTCTA 384
Qy 81 PheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAspAsp 100
Db 385 TTTCAGGCTTGAATGAGCAAAAGCTTTTTCATCAGACATCAGAAAGAGACTTGACGAT 444
Qy 101 LeuAlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAspPheTyrProLeu 120
Db 445 TTGGCTCAGATTAAAGAGACTGTACATACCATCTTTTGTGAAATTTTATCCCTT 504
Qy 121 GlyGluAspLleAspLleIlePheAsnLeuLysSerThrPheThrGluProValLeuTyr 140
Db 505 GGTGAAGATATTGACATATTATTATTAACTTGAAGAACACCTTCACGAACCTGCTGTGG 564
Qy 141 ArgYsAspGlnHisHisArgValGluGlnLeuThrLysAsnGlyLeuGlnAla 160
Db 565 AGGAGGACCAACACATACCGCGTGAGAGCTGAGACCTGAATGGCTCTGTGAGCT 624
Qy 161 LeuGlnSerProCysLleIleGluGlyLysSerGlyLysGlyLysSerThrLeuGln 180
Db 625 CTTCAGAGCCCTCGATCATTTGAAGGGGAATCTGGCAAGGCAAGTCCACTGTGTCAG 684
Qy 181 ArgIleAlaMetLeuTyrGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 200
Db 685 CGAATTTGCATGCTCTGGGGCTCCGGAAAGTCAAGGCTTCGACCAAGTTAAATTCCTC 744
Qy 201 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuCysAspGlnLeu 220
Db 745 TTCTTCTCCGCTCAGCAGGAGGCCAGGGTGAACCTTTTGAACCTCTGTGATCAACTC 804
Qy 221 LeuAspLleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLysLeuArg 240
Db 805 CTGATATTAAGTGGACAAATCAGAGAGCAGACATTCAATGAGGCTGCTAAGTGGGG 864
Qy 241 GlnArgValLeuPheLeuLysAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 260
Db 865 CAGAGGGTCTTTCTCTTGTGATGGCTACAAATGAATCAAGCCCAACAACTGGCCCAAA 924
Qy 261 IleGluAlaLeuLleYsGluAsnHisArgPheLysAsnMetValIleValThrThrThr 280
Db 925 ATCGAAGCCGTGATTAAGAAACCAACCGCTTCAAGAAACAGTGCATGCCACATACC 984
Qy 281 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 300
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Db 985 ACTGAGTCCTGAGGACATACGGCAGTTTGGGCCCTGACTGCTGAGGTGGGGATATG 1044  
QY 301 ThrGluAspSerAlaGlnAlaLeuIleargGluValLeuIleuysgluLeuAlaGluGly 320  
|||||  
Db 1045 ACAGAAAGACGGCCCGCAGGCTCTCATCCGAGAAAGTGCTGATCAAGGAGCTTGCGTAAGGC 1104  
QY 321 LeuLeuLeuGlnIleGlnIlySerArgCysLeuArgAsnLeuMetLysThrProLeuPhe 340  
|||||  
Db 1105 TTGTGCTCCCAATTCAGAAATCCAGGTGCTTGAGCAATCTCATGAAGACCCCTCTCTTT 1164  
QY 341 ValValIleIleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnThr 360  
|||||  
Db 1165 GTGGTATCATCTGTGAAATCCAGATGGGTGAAGAGTAGTTCCACTCTCCACACCAACACA 1224  
QY 361 ThrLeuPheHisThrPheArgAspLeuLeuIleGlnIlyAsnLysHisLysHisLysGly 380  
|||||  
Db 1225 AGCCTGTCCATACCTCTCTGATCTGTATACAGAAAAACAACAAACAAACATAAAGGT 1284  
QY 381 ValAlaAlaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGly 400  
|||||  
Db 1285 GTGGCTGCAAGTACCTTCATTCGAGCGCTGACCACTGTGAGACCTAGACTCTTGAGAGGT 1344  
QY 401 ValPheSerHisLysPheAspPheGlnLeuGlnAspValSerSerValAsnGluAspVal 420  
|||||  
Db 1345 GTGTCTCCACCAAGTTGATTCGAATCTGCACTGAGATGTTCACAGCGTGAATGAGATGTC 1404  
QY 421 LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys 440  
|||||  
Db 1405 CTGCTGCAACCTGGCGCTCCTGTGAATATACAGCTCAAAAGTTCAAGCCCAAGATATAAA 1464  
QY 441 PhePheHisLysSerPheGlnGluTyrThrAlaGlyArgLeuSerSerLeuLeuThr 460  
|||||  
Db 1465 TTCTTTCACAAAGTCATTCACGAGGTACACAGAGCAGAAAGACTCACAGATTATTACAG 1524  
QY 461 SerHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle 480  
|||||  
Db 1525 TCTCATAGCCAGAGGAGGAGCCACAGGGAGATGTTACTTGCGAAATAAGTGTTCATTT 1584  
QY 481 SerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu 500  
|||||  
Db 1585 TCGGACATTCATCCATTCATAGCAGCGCTCGGTGACACCTGTGGGTATCTGTGGAA 1644  
QY 501 AlaThrArgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCysLeuLeuGly 520  
|||||  
Db 1645 GCCACCGAGGCTGTATGAGACACCTCGACAGCTGATCAACACGCGCTGCTCTCGGA 1704  
QY 521 LeuSerIleAlaLysArgProLeuThrArgGlnIleSerLeuGlnSerValLysAsnThr 540  
|||||  
Db 1705 CTTTCCATCCGCCAAGAGGCTCTCTGAGACAGGAATCTTTGCAAAAGTGTGAAAAACACC 1764  
QY 541 ThrGlnGlnIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHis 560  
|||||  
Db 1765 ACTGAGCAAGAAATTCGAAAGCCATCAATCAATTCCTTTGTAGAGTGTGGCATCCAT 1824  
QY 561 LeuTyrGlnIleuSerThrSerLysSerAlaLeuSerGlnIlePheGlnIleAlaPhePheGln 580  
|||||  
Db 1825 TTATATCAAGAGATACATCCAAATCAAGCCCTGAGCCCAAGAAATTTGAAGCTTCTTCAA 1884  
QY 581 GlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLeuPheAspPhePheGln 600  
|||||  
Db 1885 CGTAAAGGCTTATATCACTCACTCGAGCAACATCCCGATTACTTATTTGATCTTTGAA 1944  
QY 601 HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyrGlyAla 620  
|||||  
Db 1945 CATTTCGCCAATTTGCAAGGCGCTGACTTCATTAACATGCACTTTTATAGGGGAGCT 2004  
QY 621 MetLaserThrProGluLysAlaAlaGluAspThrGlyIleHisMetGluGluAlaPro 640  
|||||  
Db 2005 ATGGCTTCATGGGAAAGCGTCGACAAAGACACAGGTGAATCCACATGGAAGAGGCCCA 2064  
QY 641 GluThrTyrIleProSerArgAlaValSerLeuPheAsnThrPylsGlnIlePheArg 660  
|||||  
Db 2065 GAAACCTACATTCACAGAGGCTGTATCTTTGTTCTTCAACGTGAGACAGGAATTCAGG 2124

QY 661 ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeu 680  
|||||  
Db 2125 ACTCTGAGGCTCACACTCCCGGATTTTCAGCAAGTTGATTAAGCAATATACAGATCTCTG 2184  
QY 681 GlyLysIlePheSerSerAlaThrSerLeuArgGlnIleLysArgCysAlaGlyVal 700  
|||||  
Db 2185 GGGAAAAATATTCAGCTCTGCGACAGGCTTCAGCTGCAAAATTAAGATGTGCTGGTGTG 2244  
QY 701 AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetValGlu 720  
|||||  
Db 2245 GCTGGAAGCTCAGTTTGGTCTCAGCAGCCTGTGAAGAACTTTATCTCTCATGGTGGAA 2304  
QY 721 AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr 740  
|||||  
Db 2305 GCCAGTCCCTCACCATAGAAAGTAGAGGACACATCACTGTAACTCAACAACTGAAAAACC 2364  
QY 741 LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyLysLeuThrAspSerLeuGly 760  
|||||  
Db 2365 TTGAGTATTCATGACCTTACAGAAATCAACGGCTCGGGGTGCTGACTGACAGCTTGGGT 2424  
QY 761 AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluAspAla 780  
|||||  
Db 2425 AACTTGAAGAACCCTTACAAAGCTCATATATGATTAACATTAAGATGAAGAAGATGCT 2484  
QY 781 IleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisIleThrHis 800  
|||||  
Db 2485 ATAAACTACTGTAAGGCTCGAAAAACCTGAAAGATGTGTTATTTACTTTGACCCAC 2544  
QY 801 LeuSerAspIleGlyGlnGlyMetAspTyrIleValLysSerLeuSerGluProCys 820  
|||||  
Db 2545 TTGTCTACATTTGAGAGGGAAATGATACATGTCAGTCTCGTCAAGTGAACCTGTG 2604  
QY 821 AspLeuGlnGluIleGlnLeuValSerCysLysSerLeuSerAlaAsnAlaValLysIleLeu 840  
|||||  
Db 2605 GACCTTGAAGAAATTCATTAATAGTCTCCTGCTGCTGTCTGCAAAATGCAAGAAATCTTA 2664  
QY 841 AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeu 860  
|||||  
Db 2665 GCTCAGAAATCTTCACAATTTGGTCAAACTGAACTGACATCTTATATTATTCAGAAATTTACTCTG 2724  
QY 861 GluLysAspGlyAsnGlnIleAlaLeuHisGlnLeuIleAspArgMetAsnValLeuGlnGln 880  
|||||  
Db 2725 GAAAAAGATGGAATGAAGGCTTTCATGAACCTGATCAACAGATGAACGCTGTGAAACAG 2784  
QY 881 LeuThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerLeuSerSerLeuLeu 900  
|||||  
Db 2785 CTCACGGCAGTGAATGCTGCCCTGGGCTGTGAGCTGCAAGGACGCTGAGCAGCCTGTGTG 2844  
QY 901 LysHisLeuGlnGluValProGlnLeuValLysLeuIleLysLeuLysAsnThrPheGluThr 920  
|||||  
Db 2845 AAACATTTGGAGGAGGCTCCCAACCTGCTCAAGCTTGAGTGAAGAACTGAGACCTACA 2904  
QY 921 AspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln 940  
|||||  
Db 2905 GATACAGAGATAGAAATTTAGATGCAATTTTGGAAAGAACCTCTCGAAAAACTTCCAG 2964  
QY 941 GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrLeuAlaPheMetGlyVal 960  
|||||  
Db 2965 CAGTTGAATTTGGCGGGAATTCGTGTAGCAGTATGATGATGCTTGCTTCATGAGGTGA 3024  
QY 961 PheGluAsnLeuLysGlnLeuValPhePheAspPheSerThrLysGluPheLeuProAsp 980  
|||||  
Db 3025 TTATGAGATCTTAAGCAATTAAGTGTTTTGTGACTTTAGTAAAGAAATTTCTACCTGAT 3084  
QY 981 ProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGluAla 1000  
|||||  
Db 3085 CCAGCATTTAGTCAAAAACTTAGCCAGGTGTATCCAAAGTTAACTTTCTGCAAGAAAGCT 3144  
QY 1001 ArgLeuValGlyTyrGlnPheAspAspAspAspLeuSerValIleThrGlyAlaPheLys 1020  
|||||  
Db 3145 AGGCTGTGGTGGCGCAATTTGATGATGATGATCTCAGTGTATTAACAGGTGCTTTAAA 3204

Oy 1021 LeuValThrAla 1024  
|  
Db 3205 CTAGTAAGTCT 3216

RESULT 3  
US-10-276-781-111  
; Sequence 111, Application us/10276781  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides  
; FILE REFERENCE: 21272-018 (785 conf19)  
; CURRENT APPLICATION NUMBER: us/10/276,781  
; PRIOR FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 09/491,404  
; NUMBER OF SEQ ID NOS: 2018  
; SOFTWARE: FASTSEQ for Windows Version 3.0  
; SEQ ID NO 111  
; LENGTH: 3545  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-276-781-111

Alignment Scores:  
Pred. No.: 0 Length: 3545  
Score: 5438.00 Matches: 1021  
Percent Similarity: 99.71% Conservative: 0  
Best Local Similarity: 99.71% Mismatches: 3  
Query Match: 99.62% Indels: 0  
Gaps: 0

US-09-697-089-2 (1-1024) x US-10-276-781-111 (1-3545)

Oy 1 MetAsnPhelIeLysAspAsnSerArgAlaLeuIleGlnArgMetClyMetThrValIle 20  
Db 212 ATGAATTTTCATAAAGACAAATAGCCGACCCCTTATTCAAGAATGGATGACTGTATA 291

Oy 21 LysGlnIleThrAspAspLeuPheValIleTrpAsnValIleAsnArgGluGluValAsnIle 40  
Db 292 AAGCAAAACACAGATGACCTATTGTGTATGAAATGTCGAATCCGGAAGATAAACATC 351

Oy 41 IleCysCysGluLysValGluGlnAspAlaIleArgGlyIleIleHisMetIleLeuLys 60  
Db 352 ATTGGCTCCGGAAGGTGAGCAGGATCTGCTAGAGGATCATTCACATGATTTTGAA 411

Oy 61 LysGlySerGlnSerCysAsnLeuPheLeuLysSerLeuLysGluIleTrpAsnTyrProLeu 80  
Db 412 AAGGGTTCAGAGTCCCTGTAACCTCTTCTTAATCCCTTAAGAGTGAACATACCTCTA 471

Oy 81 PheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGluGlyAspLeuAspAsp 100  
Db 472 TTTCAGGACTTGAAATGCAAGATCTTTTCATCAGACATCAGAAAGGAGACTTGACGAT 531

Oy 101 LeuAlaGlnAspLeuLysAspLeuTyrHisThrProSerPheLeuAsnPheTyrProLeu 120  
Db 532 TTGGCTCCGGAATTAAGGACTTGTACCATACCCCATCTTTCTGAACTTTTATCCCTT 591

Oy 121 GlyIleAspIleAspIleIlePheAsnLeuLysSerThrPheThrGluProValLeuTrp 140  
Db 592 GGTGAAGATATTGACATATTATTTAACTTGAAGAACACCTTCACAGAACCTGCTGTGG 651

Oy 141 ArgIleAspGlnHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAla 160  
Db 652 AGGAGAGCCAAACACACACACCGGTGAGACGTCGAACTGGAATGGCTCTGACAGCT 711

Oy 161 LeuGlnSerProCysIleIleGluGlyLysSerGlyLysSerThrLeuLeuGln 180  
Db 712 CTTCAGAGCCCTGCATATTGAAGGGGAATCTGGCAAGGCAAGTCCACTGCTGTGAG 771

Oy 181 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 200  
Db 772 CGCATTCGCAATGCTCTGGGGCTCCGGAAGATGCAAGGCTCTGACCAAGTTCAAAATTCGTC 831

Oy 201 PhePheLeuArgLeuSerArgAlaGlnGlyGluPheGlnThrLeuCysAspGlnLeu 220  
Db 832 TTCTTCCTCCGCTCAGCAGGGCCGAGGGTGACTTTTGAACCCCTGTGATCACTC 891

Oy 221 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLysLeuArg 240  
Db 892 CTGGAATATACCGGACACATCAGAGACGACATTCATGGCCATCTGTAAGCTGGGG 951

Oy 241 GlnArgValIleuPheLeuLysPclYTrpAsnGluPheLysProGlnAsnCysProGlu 260  
Db 952 CAGAGGGTCTCTTCTCTTGATGCTACATGAATCAAGCCCCCAAGCTGCCAGAA 1011

Oy 261 IleGluAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValIleThrThr 280  
Db 1012 ATCGAAGCCCTGATTAAGGAAACCCAGCTTCAAGAACATGATGCTGACCACTACC 1071

Oy 281 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 300  
Db 1072 ACTGAGTCCCTGAGGACATACGAGGAGTTGGTGGCCCTGAGCTGAGAGTGGGAGATAG 1131

Oy 301 ThrGluAspSerAlaGlnAlaLeuIleArgGluValIleuLysGluLeuAlaGluGly 320  
Db 1132 ACAGAAAGACAGGCCCGCCAGGCTCTCATCCGAGAACTGATCAAGAGACTTGTAAGGC 1191

Oy 321 LeuLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPhe 340  
Db 1192 TTGGTGTCCAAATTCACAAATCCAGGTGCTGAGGAATCTCATGAACCCCTCTCTTT 1251

Oy 341 ValValIleThrCysAlaIleGlnMetGlyLysSerGluPheHisSerHisThrGlnThr 360  
Db 1252 GTGGTCATCAGCTTGTCATATCAGATGGGTGAATGATGATTCACATCCACACAAACA 1311

Oy 361 ThrLeuPheHisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysGly 380  
Db 1312 ACGCTGTTCACATCCCTTATGATCTGTGATACAGAAAACAAACAAACATTAAGGT 1371

Oy 381 ValAlaIleAspAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGlnGly 400  
Db 1372 GTGGCTGCAGGACTTATTCGAGGCTGAGCCCTGTGGATCTGACTCTGGAGGGT 1431

Oy 401 ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAsnGluAspVal 420  
Db 1432 GTGTTCTCCCAACAGTTGATTTGCACTGCAGATGTGTCAGGCTGAATAGAGATGTC 1491

Oy 421 LeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLys 440  
Db 1492 CTGCTGACAACTGGGCTCTCTGTAATATACAGCTCAAGGTTCAAGCCAAAGTATGAA 1551

Oy 441 PhePheHisLysSerPheGlnGluTyrThrAlaGlyArgLeuSerSerLeuLeuThr 460  
Db 1552 TTCTTTCACAAAGTCAATTCAGAGATACACAGCAGACCAACAGTCAAGATTTATGGCG 1611

Oy 461 SerHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIle 480  
Db 1612 TCTCATGAGCCAGAGAGGTGACCAAGGGAAATGTTACTTGCAAAAATGCTTTCCATT 1671

Oy 481 SerAspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu 500  
Db 1672 TCGGACATTAATCATTATATAGCAGCTGCTCCGGTACACTGAGGTCATCTGTGAA 1731

Oy 501 AlaThrArgAlaValMetLysHisLeuAlaValIleTrpGlnHisGlyCysLeuLeuGly 520  
Db 1732 GCCACCAAGGCTGTTATAGACACTCCAGCAGAGTATCAACAGCGGCTGCTTCGGA 1791

Oy 521 LeuSerIleAlaLysArgProLeuTrpArgGlnGlnSerLeuGlnSerValLysAsnThr 540  
Db 1792 CTTCATATCGCCAGAGGCTCTCTGAGACAGGAATCTTTGCAAAAGTGTAAAAACACC 1851

Oy 541 ThrGluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysGlyIleHis 560  
Db 1852 ACTGAGCAAGAAATTCCTAAGGCCATTAACATCAATCTCTTGTAGAGTGGGATTCAT 1911



QY 561 LeuTYrGlnGlnSerThrSerLysSerAlaLeuSerGlnGlnupheGlnAlaPhepHeGln 580  
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 Db 1912 TTATATCAAGAGATACATCCAAATCAGCCCTGAGCCAAAGAAATTTGAAGCTTCTTCA 1971  
 QY 581 GlyLysSerLeuYrIleAsnSerGlyAsnIleProAspYrIleuPheAspPhepHeGlu 600  
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 Db 1972 GGTAAGGCTTATATCAACTCAGGGAGACATCCCGATTACTTATTTGACTCTTTGAA 2031  
 QY 601 HisLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheYrGlyAla 620  
 |||||  
 Db 2032 CATTGCCCAATGTGCAAGTGCCTGCTGACTTCACTTAAGCTGGCTTTTATGGGGAGCT 2091  
 QY 621 MetAlaSerTrpGluLysAlaAlaGluAspThrGlyIleHisMetGluAlaPro 640  
 |||||  
 Db 2092 ATGGCTTCATGGGAAAGGCTGAGAGACACAGGTGGAATCCACATGGAAGAGGCCCA 2151  
 QY 641 GluThrYrIleProSerArgAlaValSerLeuPheAsnTrpLysGlnGluPheArg 660  
 |||||  
 Db 2152 GAACCTTACTTCCACAGGCTGATCTTTGTTCTTCAAGTGGAGAGCAAGAAATTCAGG 2211  
 QY 661 ThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrYrLeu 680  
 |||||  
 Db 2212 ACTCTGGAGTTCACACCTCCGGGATTCAGCAAGTTGAATGAAGATATCAGATATCTG 2271  
 QY 681 GlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyVal 700  
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 Db 2272 GGGAAATATTCAGCTCTGCCACACAGCTCAGGCTGCAAAATAAGATGTGCTGCTGTG 2331  
 QY 701 AlaglySerLeuSerLeuValLeuSerThrCysLysAsnIleYrSerLeuMetValGlu 720  
 |||||  
 Db 2332 GCTGGAGGCTCAGTGTGGCTCAGCAGCTGTAAGAACATTATCTCATGTGTGAA 2391  
 QY 721 AlaSerProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLysThr 740  
 |||||  
 Db 2392 GCCAGTCCCTCACCACATAGAAGATGAGAGACATCATCTGTGAACAACTGAAACCC 2451  
 QY 741 LeuSerIleHisAspLeuGlnAsnGlnArgLeuProGlyLeuThrAspSerLeuGly 760  
 |||||  
 Db 2452 TTGGTGTTCATGACCTCAGCAAGAAACAGGCTGCCGGGTGTGTGACTGTGACAGCTTGG 2511  
 QY 761 AsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluAlaAspAla 780  
 |||||  
 Db 2512 AACTTGAAGAACCTTACAAACCTCATATATGATATCAATAAGATGAAGAAAGATGCT 2571  
 QY 781 IleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis 800  
 |||||  
 Db 2572 ATAAACTACTGAAAGCCCTGAAACCTGAAAGATGTGTATTTATTCATTGATGCCAC 2631  
 QY 801 LeuSerAspIleGlyGluGlyMetAspYrIleValLysSerLeuSerSerGluProCys 820  
 |||||  
 Db 2632 TTGTCTGACATTTGAGAGGAGGATGATTAATGATCAAGTCTCTGTCAAGTGAACCTGT 2691  
 QY 821 AspLeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu 840  
 |||||  
 Db 2692 GACCTTGAAGAAATTCATTAATAGTCTCTGCTGTGTCTGCAAAATGCAGTAAAAATCTTA 2751  
 QY 841 AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTrpLeu 860  
 |||||  
 Db 2752 GCTCAGATCTTCAACAATTTGGTCAAACTGAGCATCTCTTGATTTATCAGAAATTAACCTG 2811  
 QY 861 GluLysAspGluAsnGluAlaLeuHisGlnLeuIleAspArgMetAsnValLeuGluGln 880  
 |||||  
 Db 2812 GAAAAAGATGGAATGGAAGCTTTCATGAACGTATGCACAGAGATGAACGTCTCTGAACAG 2871  
 QY 881 LeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeu 900  
 |||||  
 Db 2872 CTACCCCACTGATGCTGCTGCTGGGCTGTGACTGCAAGGACACCTTGAGAGCTGTG 2931  
 QY 901 LysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThr 920  
 |||||  
 Db 2932 AAACATTTGGAGAGGATCCCAACACCTGTCAAGCTTGGGTTGAAAACTGAGAGCTACA 2991  
 QY 921 AspThrIleuIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln 940

Db 2992 GATACAGAGATGGAATTTAGGCGCATTTTGGAAAGAACCTCTGAAAACTCCAG 3051  
 QY 941 GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGlyVal 960  
 |||||  
 Db 3052 CAGTTGAATTTGGCGGAAATTCGTGTGACGACGATGATGAGCTTGCCTTCATGGGTGA 3111  
 QY 961 PheGluAsnLeuLysGlnLeuValPheAspAspPheSerThrLysGluPheLeuProAsp 980  
 |||||  
 Db 3112 TTGAGAAATCTTAAGCAATTAATGTTTGTGACTTGTACTAAAGAAATTTCTAAGTGA 3171  
 QY 981 ProAlaLeuValArgLysLeuSerGlnValLeuSerLysLeuThrPheLeuGlnGluAla 1000  
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 Db 3172 CCAGCATTTAGTCAGAAAACTTACGCCAGGTGTATCCAAAGTTACTTTGCAAGAGCT 3231  
 QY 1001 ArgLeuValGlyTrpGlnPheAspAspAspLeuSerValIleThrGlyAlaPheLys 1020  
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 Db 3232 AGGCTTTGGGTGGCAGAAATTTGATGATGATGATCTGATTTATTCAGGTTGCTTAA 3291  
 QY 1021 LeuValThrAla 1024  
 |||||  
 Db 3292 CTAGTACTGCT 3303

RESULT 4  
 US-10-203-138A-4307  
 ; Sequence 4307, Application US/10203138A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Molecular Dynamics, Inc.  
 ; APPLICANT: Penn, Sharon G.  
 ; APPLICANT: Rank, David R.  
 ; APPLICANT: Hanzel, David K.  
 ; APPLICANT: Chen, Wenshang  
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
 ; FILE REFERENCE: PB 0004 WO 8  
 ; CURRENT APPLICATION NUMBER: US/10/203,138A  
 ; CURRENT FILING DATE: 2002-08-02  
 ; PRIOR APPLICATION NUMBER: US 60/180,312  
 ; PRIOR FILING DATE: 04 February 2000 (04.02.00)  
 ; PRIOR APPLICATION NUMBER: US 60/207,456  
 ; PRIOR FILING DATE: 26 May 2000 (26.05.00)  
 ; PRIOR APPLICATION NUMBER: US 09/632,366  
 ; PRIOR FILING DATE: 03 August 2000 (03.08.00)  
 ; PRIOR APPLICATION NUMBER: GB 24263,6  
 ; PRIOR FILING DATE: 03 October 2000 (03.10.00)  
 ; PRIOR APPLICATION NUMBER: US 60/236,359  
 ; PRIOR FILING DATE: 27 September 2000 (27.09.00)  
 ; PRIOR APPLICATION NUMBER: US 60/234,687  
 ; PRIOR FILING DATE: 21 September 2000 (21.09.00)  
 ; PRIOR APPLICATION NUMBER: US 09/608,408  
 ; PRIOR FILING DATE: 30 June 2000 (30.06.00)  
 ; SOFTWARE: Molecular Dynamics Sequence Listing Engine  
 ; SEQ ID NO 4307  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: MAP TO AC011232.3  
 ; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.5  
 ; US-10-203-138A-4307

Alignment Scores:  
 Pred. No.: 1,15e-55 Length: 421  
 Score: 435.00 Matches: 80  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 7.97% Indels: 0  
 DB: 6 Gaps: 0  
 US-09-697-089-2 (1-1024) x US-10-203-138A-4307 (1-421)

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OY 928 GJALAlaphbPhgLYlysaSnProleuYsaSnPheglInlInleuaSnleAlaIagLYsaN 947
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Db 181 GGtGCAATTTTTGGAAAGAACCCCTCTGAAAAACCTTCACAGAGTTGGAAATTTGGCGGGAAT 240
OY 948 ArGvaIseSerAspGlyrPleuAlaPheMeGlYvaIphGluAaSnleuYsGluen 967
      |||||||
Db 241 CGTGTGAGAGAGTGAATGATGGCTTGCTTCATCGTGTATTTGAGAAATCTTAACCAATTA 300
OY 968 ValPhepheaSpPheSerThrylsGluPheleuProaSpProAlaIeuaValArgLYsleu 987
      |||||||
Db 301 GGTGTGTTTGAACCTTAGTACTAAAGAAATTTCTACGTGATCCAGCATATGTCAGAAAACCTT 360
OY 988 SerGlnValleuSerLYsleuThrPheleuGlnGluAlaArgleuValIgyTrpGlnPhe 1007
      |||||||
Db 361 ACCCAAGTGTATTCCAAAGTTAACTTTTCGCAAGAAGCTAGGCTGTGTGGGTGCAAAATTT 420

RESULT 5
US-10-203-138A-9429
/ Sequence 9429, Application US/10203138A
/ GENERAL INFORMATION:
/ APPLICANT: Molecular Dynamics, Inc.
/ APPLICANT: Penn, Sharon G.
/ APPLICANT: Rank, David R.
/ APPLICANT: Hanzel, David K.
/ APPLICANT: Chen, Wensheng
/ TITLE OF INVENTION: HUMAN GENOME- DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
/ FILE REFERENCE: PB 0004 WO 8
/ CURRENT APPLICATION NUMBER: US/10/203,138A
/ CURRENT FILING DATE: 2002-08-02
/ PRIOR APPLICATION NUMBER: US 60/180,312
/ PRIOR FILING DATE: 04 February 2000 (04.02.00)
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 26 May 2000 (26.05.00)
/ PRIOR APPLICATION NUMBER: US 09/632,366
/ PRIOR FILING DATE: 03 August 2000 (03.08.00)
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 03 October 2000 (03.10.00)
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 27 September 2000 (27.09.00)
/ PRIOR APPLICATION NUMBER: US 60/234,687
/ PRIOR FILING DATE: 21 September 2000 (21.09.00)
/ PRIOR APPLICATION NUMBER: US 09/608,408
/ PRIOR FILING DATE: 30 June 2000 (30.06.00)
/ NUMBER OF SEQ ID NOS: 15438
/ SOFTWARE: Molecular Dynamics Sequence Listing Engine
/ SEQ ID NO 9429
/ LENGTH: 220
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: MAP TO AC011232.3
/ FEATURE:
/ OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.5
/ FEATURE:
/ OTHER INFORMATION: NT HIT: U75273.1, EVALUE 8.20e+00
/ FEATURE:
/ OTHER INFORMATION: EST_HUMAN HIT: AI263294.1, EVALUE 1.00e-121
/ OTHER INFORMATION: SWISSPROT HIT: P24583, EVALUE 1.60e+00
US-10-203-138A-9429

Alignment Scores:
Pred. No.: 2,37e-49 length: 220
Score: 391.00 Matches: 73
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 7.16% Indels: 0
DB: 6 Gaps: 0

OY 944 LeuAlaGlyAsnArgValSerSerAspGlyTrPleuAlaPheMeGlYvaIphGluAaSn 963
US-09-697-089-2 (1-1024) x US-10-203-138A-9429 (1-220)

```

[illegible]





Best Local Similarity: 32.61% Mismatches: 156  
 Query Match: 5.11% Indels: 15  
 DB: 5 Gaps: 6  
 US-09-697-089-2 (1-1024) x US-09-949-002-656 (1-60194)

QY 150 GUGLInleuThrLeuAnGLyLeuLeuGlnAlaLeuInserProCysIleIleGluGly 169  
 DB 40978 GAACCTGTGGCTGCTGAGCTGTTGGCAACTTGAACCTGTGATGTGTGGAGGGT 41037  
 QY 170 GUGSerIlySGlyLysSerThrLeuLeuGlnArgIleAlaMetLeuTrpGlySerGly 189  
 DB 41038 GAACCTGGAAGTGAAGAGAGCGCTCTCTGAAGAAATAGCTTTCTGTGGCATCTGGA 41097  
 QY 190 LysCysLysAlaLeuThrLysPheValPhePheLeuArgLeuSer-----Arg 207  
 DB 41098 TGCTGTCCCTGTTAAACAGAGTTCACAGCTGTTTCTACCTCCCTAGTTCACACAGA 41157  
 QY 208 AlagInIlyGlyLeuPheGluThrLeuCysAspGlnIleLeuAspIleProGlyThrIle 227  
 DB 41158 CCACAGCAGGGGGCGCCAGTATCATCTGTGACCACTCCCTAGAGAAAGAGATCTGTT 41217  
 QY 228 ArgGlySlnThrPheMetAlaMetLeuLeuLeuArgGlnArgValLeuPheLeu 247  
 DB 41218 ACTGAATGTGCATGAGGAACATTAATCCAGCAGTTAAAGATCAGGCTTAATCTTTTA 41277  
 QY 248 AspGlyTyraSngluPheLysProGlnAsnCysProGluIleGluAlaLeuLysGlu 267  
 DB 41278 GATGACTACCAAGAAATATGTCAATCCCT---CAAGTCATAGCAAAACGATTCATAAAA 41334  
 QY 268 AsnHisArgPheLysAsnMetValIleValIleThrThrThrGlyCysLeuArgHisIle 287  
 DB 41335 AACCACTATCCCGACCTGCTATGATGCTGCTCCGTCACAAACAGGCCAGGACATC 41394  
 QY 288 ArgGlnPheGlyAlaLeuThrAlaGluValaGlyAspMetThrGluAspSerAlaGlnAla 307  
 DB 41395 CGCCGATACCTAGACCACTTATAGATGATCAAGCAATTCCTTTTAAATACGTCTGT 41454  
 QY 308 LeuIleArgGluValLeuIleLysGluLeuAla-----GluGlyLeuLeuGlnIle 325  
 DB 41455 ATATTACGAAGCTCTTTACATAATATAGCTGTGCGAAGTTTAAATGTTTACTT 41514  
 QY 326 GlnLysSerArgCysLeuAlaGlnLeuMetLysThrProLeuPheValIleThrCys 345  
 DB 41515 GGAAGAGAACCAAACTTGCAGAGATACAGAAACTCTCTGTTGTGGCGCATCTGT 41574  
 QY 346 Ala-IleGlnMetLysGluSerGlnPheHisSerHisThrGlnThrIlePheHisIle 365  
 DB 41575 GCTCATTTGGTTTCAGTATCTTTGACCCATCTTT---GATGATGTGGCTGTTTCAAGTC 41633  
 QY 365 rPheTyraSngluPheLeuIleGlnLysAsnLysHisLysGlyValaAlaAlaSerAs 385  
 DB 41634 CTAAATGGAAGCTTTCCTTAAGCAACAA-----GCGACAGCTGAAT 41678  
 QY 385 rPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluValaPheSerHisLys 405  
 DB 41679 TCTCAAGCAACTGTCTGCTCTCTGTGAGCTGCTTGAAGAGGTTTTCATGTGTG 41738  
 QY 405 sPheAsnArgPheGluLeuGlnAspVal-----SerSerValAsnGluAspValLeuLeu 423  
 DB 41739 CTTTGAGCTTTAATGATATGATGCTCGCAAGAGCAGGGGTGATGAGATGAAGATCTAAC 41798  
 QY 423 rThrGlyLeuLeuCysLysTyrrThrAlaGlnArgPheLysProLysTyrrPhePheHis 443  
 DB 41799 CATGTGCTGTGATGAGCAAAATTTACAGCCAGACCTAAAGACATTTCAACCGGTTTTTAAG 41858  
 QY 443 LysSerPheGlnIlyuTyrrThrAlaGlyArgGluSerSerLeuLeuThrSerHisGly 463  
 DB 41859 TCCGCTCTCCCAAGAAATTTCTGCGGGAGATGAGGCTGATGAACCTCGATTCAGATAG 41918  
 QY 463 uProGluGluValThrLysGlyAsnGlyTyrrLeuGlnLysMetValSerIleSerAspIle 483  
 DB 41919 GCAGGAACATCAAGATTTGGAGCTGTATCATTTGAAACAAATCAATCAACCATGATGAC 41978

QY 483 eThrSerThrYSerSerLeuLeuArgTyrrThrCysGly---SerSerValGluAlaIle 502  
 DB 41979 TGTAAGCGGCTACAAACAATTTTGAACATATGCTCCAGCCTCTCAACAAAGACAG 42038  
 QY 502 rArgAlaValMetLysHisLeu 509  
 DB 42039 GCCCAAAATGTGTCTCATTTG 42060

## RESULT 10

US-09-949-002-697  
 ; Sequence 697, Application US/09949002  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 ; WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION  
 ; TITLE OF INVENTION: AND USES THEREOF  
 ; FILE REFERENCE: C1000790  
 ; CURRENT APPLICATION NUMBER: US/09/949,002  
 ; CURRENT FILING DATE: 2000-01-28  
 ; PRIOR APPLICATION NUMBER: 60/231,401  
 ; PRIOR FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ. ID NOS: 10823  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ. ID NO 697  
 ; LENGTH: 60195  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 ; US-09-949-002-697

Alignment Scores:  
 Pred. No.: 4,93e-29 Length: 60195  
 Score: 279.00 Matches: 120  
 Percent Similarity: 53.80% Conservative: 78  
 Best Local Similarity: 32.61% Mismatches: 156  
 Query Match: 5.11% Indels: 15  
 DB: 5 Gaps: 6

US-09-697-089-2 (1-1024) x US-09-949-002-697 (1-60195)

QY 150 GUGLInleuThrLeuAnGLyLeuLeuGlnAlaLeuInserProCysIleIleGluGly 169  
 DB 40978 GAACCTGTGGCTGCTGAGCTGTTGGCAACTTGAACCTGTGATGTGTGGAGGGT 41037  
 QY 170 GUGSerIlySGlyLysSerThrLeuLeuGlnArgIleAlaMetLeuTrpGlySerGly 189  
 DB 41038 GAACCTGGAAGTGAAGAGAGCGCTCTCTGAAGAAATAGCTTTCTGTGGCATCTGGA 41097  
 QY 190 LysCysLysAlaLeuThrLysPheValPhePheLeuArgLeuSer-----Arg 207  
 DB 41098 TGCTGTCCCTGTTAAACAGAGTTCACAGCTGTTTCTACCTCCCTAGTTCACACAGA 41157  
 QY 208 AlagInIlyGlyLeuPheGluThrLeuCysAspGlnIleLeuAspIleProGlyThrIle 227  
 DB 41158 CCACAGCAGGGGGCGCCAGTATCATCTGTGACCACTCCCTAGAGAAAGAGATCTGTT 41217  
 QY 228 ArgGlySlnThrPheMetAlaMetLeuLeuLeuArgGlnArgValLeuPheLeu 247  
 DB 41218 ACTGAATGTGCATGAGGAACATTAATCCAGCAGTTAAAGATCAGGCTTAATCTTTTA 41277  
 QY 248 AspGlyTyraSngluPheLysProGlnAsnCysProGluIleGluAlaLeuLysGlu 267  
 DB 41278 GATGACTACCAAGAAATATGTCAATCCCT---CAAGTCATAGCAAAACGATTCATAAAA 41334  
 QY 268 AsnHisArgPheLysAsnMetValIleValIleThrThrThrGlyCysLeuArgHisIle 287  
 DB 41335 AACCACTATCCCGACCTGCTATGATGCTGCTCCGTCACAAACAGGCCAGGACATC 41394  
 QY 288 ArgGlnPheGlyAlaLeuThrAlaGluValaGlyAspMetThrGluAspSerAlaGlnAla 307  
 DB 41395 CGCCGATACCTAGACCACTTATAGATGATCAAGCAATTCCTTTTAAATACGTCTGT 41454  
 QY 308 LeuIleArgGluValLeuIleLysGluLeuAla-----GluGlyLeuLeuGlnIle 325

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Db 41455 AATTATCGGAACCTCTTTACATATATGACTCGTCTCGGAAGTTTATGTTACTTT 41514
      :::::||||| :::::
Qy 326 GlnlySerArgCysLeuArgAnLeuMetLysTrhProLeuPheValAlIethrCys 345
      |||:::|||||:::
Db 41515 GGAAGAACAAGTTTGCAGAAATACAGAAACCTCTCTTGTGTGGCGGATCTGT 41574
      |||:::|||||:::
Qy 346 Ala-IleGlnMetGlyGluSerGluPheHisSerHisTrhGlnTrhTrhLeuPheHisTrh 365
      ||| ||| ::::: |||:::
Db 41575 GCTCATTTGGTTTCACTATCTTTTGAACCCATCTTT-GATGATGTGGCGTTTTCAGAGC 41633
      ::::: |||::: |||:::
Qy 365 rPheTrpAspLeuLeuIleGlnLysAsnLysHisLysHisLysGlyValAlAlAlSerAs 385
      ::::: |||::: |||:::
Db 41634 CATATGGAACCCCTTTCTCTTAAAGAACAA-----GGCAGCTGAAT 41678
      ::::: |||::: |||:::
Qy 385 PheIleArgSerLeuAspHisCysGlyAspLeuAlaleuGlnGlyValPheSerHisLys 405
      ::::: |||::: |||:::
Db 41679 TCTCAAGCAACTGTGCTCCTGTGTGAGCTGGCTTGAAGGGTTTTTTTCATGTGTG 41738
      |||:::|||||:::
Qy 405 sPheAspPheGluLeuGlnAspVal-----SerSerValAsnGluAspValLeuLeuTh 423
      |||:::|||||:::
Db 41739 CTTTGAATTTAATGATGATGATCTGCAGAACAGGGGTTGATGAAGATGAATCTAAC 41798
      |||:::|||||:::
Qy 423 rThrGlyLeuLeuCysLysTrpTrhAlaGlnArgPheLysProLysTrpLysPhePheTrh 443
      |||:::|||||:::
Db 41799 CATGTGCTTGATGACAAATTTTACAGCCAGACTAAGACCATTTCTACCGGTTTTTAAG 41858
      |||:::|||||:::
Qy 443 sLysSerPheGlnGluTrpTrhAlaGlyArgArgLeuSerSerLeuLeuTrhSerHisG1 463
      ::::: |||::: |||:::
Db 41859 TCCTGCTTCCTCAAGAAATTTCTTGGCGGGATGAGCTGATTTGAACCTGATTCAGATAG 41918
      ::::: |||::: |||:::
Qy 463 uProGluGluValThrLysGlyAsnGlyTrpLeuGlnLysMetValSerIleSerAspI1 483
      ||| ||| |||
Db 41919 GCAGGAACATCAAGATTGGGAGCTGATCATTTGAAACAATCAACTCCCATGATGAC 41978
      ||| ||| |||
Qy 483 eThrSerThrTrpSerSerLeuLeuArgTrpTrhCysGly---SerSerValGluAlaTh 502
      |||:::|||||:::
Db 41979 TGTAAAGCGGCTACAAACATTTTGTGAACATATGCTCCAGCCCTCTTCAACAAAGCAG 42038
      |||:::|||||:::
Qy 502 rArgAlaValMetLysHisLeu 509
      ::::: |||:::
Db 42039 GCCCAAAATTTGTCTCATTTG 42060
      ::::: |||:::
RESULT 11
US-09-724-676-6819
; Sequence 6819, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6819
; LENGTH: 3210
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-6819

Alignment Scores:
Pred. No.: 2,22e-29 Length: 3210
Score: 270.00 Matches: 116
Percent Similarity: 53.13% Conservative: 79
Best Local Similarity: 31.61% Mismatches: 159
Query Match: 4.95% Indels: 13
DB: 5 Gaps: 9

US-09-697-089-2 (1-1024) x US-09-724-676-6819 (1-3210)
Qy 150 GlnGlnLeuTrhLeuAsnGlyLeuLeuGlnAlaLeuGlnSerProCysIleIleGlnGly 169
      ||| ||| |||
Db 693 GAACCTTGCTGCTGCTGCTGCTGCTTTGGCAACTGTGAACCTGTGATGTGTGAGGGGT 752
```

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Qy 170 GluSerGlyLysGlyLysSerTrhLeuLeuGlnAlaGlyIleAlaMetLeuTrpGlySerGly 189
      |||:::|||||:::
Db 753 GAAGCGGAAGTGCAGAAAGGCTCTCGAAGAAATATGCTTTGTGTGGCATCTGCA 812
      |||:::|||||:::
Qy 190 LysCysLysAlaLeuThrLysPheLysPheValPhePheLeuArgLeuSer-----Arg 207
      ||| ||| ::::: |||:::
Db 813 TCGTGTCCCTGTTAAACAGGTTCCAGCTGGTTTCTACTCTCTCCCTTAGTTCCACCAGA 872
      ||| ||| |||
Qy 208 AlaGlnGlyLysLeuPheGluTrhLeuCysAspGlnLeuLeuAspIleProGlyTrhIle 227
      ::::: |||::: |||:::
Db 873 CCAGACGAGGGGCTGGCCAGTATCATCTGTGACCGAGCTCTAGAGAAAGAGATCTGTT 932
      |||:::|||||:::
Qy 228 ArgLysGlnTrhPheMetAlaMetLeuLeuLysLeuArgGlnArgValLeuPheLeuLeu 247
      ::::: |||::: |||:::
Db 933 ACTGAATGCTGRTGAGAACATTTCCAGCAGTTAAACAAAGAGTCTTATCTCTTTTA 992
      ||| ||| |||
Qy 248 ASPGLYTYRAsnGluPheLysProGlnAsnGlyProGluIleGluAlaLeuIleLysGlu 267
      ||| ||| |||
Db 993 GATGACTACAAAGAAATATATGTTCAATCCT---CAAGTCATAGAAACTGATCAAAA 1049
      ||| ||| |||
Qy 268 AsnHisArgPheLysAsnMetValIleValIleTrhTrhTrhGluCysLeuArgHisIle 287
      ||| ||| |||
Db 1050 AACCACTTATCCCGGACCTGCTATGATGCTGTCGCCAGAACAGGGCCAGGACATC 1109
      ||| ||| |||
Qy 288 ArgGlnPheGlyAlaLeuTrhAlaGluValAlaAspMetTrhGluAspSerAlaGlnAla 307
      |||:::|||||:::
Db 1110 CCCCAGTACCTAGAACACATTTCTAGAGATCAAGCATTTCCCTTTATATATCTGTCTGT 1169
      |||:::|||||:::
Qy 308 LeuIleArgGluValLeuIleLysGluLeuAla-----GluGlyLeuLeuLeuGlnIle 325
      ::::: |||::: |||:::
Db 1170 AATTATCGGAACCTCTTTACATATATGATGATGCTGCTCGGAAAGTTATGTTACTTT 1229
      ::::: |||::: |||:::
Qy 326 GlnlySerArgCysLeuArgAnLeuMetLysTrhProLeuPheValAlIethrCys 345
      |||:::|||||:::
Db 1230 GGAAGAACAAGTTTGCAGAAATACAGAAACCTCTCTGTGTGGCGGCGATCTGT 1289
      |||:::|||||:::
Qy 346 AlaIleGlnMetGlyGluSerGluPheHisSerHisTrhGlnTrhTrhLeuPheHisTrh 365
      ||| ||| |||
Db 1290 GCT---CATTTGTTTCAATATCTTTGACCCATCTTTGAAGGTTTTTTTCATGTTGC 1340
      ||| ||| |||
Qy 366 PheTrpAspLeuLeuIleGlnLysAsnLysHisLysHisLysGlyValAlAlAlaSerAsp 385
      ||| ||| |||
Db 1341 TTCAGTCTCTATATG---GAAGCCTTCTCTTAAGAACAAAGCCAGACGCTAAAT--- 1394
      ||| ||| |||
Qy 386 PheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGlnGlyValPheSerHisLys 405
      ::::: |||::: |||:::
Db 1395 CTCAAGCAACTGTGCTCCCTGCTGTGAGCTGGCTTGAAGGGTTTTTTTCATGTTGC 1454
      |||:::|||||:::
Qy 406 PheAspPheGluLeuGlnAspVal-----SerSerValAsnGluAspValLeuLeuThr 423
      |||:::|||||:::
Db 1455 TTTGAGTTTAAATGATGATATCTCGCAGAACAGGGGTTGATGAAGATGAACATCTAAC 1514
      |||:::|||||:::
Qy 424 rThrGlyLeuLeuCysLysTrpTrhAlaGlnArgPheLysProLysTrpLysPhePheHis 443
      |||:::|||||:::
Db 1515 ATGTGCTTGTATGACAAATTTTACAGCCAGACACATTAAGCATTTCTACCGGTTTTTAAGT 1574
      |||:::|||||:::
Qy 444 LysSerPheGlnGluTrpTrhAlaGlyArgArgLeuSerSerLeuLeuTrhSerHisGlu 463
      ::::: |||::: |||:::
Db 1575 CTTGCTTCCAGAAATTTCTTCCGGGAGTGAAGCTGATTTGAACCTCTCGATTCACATAGG 1634
      ||| ||| |||
Qy 464 ProGluGluValThrLysGlyAsnGlyTrpLeuGlnLysMetValSerIleSerAspIle 483
      ||| ||| |||
Db 1635 CAGGAACATCAAGATTGGGAGCTGATCATTTTGAACAACAACTCAACCCATGATGACT 1694
      ||| ||| |||
Qy 484 ThrSerThrTrpSerSerLeuLeuArgTrpTrhCysGly---SerSerValGluAlaTrh 502
      |||:::|||||:::
Db 1695 GTAAAGCGCTACAAACATTTTGTGAACATATGCTCCAGCTCTCCCTTCAACAAAGCAGGG 1754
      |||:::|||||:::
Qy 503 ArgAlaValMetLysHisLeu 509
      ::::: |||:::
Db 1755 CCCAAAAATTTGTCTCATTTG 1775
      ::::: |||:::
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RESULT 12
US-09-724-676A-6819
; Sequence 6819, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6819
; LENGTH: 3210
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-6819

Alignment Scores:
Pred. No.: 2,22e-29 Length: 3210
Score: 270.00 Matches: 116
Percent Similarity: 53.13% Conservative: 79
Best Local Similarity: 31.61% Mismatches: 159
Query Match: 4.95% Indels: 13
DB: Gaps: 9

US-09-697-089-2 (1-1024) x US-09-724-676A-6819 (1-3210)
QY 150 GluGlnLeuThrLeuAsnGlyLeuLeuGlnAlaLeuGlnSerProCysIleIleGluGly 169
DB 693 GAACCTCTGGTGGCTGCTCCGAGAGCTCTTGGAACCTTGGAACCTGTCATGTCGTGGAGGCT 752
QY 170 GluSerGlyLysGlyLysSerThrLeuLeuGlnArgIleAlaMetLeuTrpGlySerGly 189
DB 753 GAACCTGGAACTGGAAGACGCTCCTCCTGAAGAAATAGCTTTCTGTGGGCACTCGA 812
QY 190 LysCysLysAlaLeuThrLysPheLysPheValPhePheLeuArgLeuSer-----Arg 207
DB 813 TGGCTGTCCTCCCTGTAACAGCGTCCAGCTGTTTCTACCTCCCTCCTAGTCCACCGA 872
QY 208 AlaGlnGlyLysLeuPheGluThrLeuGlnSerGlnLeuAspIleProGlyThrIle 227
DB 873 CCAGACGAGGGGCTGGCCAGATATCATCTGTGACCACTCTCTAGAGAAAGAGATCTGTT 932
QY 228 ArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArgGlnArgValLeuPheLeu 247
DB 933 ACTGAATGTCCTGAGAGCAATATATCCAGCATTAAGAAATGAGCTGTATTCCTTTTA 992
QY 248 AspGlyTyrAsnGlnPheLysProGlnAsnGlyProGluIleGluAlaLeuIleLysGlu 267
DB 993 GATGACTGCAAGAAATATGTTCAATCCCT--CAAGTCATAGCAAAACGATTCATAAAA 1049
QY 268 AsnIleArgPheLysAsnMetValIleValThrThrThrGluLysLeuArgHisIle 287
DB 1050 AACCACTTATCCCGCACTGCTATGATGTGCTGCTTACCAAAAGGCGCAGGACATC 1109
QY 288 ArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMetThrGluAspSerAlaGlnAla 307
DB 1110 CGCGGATACCTAGAGACCATCTTAGACATCAAAAGCATTTCCCTTTTAAATACGTCTGT 1169
QY 308 LeuIleArgGluValLeuIleLysGluLeuAla-----GluGlyLeuLeuLeuGlnIle 325
DB 1170 ATATTAGCGAAGCTCTTTTCACTATATATGACTGCTGCGCAAACTTATGCTTACTTT 1229
QY 326 GlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPheValIleThrCys 345
DB 1230 GGAAGAAACCAAGTTTCCAGATACAGAAACTCCTCTTGCGTGGCGCATCTGCT 1289
QY 346 AlaIleGlnMetGlyLysSerGluPheHisSerHisThrGlnThrThrLeuPheHisThr 365
DB 1290 GCT---CATTTGCTTACATATCTTTTACCCATCTTGTATGATGTG-----GCTGCT 1340
QY 366 PheTyrAspLeuLeuIleGlnLysAsnLysHisLysHisLysGlyValAlaAlaLaserasp 385
DB 1340 GCT---CATTTGCTTACATATCTTTTACCCATCTTGTATGATGTG-----GCTGCT 1340

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DB 1341 TTCAAGTCTTATATG---GAAGGCTTTTCTTAAAGAAACCAAGGACGTAAGATT-- 1394
QY 386 PheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGlnGlyValIlePheSerHisLys 405
DB 1395 CTCAAGCAACTGTGTCTCTCTGCTGAGTGGCTGCTTGAAGGGTTTTCATGCTTC 1454
QY 406 PheAspPheGluLeuGlnAspVal-----SerSerValAsnGluAspValLeuLeuThr 423
DB 1455 TTTAGATTATGATGATGATGATCTCGCAGAGCAGGGGTGATGAAGATGAAGATCAAC 1514
QY 424 ThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLysPhePheHis 443
DB 1515 ATGTGCTTGATGAGCAAAATTTTACAGCCAGCACTTAAGCCATTCCTGCTTTTAAGT 1574
QY 444 LysSerPheGlnGlnLysThrAlaGlyArgArgLeuSerSerLeuLeuThrSerHisGlu 463
DB 1575 CCTGCTTCCAAAGATTTCTTGGCGGATGAGGCTGATGAACCTCGATTCAGATAGG 1634
QY 464 ProGluGluValThrLysGlyAsnGlyLysLeuGlnLysMetValSerIleSerAspIle 483
DB 1635 CAGGACATCAAGATTTGGAGCTGATCATTTGAACAAATCACTCACCATGATGACT 1694
QY 484 ThrSerThrTyrSerSerLeuLeuArgTyrThrCysGly---SerSerValGluAlaThr 502
DB 1695 GTAAGCGGCTTACCAAAATTTTGAAGTATGTCACAGCTTCCTTCACCAAAAGCAGGG 1754
QY 503 ArgAlaValMetLysHisLeu 509
DB 1755 CCCAAATGTGTCTCATTTG 1775

RESULT 13
US-09-724-676-6801
; Sequence 6801, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6801
; LENGTH: 3597
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-6801

Alignment Scores:
Pred. No.: 2.59e-29 Length: 3597
Score: 270.00 Matches: 116
Percent Similarity: 53.13% Conservative: 79
Best Local Similarity: 31.61% Mismatches: 159
Query Match: 4.95% Indels: 13
DB: Gaps: 9

US-09-697-089-2 (1-1024) x US-09-724-676-6801 (1-3597)
QY 150 GluGlnLeuThrLeuAsnGlyLeuLeuGlnAlaLeuGlnSerProCysIleIleGluGly 169
DB 1080 GAACCTCTGGTGGCTGCTCCGAGAGCTCTTGGAACCTTGGAACCTGTCATGTCGTGGAGGCT 1139
QY 170 GluSerGlyLysGlyLysSerThrLeuLeuGlnArgIleAlaMetLeuTrpGlySerGly 189
DB 1140 GAACCTGGAATGGAAGACGCTCCTCCTGAAGAAATAGCTTTCTGTGGGCACTGGA 1199
QY 190 LysCysLysAlaLeuThrLysPheLysPheValPhePheLeuArgLeuSer-----Arg 207
DB 1200 TGGCTGTCCTCCCTGTAACAGCGTCCAGCTGTTTCTACCTCCTCCTAGTTCCACCGA 1259
QY 208 AlaGlnGlyLysLeuPheGluThrLeuGlnSerGlnLeuAspIleProGlyThrIle 227
DB 1260 CCAGACGAGGGGCTGGCCAGATATCATCTGTGACCACTCTCTAGAGAAAGAGATCTGTT 1319

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Qy	228	ArgylsGlnThrPheMetAlaMetLeuLeuLysLeuArgGlnArgValLeuPheLeu	247
Db	1320	ACTGAATGTCRCRGGAGGAACATTATTCACGAGTATTAACATACAGCTTTATTCCTTTTA	1379
Qy	248	AspGlyTyrAsnLLeuPheLysProGlnAsnCysProGluIleGluAlaLeuIleLysGlu	267
Db	1380	GATGACCTACAAATAATTTGTTCAATCCCT---CAAGTCATAGGAAACTGATTTCAAAA	1436
Qy	268	AsnHisArgPheLysAsnMetValIleValThrThrThrThrGluCysLeuArgHisIle	287
Db	1437	AACCACTTATCCCGACACTCCGCTATGTATGCTGTCCGTCCATCAACACAGGCGCAGGACATC	1496
Qy	288	ArgGlnPheLysAlaLeuThrAlaGluValIleGlyAspMetThrGluAspSerAlaGln	307
Db	1497	CGCGGATCCCTAGACACCATTTCTAGATCAACAAAGCATTTCCCTTTATATATCTCTGT	1556
Qy	308	LeuIleArgGluValLeuIleLysGluLeuAla-----GluGlyLeuLeuGlnIle	325
Db	1557	ATATTACGGAAGCTCTTTTACATATATATGACTCGTCTCCGAAGTTATGGTTTACTTT	1616
Qy	326	GlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPheValIleThrCys	345
Db	1617	GGAAGAGCAACAAAGTTTGACAGAGATACAGAAAACCTCTCTGTGGCGGCGCATCTGT	1676
Qy	346	AlaIleIleMetGlyLysSerGluPheHisSerHisThrGlnThrThrLeuPheHisThr	365
Db	1677	GCT---CATGGGTTCAGTATCTCTTTGACCAATCCCTTTGAAGATGATGTC-----GCTCCT	1727
Qy	366	PheTyrAspLeuLeuIleGlnLysAsnLysHisLysGluValAlaAlaIleAsp	385
Db	1728	TTTCAAGTCCTATATG---GACGCTCTTCTTAAAGAACAAAGCCACAGCTGAAT---	1781
Qy	386	PheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGlyValPheSerHisLys	405
Db	1782	CTCAACACCACTGTCTCTCTCTGTGGTGAAGCGCTTGAAGGGTTTTCATGTTGC	1841
Qy	406	PheAspPheLysLeuGlnAspVal-----SerSerValAsnGluAspValLeuLeuThr	423
Db	1842	TTTTCAGTTTATATGATGATGATGATCCGACAGACAGAGGGTTGATGAAGATGAAGATCTAAC	1901
Qy	424	ThrGlyLeuLeuLysLysTyrThrAlaGlnAspCysPheLysProLysTyrLysPheHis	443
Db	1902	ATGCGCTTGATGAGCAATTTTACAGCCGACAGACTRAAGCCATTCTACCGGTTTAACT	1961
Qy	444	LysSerPheGlnLysTyrThrAlaGlyArgArgSerSerLeuLeuThrSerHisGlu	463
Db	1962	CTGCGCTTCCAAAGATTTCTGGGGGAGAGAGCGTATGAACCTCTGGATTCAATFAGG	2021
Qy	464	ProGluGluValThrLysGlnGlyTyrLeuGlnLysMetValSerLysSerAspIle	483
Db	2022	CAGGACATCAATGATTTGGAGCTGATCATTTTGAACAAATCAATCACTACCATGATGACT	2081
Qy	484	ThrSerThrTyrSerSerLeuLeuArgTyrThrCysGly---SerSerValGluAlaThr	502
Db	2082	GTAAGCGCCCTACACAAATTTTGGACATGTATGCTCCAGCTCCCTTCAACAAAACAGG	2141
Qy	503	ArgAlaValMetLysHisLeu 509	
Db	2142	CCCAAAATTTGTCTCATTTTG 2162	
RESULT 14			
US-09-724-676A-6801			
: Sequence 6801, Application US/09724676A			
: GENERAL INFORMATION:			
: APPLICANT: Comugen LTD			
: TITLE OF INVENTION: Variants of alternative splicing			
: FILE REFERENCE: 129181.4 Comugen			
: CURRENT APPLICATION NUMBER: US/09/724.676A			
: CURRENT FILING DATE: 2000-11-28			
: NUMBER OF SEQ ID NOS: 97222			
: SOFTWARE: PatentIn version 3.2			
: SEQ ID NO 6801			
LENGTH: 3597			

[illegible]

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QY 444 LysSerPheGlnGluTyrThrAlaGlyArgLeuSerSerLeuLeuThrSerHisGlu 463
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QY 464 ProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIleSerAspIle 483
    ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2022 CAGGAACATCAAGATTGGGACTGTATCATTTGAACAATCAATCAACCCATGATGACT 2081
QY 484 ThrSerThrTyrSerSerLeuLeuArgTyrThrCysGly---SerSerValGluAlaThr 502
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Db 2082 GTAAAGGCTTACACAAATTTTGAACATATGCTCCAGCTCCCTTCAACAAAGCAGGG 2141
QY 503 ArgAlaValMetLysHisLeu 509
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Db 2142 CCCAAATGTGTCTCATTTG 2162

RESULT 15
US-09-724-676-6810
; Sequence 6810, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6810
; LENGTH: 4143
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-6810

Alignment Scores:
Pred. No.: 3,136-29 Length: 4143
Score: 270.00 Matches: 116
Percent Similarity: 53.13% Conservative: 79
Best Local Similarity: 31.61% Mismatches: 159
Query Match: 4,95% Indels: 13
DB: 5 Gaps: 9

US-09-697-089-2 (1-1024) x US-09-724-676-6810 (1-4143)
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Db 1626 GAACCTCTGCTGCTGCTGAGGCTTTGGCACTTGAACCTGCTATGCTGTCGAGGGT 1685
QY 170 GluSerGlyLysGlyLysSerThrLeuLeuGlnArgIleAlaMetLeuTrpGlySerGly 189
    ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1686 GAAGCTGAAGTGGAAAGCGGCTCTCTGAAGAAATAGCTTTTCTGTGGCATCTGGA 1745
QY 190 LysCysLysAlaLeuThrLysPheLysPheValPhePheLeuArgLeuSer-----Arg 207
    ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1746 TGTCTGCTCCCTGTTAAACAGGTTCCAGCTGCTTTTCTACCTCTCCCTTAGTTCACACGA 1805
QY 208 AlaGlnGlyLysLeuPheGlnThrLeuCysAspGlnLeuLeuAspIleProGlyThrIle 227
    :::::::::: ||||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1806 CCAGACGAGGGGCTGGCCAGTATCATCTGTGACACAGCTCCTAGAGAAAGAGATCTGTT 1865
QY 228 ArgLysGlnThrPheMetAlaMetLeuLysLeuArgGlnArgValLeuPheLeuLeu 247
    :::::::::: ||||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1866 ACTGAATGTCGRTGAGAACATTTATCCAGCATTTAAAGATCAGCTTATTCCTTTTA 1925
QY 248 AspGlyTyrAsnGluPheLysProGlnAsnCysProGluIleGluAlaLeuIleLysGlu 267
    ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1926 GATGACTACAAAGAAATATGTTCAATCCT---CAAGTCATAGAAACTGATTCAAAAA 1982
QY 268 AsnHisArgPheLysAsnMetValIleValIleThrThrThrGluCysLeuArgHisIle 287
    ||||| :::::::::: ||| ||| ||| ||| ||| ||| ||| |||
Db 1983 AACCACTTATCCCGGACGCTGCTATGATGCTGTCCGACAAACAGGGCCAGGGACATC 2042
QY 288 ArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMetThrGluAspSerAlaGlnAla 307

```

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Db 2043 CCGCGATACCTAGAGACCATTTCTAGAGATCAAGCATTTCCCTTTATATATCTGCTGT 2102
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QY 308 LeuIleArgGluValLeuIleLysGluLeuAla-----GluGlyLeuLeuLeuGlnIle 325
    :::::::::: ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2103 ATATTACGGAACCTCTTTTACATATATAGACTGCTGCGAAAGTTATGGTTACTTTT 2162
QY 326 GlnLysSerArgCysLeuArgAsnLeuMetLysThrProLeuPheValIleThrCys 345
    ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2163 GGAAGAACCAAGTTTGGAGAGATACAGAAATACTCTCTTGTGTGGCGGCGATCTGT 2222
QY 346 AlaIleGlnMetGlyGluSerGluPheHisSerHisThrGlnThrThrLeuPheHisThr 365
    ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2223 GCT---CATTTGTTACAGATCTTTTGAACCATCTTGAACCATCTTGAAGATGTG-----GCTGCT 2273
QY 366 PheTyrAspLeuLeuIleGlnLysAsnLysHisLysHisLysGlyValAlaAlaSerAsp 385
    ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2274 TTCAGTCTCTATATG---GAACGCTTTCTTACAGAACAAAGCAGACACTGAAT--- 2327
QY 386 PheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGlyValPheSerHisLys 405
    ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2328 CTCAAAGCAACTGTGCTCCCTGCTGCTGAGCTGGCTTGAAGGGTTTTTTTCATGTTGC 2387
QY 406 PheAspPheGlnLeuGlnAspVal-----SerSerValAsnGluAspValLeuLeuThr 423
    ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2388 TTGAGATTAAATGATGATGATCTCCGCAAGCAGGGGTTGATGAAGATGAAGATCTAAC 2447
QY 424 ThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLysPheHis 443
    ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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QY 444 LysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerSerLeuLeuThrSerHisGlu 463
    :::::::::: ||||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2508 CCTGCTTCAGAAATTTCTTGCGGGATGAGGCTGATTAAGTCTCTGATTCAGATAGG 2567
QY 464 ProGluGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIleSerAspIle 483
    ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2568 CAGGAACATCAAGATTGGGACTGTATCATTTGAACAATCAACTCAACCCATGATGACT 2627
QY 484 ThrSerThrTyrSerSerLeuLeuArgTyrThrCysGly---SerSerValGluAlaThr 502
    ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2628 GTAAAGGCTTACACAAATTTTGAACATATGCTTCACAGCTCCCTTCAACAAAGCAGGG 2687
QY 503 ArgAlaValMetLysHisLeu 509
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Db 2688 CCCAAATGTGTCTCATTTG 2708

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Search completed: January 31, 2003, 11:50:02  
 Job time : 402 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OW protein - nucleic search, using frame\_plus\_p2n model

Run on: January 31, 2003, 11:41:11 ; Search time 1277.45 Seconds

(without alignments)  
2004.811 Million cell updates/sec

Title: US-09-697-089-2\_COPY\_1\_88  
Perfect score: 461  
Sequence: 1 MNFKDSRALIQRMGWTVI.....FLKSLKEMNYPLFODLNGQS 88

Scoring table: BIOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n model -DEV=rlh  
-Q/cgna2\_1/USPIO.spool/US09697089/rnuc\_29012003\_092753\_19716/app-query.fasta.1.981  
-DB=GenEmbl -QPM=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=BIOSUM62 -TRANS=human40.cdi -LIST=45  
-DOCALLIGN=200 -THR\_SCORE=pcr -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09697089 @CGN 1.1.3568 @rnuc\_29012003\_092753\_19716 -NCPU=6 -ICPU=3  
-NO\_XLPPY -NO\_MMAP -LARGENQURY -NEG\_SCORES=0 -RAIT -LONGLOG -DEV.TIMEOUT=120  
-MARK.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FEAPOP=6 -FEAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_cm:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_com:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
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28: em\_un:\*

29: em\_vl:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htg\_mus:\*  
34: em\_htg\_pln:\*  
35: em\_htg\_rtd:\*  
36: em\_htg\_mam:\*  
37: em\_htg\_vrt:\*  
38: em\_sy:\*  
39: em\_htgo\_hum:\*  
40: em\_htgo\_mus:\*  
41: em\_htgo\_other:\*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	461	100.0	578	AX318095	AX318095 Sequence
2	461	100.0	578	AY027790	AY027790 Homo sapi
3	461	100.0	768	AX318097	AX318097 Sequence
4	461	100.0	768	AY027789	AY027789 Homo sapi
5	461	100.0	1395	AX318093	AX318093 Sequence
6	461	100.0	1395	AY027788	AY027788 Homo sapi
7	461	100.0	3133	AY032589	AY032589 Homo sapi
8	461	100.0	3219	AY035391	AY035391 Homo sapi
9	461	100.0	3355	AK095467	AK095467 Homo sapi
10	461	100.0	3360	BC031555	BC031555 Homo sapi
11	461	100.0	3396	AX318091	AX318091 Sequence
12	461	100.0	3396	AY027787	AY027787 Homo sapi
13	461	100.0	3581	AF376061	AF376061 Homo sapi
14	457	99.1	261	AX318172	AX318172 Sequence
15	457	99.1	138909	CNS01053	AL121653 BAC seque
16	457	99.1	160583	AC010968	AC010968 Homo sapi
17	341	74.0	107885	AC107111	AC107111 Rattus no
18	311	67.5	185465	AC101793	AC101793 Mus muscu
19	123.5	26.8	1233	AF135968	AF135968 Felis cat
20	118.5	25.7	1215	AF135967	AF135967 Canis fam
21	118.5	25.7	1215	E32836	E32836 Canine inte
22	118.5	25.7	1560	E32838	E32838 Canine inte
23	113	24.5	146451	AC019309	AC019309 Homo sapi
24	113	24.5	161218	AC011171	AC011171 Homo sapi
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26	113	24.5	214484	AP001830	AP001830 Homo sapi
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29	108	23.4	2380	BC016174	BC016174 Homo sapi
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31	108	23.4	2589	AR129832	AR129832 Sequence
32	108	23.4	3532	AR076334	AR076334 Sequence
33	108	23.4	3532	AX410708	AX410708 Sequence
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35	108	23.4	3732	AR106399	AR106399 Sequence
36	108	23.4	3732	AR116701	AR116701 Sequence
37	108	23.4	4089	BC028578	BC028578 Homo sapi
38	106	23.0	257047	AC090879	AC090879 Mus muscu
39	104.5	22.7	156684	AP002787	AP002787 Homo sapi
40	104.5	22.7	172488	AP001153	AP001153 Homo sapi
41	104	22.6	1770	AF184331	AF184331 Rattus no
42	104	22.6	3290	AF190020	AF190020 Rattus no
43	103.5	22.5	1215	AB027296	AB027296 Sus scrofa
44	103.5	22.5	1218	AF090119	AF090119 Equus cab
45	102.5	22.2	321	AX318084	AX318084 Sequence

RESULT 1

## ALIGNMENTS

AX318095 AX318095 578 bp DNA linear PAT 14-DEC-2001  
LOCUS Sequence 100 from Patent WO0190156.  
DEFINITION AX318095  
ACCESSION AX318095.1 GI:17900824  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
human.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
Patent: WO 0190156-A 100 29-NOV-2001;  
The Burnham Institute (US)  
FEATURES  
source  
Location/Qualifiers  
1..578  
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/db\_xref="taxon:9606"  
277..555  
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BASE COUNT 172 a 106 c 143 g 157 t  
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Alignment Scores:  
Pred. No.: 1..4e-51 Length: 578  
Score: 461.00 Matches: 88  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0  
US-09-697-089-2\_COPY\_1\_88 (1-88) x AX318095 (1-578)  
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DB 277 ATGAATTTCAATAAGGCAATAGCCGAGCCCTTATTCAGAAATGGGAATGACGTATATA 336  
QY 21 LysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluGluValAsnIle 40  
DB 337 AAGCAATTCACAGATGACCTATTGTTGATGGAATGTTCTGAATCGCGAAGAAAGTAAACATC 396  
QY 41 IleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60  
DB 397 ATTGCTGCGAGAGAGGTGAGACAGATGCTCTAGAGGATCATTCACATGATTTTGAAA 456  
QY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTrpProLeu 80  
DB 457 AAGGTTTCAGAGTCTCTGTAACCTCTTCTTAATCCCTTAAGAGATGGAACATATCTCTTA 516  
QY 81 PheGlnAspLeuAsnGlyGlnSer 88  
DB 517 TTTCAGGACTTGAAATGACAAAGT 540  
RESULT 2  
LOCUS AY027790 578 bp mRNA linear PRI 20-JUL-2001  
DEFINITION Homo sapiens CLAND (CLAN1) mRNA, complete cds.  
ACCESSION AY027790  
VERSION AY027790.1 GI:14324118  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE  
1 (bases 1 to 578)

AUTHORS Damiano, J.S., Stehlik, C., Pio, F., Godzik, A. and Reed, J.C.  
TITLE Clan, a novel human ced-4-like gene  
JOURNAL Genomics 75 (1-3), 77-83 (2001)  
MEDLINE 21365712  
PUBMED 11472070  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
2 (bases 1 to 578)  
Stehlik, C., Damiano, J.S., Pio, F., Godzik, A. and Reed, J.C.  
Direct Submission  
Submitted (21-FEB-2001) Program on Apoptosis and Cell Death  
Research, The Burnham Institute, 10901 North Torrey Pines Road, La  
Jolla, CA 92037, USA  
FEATURES  
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/product="CLAND"  
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/db\_xref="GI:14324119"  
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KYEDPARGIHMLIKKSESCNLFKSKENNYPLFQDLNGSLTLTA"  
BASE COUNT 172 a 106 c 143 g 157 t  
ORIGIN

Alignment Scores:  
Pred. No.: 1..4e-51 Length: 578  
Score: 461.00 Matches: 88  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0  
US-09-697-089-2\_COPY\_1\_88 (1-88) x AY027790 (1-578)  
QY 1 MetAsnPhelIeLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20  
DB 277 ATGAATTTCAATAAGGCAATAGCCGAGCCCTTATTCAGAAATGGGAATGACGTATATA 336  
QY 21 LysGlnIleThrAspAspLeuPheValTrpAsnValLeuAsnArgGluGluValAsnIle 40  
DB 337 AAGCAATTCACAGATGACCTATTGTTGATGGAATGTTCTGAATCGCGAAGAAAGTAAACATC 396  
QY 41 IleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60  
DB 397 ATTGCTGCGAGAGAGGTGAGACAGATGCTCTAGAGGATCATTCACATGATTTTGAAA 456  
QY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTrpProLeu 80  
DB 457 AAGGTTTCAGAGTCTCTGTAACCTCTTCTTAATCCCTTAAGAGATGGAACATATCTCTTA 516  
QY 81 PheGlnAspLeuAsnGlyGlnSer 88  
DB 517 TTTCAGGACTTGAAATGACAAAGT 540  
RESULT 3  
LOCUS AX318097 768 bp DNA linear PAT 14-DEC-2001  
DEFINITION Sequence 102 from Patent WO0190156.  
ACCESSION AX318097  
VERSION AX318097.1 GI:17900826  
KEYWORDS  
SOURCE  
ORGANISM  
human.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE

REFERENCE 1  
AUTHORS Reed,J.C., Plo,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H.,  
Oliveira,V.A., Hayashi,H. and Pawlowski,K.  
TITLE Card domain containing polypeptides, encoding nucleic acids, and  
METHODS OF USE  
PATENT: WO 0190156-A 102 29-NOV-2001;  
JOURNAL The Burnham Institute (US)  
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Pred. No.: 1.94e-51 Length: 768  
Score: 461.00 Matches: 88  
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DB: 6 Gaps: 0  
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QY 61 LysglYsergluSerCysAsnLeupheLeuIysSerLeuIysgluITrpAsnTyProleu 80  
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DB 517 TTTCAGGACTTGAAATGACAAAGT 540  
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DEFINITION Homo sapiens CLANC (CLANI) mRNA, complete cds.  
ACCESSION AY027789  
VERSION AY027789.1 GI:14324116  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Damiano,J.S., Stehlik,C., Plo,F., Godzik,A. and Reed,J.C.  
TITLE Clanc, a novel human ced-4-like gene  
JOURNAL Genomics 75 (1-3), 77-83 (2001)  
MEDLINE 21365712  
PUBMED 11472070  
REFERENCE 2 (bases 1 to 768)  
AUTHORS Stehlik,C., Damiano,J.S., Plo,F., Godzik,A. and Reed,J.C.  
TITLE Direct Submission  
JOURNAL Submitted (21-FEB-2001) Program on Apoptosis and Cell Death

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BASE COUNT 218 a 157 c 180 g 213 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 1.94e-51 Length: 768  
Score: 461.00 Matches: 88  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
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QY 1 Metasnphelleyaspsasnserrargalaleuileglnargmetglymethrvalille 20  
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QY 21 LysglnlierhraspaspLeupheValITrpasnValleuasnarggluValasnlle 40  
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QY 61 LysglYsergluSerCysAsnLeupheLeuIysSerLeuIysgluITrpAsnTyProleu 80  
DB 457 AAGGTTTCAGAGTCCTCTTAACCTTCTTAATCCCTTAAGAGATGGAATATCCCTTA 516  
QY 81 PheGlnaspLeuAsnGlyGlnSer 88  
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RESULT 5  
LOCUS AX318093 1395 bp DNA linear PAT 14-DEC-2001  
DEFINITION Sequence 98 from Patent WO0190156.  
ACCESSION AX318093  
VERSION AX318093.1 GI:17900822  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Reed,J.C., Plo,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H.,  
Oliveira,V.A., Hayashi,H. and Pawlowski,K.  
TITLE Card domain containing polypeptides, encoding nucleic acids, and  
METHODS OF USE  
PATENT: WO 0190156-A 98 29-NOV-2001;  
JOURNAL The Burnham Institute (US)  
FEATURES  
location/Qualifiers







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Qy      81  PheGlnAspLeuAsnGlyGlnSer 88
Db      385 TTTCAGGACTTGAAATGACAAAGT 408

RESULT 9
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DEFINITION
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to Homo sapiens ICE-protease activating factor mRNA.
ACCESSION
AK093467
VERSION
AK093467.1 GI:21754727
KEYWORDS
oligo capping; fis (full insert sequence).
SOURCE
Homo sapiens CD34+ Cells cDNA to mRNA, clone_1lb:D90ST2
clone:D90ST2003791.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1
Miyoshi, K., Nagatsuma, M., Kanda, K., Kondo, H., Yokoi, T.,
Kodaira, H., Furuya, T., Takahashi, M., Kikkawa, E., Omura, Y., Abe, K.,
Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M.,
Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S.,
Yamamoto, K., Isono, Y., Kawai, H., Saito, K., Nishikawa, T.,
Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M.,
Kikuchi, H., Murakawa, K., Kaneshiro, K., Takahashi-Fujii, A.,
Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S.,
Nagahara, K., Masuno, Y., Nagai, K. and Isogai, T.
NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 3355)
Isogai, T. and Yamamoto, J.
Direct Submission
Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
(E-mail: genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan: cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.
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Score:      461.00      Matches:      88
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RESULT 10
BC031555
LOCUS
DEFINITION
Homo sapiens, caspase recruitment domain protein 12, clone
MGC:35330 IMAGE:5179909, mRNA, complete cds.
ACCESSION
BC031555
VERSION
BC031555.1 GI:21594975
KEYWORDS
MGC.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 3360)
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS
Strausberg, R.
TITLE
Direct Submission
JOURNAL
Submitted (06-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
CONTACT
MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Guarantee, P.H., Garcia, A.M., Lu, X., Huylk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILN at: http://image.llnl.gov
Series: IRAP Plate: 50 Row: 10
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis.
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Db 412 AAGGTTTCAGAGTCTCTTAACCTCTTCTTAATCCCTTAAGAGATGGAACATATCCTCTA 471  
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LOCUS Sequence 96 from Patent W00190156.  
ACCESSION AX318091  
VERSION AX318091.1 GI:17900820  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
1 Reed,J.C., Pio,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H.,  
Oliveira,V.A., Hayashi,H. and Pawlowski,K.

TITLE Card domain containing polypeptides, encoding nucleic acids, and  
JOURNAL methods of use  
Patent: WO 0190156-A 96 29-NOV-2001;  
The Burnham Institute (US)  
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Qy 1 Metanphelellasaspasnserrargalaleuileglnargmetglymetrvalille 20  
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Qy 21 Lysglnlethraspaleuphevalitrrasnvalleuasarggluglvaisnille 40  
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RESULT 12  
AY027787 3396 bp mRNA linear PRI 20-JUL-2001  
LOCUS AY027787  
DEFINITION AY027787 Homo sapiens CLAN1 (CLAN1) mRNA, complete cds.  
ACCESSION AY027787  
VERSION AY027787.1 GI:14324112  
KEYWORDS  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
2 (bases 1 to 3396)  
Stehlik,C., Damiano,J.S., Plo,F., Godzik,A. and Reed,J.C.  
Direct Submission  
Submitted (21-FEB-2001) Program on Apoptosis and Cell Death  
Research, The Burnham Institute, 10901 North Torrey Pines Road, La  
Jolla, CA 92037, USA

## FEATURES

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OY 81 Pheglaspheulansglylinsr 88  
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RESULT 13  
AF376061 3581 bp mRNA linear PRI 15-MAY-2001  
LOCUS  
DEFINITION  
Homo sapiens caspase recruitment domain protein 12 mRNA, complete  
cds

ACCESSION  
AF376061  
AF376061.1 GI:14040074  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
2 (bases 1 to 3581)  
Gingras,M.-C., Qiu,J. and Margolin,J.F.  
Differential expression of the caspase recruitment domain protein  
12 (CARD12) during monocytic differentiation  
Unpublished

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
2 (bases 1 to 3581)  
Gingras,M.-C., Qiu,J. and Margolin,J.F.  
Direct Submission  
Submitted (03-MAY-2001) Pediatric/Texas Children's Cancer Center,  
Baylor College of Medicine, 6621 Fannin St. MC3-3320, Houston, TX  
77030, USA

## FEATURES

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## misc\_feature

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Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0

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DB: 9 Gaps: 0  
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DB 550 AAGCAAAATCACAGATGACCTATTGTATGCAATGTTCTGAATCCGGAAGATAACATC 609  
QY 41 IlecyScyglulysvalgluInaspalaalaarqglylleleHismetlleulelys 60  
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RESULT 14  
AX318172 261 bp DNA linear PAT 14-DEC-2001  
LOCUS AX318172  
DEFINITION Sequence 177 from Patent WO0190156.  
ACCESSION AX318172  
VERSION AX318172.1 GI:17900863  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Reed,J.C., Pio,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H.,  
Oliveira,V.A., Haysht,H. and Pawlowski,K.  
TITLE Card domain containing polypeptides, encoding nucleic acids, and  
methods of use  
JOURNAL Patent: WO 0190156-A 177 29-NOV-2001;  
The Burnham Institute (US)  
FEATURES  
source location/Qualifiers  
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DB 61 AAGCAATACAGATGACCTATTGTATGCAATGTCGAGAAAGATACATC 120  
QY 41 IlecyScyglulysvalgluInaspalaalaarqglylleleHismetlleulelys 60  
DB 121 ATTTCCTCGAGAAAGTGAGAGATGCTGTAAAGGATCATTCACATGATTTTGAAA 180  
QY 61 LysglSerGluSerCyAsnleupheleuysSerleuysgluTrpAsnTyProleu 80  
DB 181 AAGGTTCAAGAGTCTGTACCTTTCTTAATCCCTTAAGAGATGAGACTATCTCTTA 240  
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DB 241 TTTCAGACTTGAATGACAA 261  
RESULT 15  
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LOCUS CNS01DS3  
DEFINITION BAC sequence from the SPG4 candidate region at 2p21-2p22 BAC 164M19  
of library CITB\_978\_SKB from chromosome 2 of Homo sapiens (Human).  
ACCESSION AL121653  
VERSION AL121653.2 GI:7159616  
KEYWORDS SPG4 genomic DNA interval.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 138909)  
AUTHORS Hazan,J., Fonknechten,N., Mavel,D., Paternotte,C., Samson,D.,  
Artiguenave,F., Davoine,C.S., Cruaud,C., Durf,A., Wincker,P.,  
Brotlier,P., Catolico,L., Barbe,V., Burgunder,J.M.,  
Prud'Homme,J.F., Brice,A., Fontaine,B., Hellis,R. and  
Weissenbach,J.  
TITLE Spastin, a novel AAA protein, is altered in the most frequent form  
of autosomal dominant spastic paraplegia  
Natl. Genet. (1999) In press  
REFERENCE 2 (bases 1 to 138909)  
AUTHORS Genoscope.  
TITLE Direct Submission  
JOURNAL Submitted (18-APR-2002) Genoscope - Centre National de Sequencage :  
BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
COMMENT On Mar 6, 2000 this sequence version replaced gi:6002386.  
FEATURES  
source location/Qualifiers  
1..138909  
BASE COUNT 39243 a 28424 c 29121 g 42121 t  
ORIGIN  
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Score: 457.00 Matches: 87  
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Best Local Similarity: 98.86% Mismatches: 0  
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Search completed: January 31, 2003, 15:14:45  
 Job time : 1289.45 secs

GenCore version 5.1.3  
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## OM protein - nucleic search, using frame\_plus.p2n model

Run on: January 31, 2003, 10:49:01 : Search time 104.246 Seconds  
(without alignments)  
1901.038 Million cell updates/sec

Title: US-09-697-089-2\_COPY\_1\_88

Perfect score: 461  
Sequence: 1 MAFKDNKSAALQRMGMVYI.....FLKSLKENVYPLFQDLNGS 88

## Scoring table:

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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2185239 segs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Command line parameters:

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-Q=/cgn2.1/USPTO.spool/US09697089/r/unat\_29012003\_092753\_19709/app\_query.fasta\_1.981  
-DB=N-Geneseq.101002 -OFMT=fastap -SUFFIX=p2n.rng -MIMATCH=0.1 -LOOPL=0  
-LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blonsun62 -TRANS=human40.cdi  
-LIST=45 -DOCLIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
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-USER=US09697089\_@cgn\_1\_1\_276.@unat\_29012003\_092753\_19709 -NCP=6 -ICPU=3  
-NO\_XLPEX -NO\_MMMP -LARGEQUERY -NEG\_SCORES=0 -MAIT -LONGLOG -DEV\_TIMEOUT=120  
-MARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELop=6 -DELEXT=7

## Database :

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24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	461	100.0	578	24	ABK22733	Human CDNA encodin
2	461	100.0	768	24	ABK22734	Human CDNA encodin
3	461	100.0	1395	24	ABK22732	Human CDNA encodin
4	461	100.0	3133	22	AA503945	Human caspase recr
5	461	100.0	3396	24	ABK22731	Human CDNA encodin
6	461	100.0	3545	22	AAH98254	Murine EST-derived
7	458	99.3	3213	22	AAH78219	Nucleotide sequenc
8	457	99.1	261	24	ABK22765	Human CDNA encodin
9	457	99.1	3615	22	AA503946	Human caspase recr
10	392	85.0	2215	22	AAH78218	Nucleotide sequenc
11	118.5	25.7	1215	20	AAH72725	Canine interleukin
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13	118.5	25.7	1560	20	AAH27727	Canine interleukin
14	118.5	25.7	1560	21	AAH13796	Canine interleukin
15	108	23.4	1435	17	AAH43709	Human inhibitor of
16	108	23.4	2589	18	AAH61590	Human c-IAP1. Hom
17	108	23.4	3532	18	AAH72711	Human inhibitor of
18	108	23.4	3532	20	AAH22143	Human cellular inh
19	108	23.4	3532	24	ABH96857	Gene #3355 used to
20	108	23.4	3732	19	AAH55040	Human HIRP-2 codin
21	103.5	22.5	429	22	ABH09527	Human secreted pro
22	103.5	22.5	1215	22	AAH6509	Pig caspase coding
23	102.5	22.2	321	24	ABK22730	Human CDNA encodin
24	102	22.1	2580	18	AAH70838	Human apoptosis in
25	102	22.1	2580	24	ABK93871	Human CDNA encodin
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27	100	21.7	3151	19	AAH55043	Murine HIRP-2 codi
28	97	21.0	1183	22	AAH35011	CDNA encoding nove
29	97	21.0	1487	22	AAH02763	Human CARD contain
30	97	21.0	3863	22	AAH34888	CDNA encoding nove
31	97	21.0	4466	22	AAH02765	Human NAC gamma or
32	97	21.0	4556	22	AAH02762	Human NAC beta iso
33	97	21.0	5059	22	AAH83652	Human CARP-8 polyP
34	96.5	20.9	549	24	ABK12898	Human protease PPT
35	96.5	20.9	879	23	AAH55669	DNA encoding novel
36	96.5	20.9	1252	24	ABK14805	DNA encoding human
37	96.5	20.9	2662	22	AAH86924	Human immune/haema
38	96.5	20.9	2662	22	AAH86925	Human immune/haema
39	96.5	20.9	2669	22	AAH86923	Human immune/haema
40	95	20.6	1215	17	AAH03137	Human interleukin-1-beta
41	95	20.6	1215	20	AAH81217	Nucleotide sequenc
42	95	20.6	1215	22	AAH24471	Human pre-interleu
43	95	20.6	1215	24	AAH03964	Human caspase-1 co
44	95	20.6	1216	20	AAH01277	Human ICE coding s
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## ALIGNMENTS

RESULT 1  
ABK22733 standard; CDNA; 578 BP.

XX ABK22733:

DT 26-MAR-2002 (first entry)

XX Human cDNA encoding CLAN C.

Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;  
abnormal cell proliferation; cancer; abnormal cell death; apoptosis;  
autoimmune disease; inflammation; keratinocyte hyperplasia;  
inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;  
balloon angioplasty; restenosis; glioma; carcinoma; sarcoma;  
leukemia; allergy; arthritis; lupus; Schrogen's syndrome;  
Crohn's disease; graft-versus-host disease; stroke;  
myocardial infarction; heart failure; neurodegenerative disease;

KW Parkinson's disease; Alzheimer's disease; HIV;  
KM human immunodeficiency virus infection.  
XX Homo sapiens.  
OS  
XX WO200190156-A2.  
PN  
XX  
XX 29-NOV-2001.  
PD  
XX  
XX 24-MAY-2001; 2001WO-US17158.  
PF  
XX  
PR 24-MAY-2000; 2000US-0579240.  
PR 10-OCT-2000; 2000US-0686347.  
PR 14-MAR-2001; 2001US-275980P.  
PR 23-MAY-2001; 2001US-0864921.  
XX  
XX  
PA (BURN-) BURNHAM INST.  
XX  
XX  
PI Reed JC, Pio FF, Godzik A, Stenlik C, Damiano JS, Lee SH;  
PI Oliveira VM, Hayashi H, Pawlowski K;  
XX  
XX MPI: 2002-083086/11.  
DR P-PSDB; AAU80863.  
XX  
XX  
PT New caspase recruitment domain (CARD)-containing polypeptides and  
PT encoding nucleic acids, useful for treating abnormal cell proliferation  
PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,  
PT arthritis or stroke -  
XX  
XX  
PS Claim 1; Page 177; 216pp; English.  
XX  
XX  
XX The invention relates to an isolated caspase recruitment domain (CARD)  
XX -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain  
XX from it, and the polynucleotides encoding them. Also included are a  
XX recombinant vector comprising the polynucleotide, recombinant cells  
XX containing the vector (e.g. bacteria, yeast, plant, animal, mammalian  
XX and insect cells) and an anti-CARD antibody. The CARD-containing  
XX polypeptide and CARD-encoding nucleic acid are useful for treating a  
XX pathology characterised by abnormal cell proliferation (e.g. cancer),  
XX abnormal cell death (apoptosis), autoimmune diseases or inflammation. In  
XX particular, the polypeptide and nucleic acid are useful for treating  
XX keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth  
XX muscle cell proliferation in arteries following balloon angioplasty  
XX (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,  
XX allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,  
XX graft-versus-host disease, stroke, myocardial infarction, heart failure,  
XX neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's  
XX disease) or immunodeficiency associated disease (e.g. human  
XX immunodeficiency virus (HIV) infection). The nucleic acids are useful  
XX in a variety of diagnostic applications. The present sequence is a  
XX cDNA encoding a CARD domain containing protein.  
SQ  
SQ Sequence 578 BP; 172 A; 106 C; 143 G; 157 T; 0 other;  
XX  
XX  
XX Alignment Scores:  
XX  
XX Pired. No.: 1,49e-54 Length: 578  
XX Score: 461.00 Matches: 88  
XX Percent Similarity: 100.00% Conservative: 0  
XX Best Local Similarity: 100.00% Mismatches: 0  
XX Query Match: 100.00% Indels: 0  
XX DB: 24 Gaps: 0  
XX  
XX US-09-697-089-2\_COPY\_1\_88 (1-88) x ABK22733 (1-578)  
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DB 277 ATGCAATTTCTAAGAGCAATACCCAGCCCTATTCAAGAGATGGGAATGACTGTATA 336  
OY 21 LysGlnIleThrAspAspLeuPheValITyrAsnValIleuAsnArgGluGluValAsnIle 40  
DB 337 AAGCAATACACAGATGACCATTTGTATGGAATGCTCTGATGCGCAAGAAGTAACATC 396  
OY 41 IleCysGluLysValGluGlnAspAlaAlaArgGlyIleIleIleHisMetIleLeuLys 60

DB 397 ATTGCTGCGAGAGAGTGAGCGATGCTGTAGAGGAGATCATTCATGATTTGAAA 456  
OY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluITyrAsnITyrProlu 80  
DB 457 AAGGTCACAGATCCGTGAACCTTCTTAAATCCCTTAAGAGATGGAATATCTCTTA 516  
OY 81 PheGlnAspLeuAsnGlyGlnSer 88  
DB 517 TTTCAGACTTGATGACCAAACT 540  
XX  
XX  
XX RESULT 2  
XX ABK22734  
XX ID ABK22734 standard; cDNA; 768 BP.  
XX  
XX  
XX ABK22734;  
XX  
XX  
XX 26-MAR-2002 (first entry)  
XX  
XX  
XX Human cDNA encoding CLAN D.  
XX  
XX  
XX Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;  
XX abnormal cell proliferation; cancer; abnormal cell death; apoptosis;  
XX autoimmune disease; inflammation; Keratinocyte hyperplasia;  
XX inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;  
XX balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;  
XX leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;  
XX Crohn's disease; graft-versus-host disease; stroke;  
XX myocardial infarction; heart failure; neurodegenerative disease;  
XX Parkinson's disease; Alzheimer's disease; HIV;  
XX human immunodeficiency virus infection.  
XX  
XX  
XX Homo sapiens.  
XX  
XX  
XX WO200190156-A2.  
XX  
XX  
XX 29-NOV-2001.  
XX  
XX  
XX 24-MAY-2001; 2001WO-US17158.  
XX  
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XX 24-MAY-2000; 2000US-0579240.  
XX 10-OCT-2000; 2000US-0686347.  
XX 14-MAR-2001; 2001US-275980P.  
XX 23-MAY-2001; 2001US-0864921.  
XX  
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XX (BURN-) BURNHAM INST.  
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XX  
XX Reed JC, Pio FF, Godzik A, Stenlik C, Damiano JS, Lee SH;  
XX Oliveira VM, Hayashi H, Pawlowski K;  
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XX MPI: 2002-083086/11.  
XX P-PSDB; AAU80864.  
XX  
XX  
XX New caspase recruitment domain (CARD)-containing polypeptides and  
XX encoding nucleic acids, useful for treating abnormal cell proliferation  
XX or cell death, autoimmune diseases or inflammation, e.g. carcinomas,  
XX arthritis or stroke -  
XX  
XX  
XX Claim 1; Page 178-179; 216pp; English.  
XX  
XX  
XX The invention relates to an isolated caspase recruitment domain (CARD)  
XX -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain  
XX from it, and the polynucleotides encoding them. Also included are a  
XX recombinant vector comprising the polynucleotide, recombinant cells  
XX containing the vector (e.g. bacteria, yeast, plant, animal, mammalian  
XX and insect cells) and an anti-CARD antibody. The CARD-containing  
XX polypeptide and CARD-encoding nucleic acid are useful for treating a  
XX pathology characterised by abnormal cell proliferation (e.g. cancer),  
XX abnormal cell death (apoptosis), autoimmune diseases or inflammation. In  
XX particular, the polypeptide and nucleic acid are useful for treating  
XX keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth  
XX muscle cell proliferation in arteries following balloon angioplasty  
XX (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,



CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,  
CC graft-versus-host disease, stroke, myocardial infarction, heart failure,  
CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's  
CC disease) or immunodeficiency associated disease (e.g. human  
CC immunodeficiency virus (HIV) infection). The nucleic acids are useful  
CC in a variety of diagnostic applications. The present sequence is a  
CC cDNA encoding a CARD domain containing protein.

XX Sequence 768 BP: 218 A; 157 C; 180 G; 213 T; 0 other;

#### Alignment Scores:

Pred. No.:	2.19e-54	Length:	768
Score:	461.00	Matches:	88
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	24	Gaps:	0

US-09-697-089-2\_COPY\_1\_88 (1-88) x ABR22734 (1-768)

Qy 1 MetasnphellielysAspAsnSerArgAlaLeuileglnArqMetGlyMetThyValIle 20  
Db 277 ATGAATTTTCATTAAGACAAATAGCCGACCTTATTTCATAAAGATGGATGACTGTTTATA 336  
Qy 21 LysGlnIleThrAspAspLeuPheValTrrpAsnValIleuAsnArqGluGluValAsnIle 40  
Db 337 AAGCAAAATCACAGATGACCTTATTGTATGAAATGTTCTGAAATCCGGAAGAAATTAACATC 396  
Qy 41 IleCysCysGluIysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuIys 60  
Db 397 ATTGCTGTCGAGAGGTGACAGATGCTCTAGAGGATCATTCACATGATTTTGA 456  
Qy 61 LysGlySerGluSerCysAsnLeuPheLeuIysSerLeuIysGluTrrpAsnTyrProleu 80  
Db 457 AAGGTTTCAGAGTCTGTACCTCTTTCTTAATCCCTTAAGAGTGAATATCTCTTA 516  
Qy 81 PheGlnAspLeuAsnGlyGlnSer 88  
Db 517 TTTCAGAGCTTGATGACAAAGT 540

#### RESULT 3

ID ABR22732 standard; CDNA: 1395 BP.

AC ABR22732;

XX 26-MAR-2002 (first entry)

XX Human cDNA encoding CLAN B.

XX Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;  
XX abnormal cell proliferation; cancer; abnormal cell death; apoptosis;  
XX autoimmune disease; inflammation; keratinocyte hyperplasia;  
XX inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;  
XX leiomyoma angiolipoma; restenosis; glioma; carcinoma; sarcoma; melanoma;  
XX leukemia; allergy; arthritis; lupus; Schrogen's syndrome;  
XX Crohn's disease; graft-versus-host disease; stroke;  
XX myocardial infarction; heart failure; neurodegenerative disease;  
XX Parkinson's disease; Alzheimer's disease; HIV;  
XX human immunodeficiency virus infection.

XX Homo sapiens.

XX MO200190156-A2.

XX 29-NOV-2001.

XX 24-MAY-2001; 2001MO-US17158.

XX 24-MAY-2000; 2000US-0579240.

XX 10-OCT-2000; 2000US-0686347.

XX 14-MAR-2001; 2001US-275980P.

XX 23-MAR-2001; 2001US-0864921.

XX (BURN-) BURHAM INST.

XX Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;

XX Oliveira VAM, Hayashi H, Pawlowski K;

XX WPI; 2002-083086/11.

XX P-PSDB; AAU80862.

XX New caspase recruitment domain (CARD)-containing polypeptides and  
XX encoding nucleic acids, useful for treating abnormal cell proliferation  
XX or cell death, autoimmune diseases or inflammation, e.g. carcinomas,  
XX arthritis or stroke

XX Claim 1; Page 174-176; 216pp; English.

XX The invention relates to an isolated caspase recruitment domain (CARD)  
XX -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain  
XX from it, and the polynucleotides encoding them. Also included are a  
XX recombinant vector comprising the polynucleotide, recombinant cells  
XX containing the vector (e.g. bacteria, yeast, plant, animal, mammalian  
XX and insect cells) and an anti-CARD antibody. The CARD-containing  
XX polypeptide and CARD-encoding nucleic acid are useful for treating a  
XX pathology characterised by abnormal cell proliferation (e.g. cancer),  
XX abnormal cell death (apoptosis), autoimmune diseases or inflammation. In  
XX particular, the polypeptide and nucleic acid are useful for treating  
XX keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth  
XX muscle cell proliferation in arteries following balloon angioplasty  
XX (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukemias,  
XX allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,  
XX graft-versus-host disease, stroke, myocardial infarction, heart failure,  
XX neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's  
XX disease) or immunodeficiency associated disease (e.g. human  
XX immunodeficiency virus (HIV) infection). The nucleic acids are useful  
XX in a variety of diagnostic applications. The present sequence is a  
XX cDNA encoding a CARD domain containing protein.

XX Sequence 1395 BP: 436 A; 248 C; 327 G; 384 T; 0 other;

#### Alignment Scores:

Pred. No.:	4.92e-54	Length:	1395
Score:	461.00	Matches:	88
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	24	Gaps:	0

US-09-697-089-2\_COPY\_1\_88 (1-88) x ABR22732 (1-1395)

Qy 1 MetasnphellielysAspAsnSerArgAlaLeuileglnArqMetGlyMetThyValIle 20

Db 277 ATGAATTTTCATTAAGACAAATAGCCGACCTTATTTCATAAAGATGGATGACTGTTTATA 336

Qy 21 LysGlnIleThrAspAspLeuPheValTrrpAsnValIleuAsnArqGluGluValAsnIle 40

Db 337 AAGCAAAATCACAGATGACCTTATTGTATGAAATGTTCTGAAATCCGGAAGAAATTAACATC 396

Qy 41 IleCysCysGluIysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuIys 60

Db 397 ATTGCTGTCGAGAGGTGACAGATGCTCTAGAGGATCATTCACATGATTTTGA 456

Qy 61 LysGlySerGluSerCysAsnLeuPheLeuIysSerLeuIysGluTrrpAsnTyrProleu 80

Db 457 AAGGTTTCAGAGTCTGTACCTCTTTCTTAATCCCTTAAGAGTGAATATCTCTTA 516

Qy 81 PheGlnAspLeuAsnGlyGlnSer 88

Db 517 TTTCAGAGCTTGATGACAAAGT 540

#### RESULT 4

ID AAS03945 standard; CDNA: 3133 BP.

XX

AC AAS03945;  
 XX 12-SEP-2001 (first entry)  
 DT XX  
 DE Human caspase recruitment domain 12 (CARD-12) cDNA.  
 XX  
 KW Caspase recruitment domain; CARD-12; apoptosis; stress-related pathway;  
 KW cancer; viral infection; poxvirus; adenovirus; autoimmune disorder;  
 KW systemic lupus erythematosus; arthritis; neurological disorder; stroke;  
 KW Alzheimer's disease; amyotrophic lateral sclerosis; haematologic disease;  
 KW aplastic anaemia; myocardial infarction; inflammatory disorder;  
 KW Crohn's disease; insulin-dependent diabetes; contact dermatitis;  
 KW psoriasis; graft rejection; bacterial infection; lepromatous leprosy;  
 KW tuberculosis; ischaemic brain injury; hypoxic brain injury; ss;  
 KW kidney ischaemia; reperfusion injury; acute bacterial meningitis;  
 KW excitotoxic brain damage; liver disease.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 36..3110  
 FT /\*tag= a  
 FT /product= "Human CARD-12"  
 XX  
 PN W0200130971-A2.  
 XX  
 PD 03-MAY-2001.  
 XX  
 PF 26-OCT-2000; 2000MO-US29643.  
 XX  
 PR 27-OCT-1999; 99US-0161822.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Berlin J, Robison KE;  
 XX WPI; 2001-308628/32.  
 DR P-PSDB; AA002880.  
 XX  
 XX  
 PT Isolated caspase recruitment domain-12 polypeptide and nucleic acids  
 PT encoding them, useful for treating and diagnosing disorders associated  
 PT with abnormal apoptosis such as cancer, arthritis and Alzheimer's  
 PT disease -  
 PT  
 PS Claim 2; Fig 1; 93pp; English.  
 XX  
 CC The sequence represents a cDNA which encodes the human caspase  
 CC recruitment domain 12 (CARD-12) polypeptide. CARD domains are found in a  
 CC number of proteins that transmit signals that activate apoptosis and  
 CC inflammatory pathways in response to stress and other stimuli. Therefore,  
 CC CARD-12 and its corresponding nucleic acid may be used in treatment and  
 CC diagnosis of patients suffering from disorders associated with an  
 CC abnormal level (an increase or a decrease) of apoptotic cell death or  
 CC abnormal activity of stress-related pathways. The disorders include  
 CC cancer, viral infections (e.g. caused by poxviruses, adenoviruses),  
 CC autoimmune disorders (e.g. systemic lupus erythematosus, arthritis),  
 CC neurological disorders (e.g. Alzheimer's disease, amyotrophic lateral  
 CC sclerosis), haematologic diseases (e.g. aplastic anaemia, myocardial  
 CC infarction, stroke), inflammatory and immune system disorders (e.g.  
 CC Crohn's disease, insulin-dependent diabetes, contact dermatitis,  
 CC psoriasis, graft rejection), bacterial infections (e.g. tuberculosis,  
 CC lepromatous leprosy), ischaemic and hypoxic brain injury, kidney  
 CC ischaemia/reperfusion injury, excitotoxic brain damage, acute bacterial  
 CC meningitis and liver disease.  
 XX  
 SQ Sequence 3133 BP; 903 A; 691 C; 729 G; 810 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 1 48e-53 Length: 3133  
 Score: 461.00 Matches: 88  
 Percent Similarity: 100.008 Conservative: 0  
 Best Local Similarity: 100.008 Mismatches: 0  
 Query Match: 100.008 Indels: 0

DB: 22 Gaps: 0  
 US-09-697-089-2\_COPY\_1\_88 (1-88) x AAS03945 (1-3133)  
 QY 1 MetaspheillelysaspanserArgAlaLeuIleGlnArgmetGlymetThrValIle 20  
 DB 36 ATGATTTTCATTAAGGCAATATGACCCGAGCCCTTATTCAAAGATGGAAAGACTGTATA 95  
 QY 21 LysGlnIleThrAspAPLeuPheValTPAspValLeuAsnArgGluValAsnIle 40  
 DB 96 AAGCAATTCACAGATGACCTATTGTATGGAATGTTGTGATGCCGAAGATTAACATC 155  
 QY 41 ILecGscGsluysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleuLys 60  
 DB 156 ATTTGCGCGAGAGAGGTGGAGAGAGATGCTAGAGAGATTCATTCACATGATTTTGAA 215  
 QY 61 LysGlnSerGlnSerCysAsnLeuPheLeuLysSerLeuLysGlnTPAsnTyrrProLeu 80  
 DB 216 AAGGTTTCAGAGTCCTCTTAACCTCTTCTTAATCCCTTAAGAGTGGAACTATCTCTA 275  
 QY 81 PheGlnAspLeuAsnGlyGlnSer 88  
 DB 276 TTTCAGGACTTGAAATGACAAAGT 299  
 RESULT 5  
 ABRK22731  
 ID ABRK22731 standard; cDNA; 3396 BP.  
 XX  
 AC ABRK22731;  
 XX  
 DT 26-MAR-2002 (first entry)  
 XX  
 DE Human cDNA encoding CLAN A.  
 XX  
 KW Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;  
 KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;  
 KW autoimmune disease; inflammation; keratinocyte hyperplasia;  
 KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;  
 KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;  
 KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;  
 KW Crohn's disease; graft-versus-host disease; stroke;  
 KW myocardial infarction; heart failure; neurodegenerative disease;  
 KW Parkinson's disease; Alzheimer's disease; HIV;  
 KW human immunodeficiency virus infection.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200190156-A2.  
 XX  
 PD 29-NOV-2001.  
 XX  
 PF 24-MAY-2001; 2001MO-US17158.  
 XX  
 PR 24-MAY-2000; 2000US-0579240.  
 PR 10-OCT-2000; 2000US-0686347.  
 PR 14-MAR-2001; 2001US-275980P.  
 PR 23-MAY-2001; 2001US-0864921.  
 XX  
 PA (BURN-) BURNHAM INST.  
 XX  
 PI Reed JC, Plo FF, Godzik A, Stehlik C, Damiano JS, Lee SH;  
 PI Oliveira VAM, Hayashi H, Pawlowski K;  
 XX WPI; 2002-083086/11.  
 DR P-PSDB; AA080861.  
 XX  
 PT New caspase recruitment domain (CARD)-containing polypeptides and  
 PT encoding nucleic acids, useful for treating abnormal cell proliferation  
 PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,  
 PT arthritis or stroke -  
 PS Claim 1; Page 166-171; 216pp; English.  
 XX

CC The invention relates to an isolated caspase recruitment domain (CARD)  
CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, IRR or SAM domain  
CC from it, and the polynucleotides encoding them. Also included are a  
CC recombinant vector comprising the polynucleotide, recombinant cells  
CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian  
CC and insect cells) and an anti-CARD antibody. The CARD-containing  
CC polypeptide and CARD-encoding nucleic acid are useful for treating a  
CC pathology characterised by abnormal cell proliferation (e.g. cancer), in  
CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In  
CC particular, the polypeptide and nucleic acid are useful for treating  
CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth  
CC muscle cell proliferation in arteries following balloon angioplasty  
CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,  
CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,  
CC graft-versus-host disease, stroke, myocardial infarction, heart failure,  
CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's  
CC disease) or immunodeficiency associated disease (e.g. human  
CC immunodeficiency virus (HIV) infection). The nucleic acids are useful  
CC in a variety of diagnostic applications. The present sequence is a  
CC cDNA encoding a CARD domain containing protein.

XX SQ Sequence 3396 BP: 992 A; 737 C; 793 G; 874 T; 0 other;

Alignment Scores:

Pred. No.: 1.65e-53 Length: 3396  
Score: 461.00 Matches: 88  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 24 Gaps: 0

US-09-697-089-2\_COPY\_1\_88 (1-88) x ABK22731 (1-3396)

OY 1 MetasphelieLyAspAsnSerArgAlaLeuIleGlnArgMetGlyMethrValIle 20  
DB 277 ATGATTTTCATTAAGACAAATAGCCGAGCCCTTATTCAAGAAATGCAATGACTGTATA 336  
OY 21 LysGlnIleThrAspAspLeuPheValITrPAsnValLeuAsnArgGluGluValAsnIle 40  
DB 337 AAGCAAAATCAGATGACCTATTGTATGAAATGTTCTGAATCGGAGAAAGTAACAATC 396  
OY 41 IleCysGluLyValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60  
DB 397 ATTTCCTCGAGAGAGCTGAGAGATGCTGTAGAGGATATTCACATGATTTTGAA 456  
OY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluITrPAsnITrProLeu 80  
DB 457 AAGGTTTCAGAGTCTCTTAACCTTTCTTAATCCCTTAAGAGATGGAATATCTCTTA 516  
OY 81 PheGlnAspLeuAsnGlyGlnSer 88  
DB 517 TTTCAGACTTGATGACAAAGT 540

RESULT 6

AAH98254  
ID AAH98254 standard; cDNA: 3545 BP.

XX AAH98254;

XX 12-OCT-2001 (first entry)

DE Murine EST-derived coding sequence SEQ ID NO: 111.

XX Human: sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;

KW Tomato; monkey; dog; sea urchin; expressed sequence tag; EST;

KW diagnostics; forensic test; gene mapping; genetic disorder;

XX biodiversity; gene therapy; nutrition; ss.

XX Mus musculus.

XX WO200154477-A2.

XX 02-AUG-2001.

XX 25-JAN-2001; 2001WO-US02687.

XX 25-JAN-2000; 2000US-0491404.

PR 17-JUL-2000; 2000US-0617746.

PR 03-AUG-2000; 2000US-0631451.

PR 15-SEP-2000; 2000US-0663870.

XX (HXSE-) HXSEQ INC.

PI Tang YF, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;

PI Cao Y, Drmanac RA, Zhang J, Werhman T;

PR WPI: 2001-476164/51.

XX P-PSDB: AAM23595.

XX Isolated polypeptide for treatment of diseases, diagnostics, raising

XX antibodies and research use -

XX Claim 1: Page 250-251; 1275bp; English.

XX The present invention provides the protein and coding sequences of novel

XX proteins from a variety of organisms, including human, dog, cat, horse,

XX cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea

XX urchin and tomato. These were derived from expressed sequence tags (ESTs)

XX from the organism of interest. They can be used in diagnostics,

XX forensics, gene mapping, identification of mutations, to assess

XX biodiversity and for nutritional purposes. The present sequence is a cDNA

XX of the invention.

XX SQ Sequence 3545 BP: 1038 A; 755 C; 816 G; 936 T; 0 other;

Alignment Scores:

Pred. No.: 1.75e-53 Length: 3545  
Score: 461.00 Matches: 88  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 22 Gaps: 0

US-09-697-089-2\_COPY\_1\_88 (1-88) x AAH98254 (1-3545)

OY 1 MetasphelieLyAspAsnSerArgAlaLeuIleGlnArgMetGlyMethrValIle 20  
DB 232 ATGATTTTCATTAAGACAAATAGCCGAGCCCTTATTCAAGAAATGCAATGACTGTATA 291

OY 21 LysGlnIleThrAspAspLeuPheValITrPAsnValLeuAsnArgGluGluValAsnIle 40  
DB 292 AAGCAAAATCAGATGACCTATTGTATGAAATGTTCTGAATCGGAGAAAGTAACAATC 351

OY 41 IleCysGluLyValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60  
DB 352 ATTTCCTCGAGAGAGCTGAGAGATGCTGTAGAGGATATTCACATGATTTTGAA 411

OY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluITrPAsnITrProLeu 80  
DB 412 AAGGTTTCAGAGTCTCTTAACCTTTCTTAATCCCTTAAGAGATGGAATATCTCTTA 471

OY 81 PheGlnAspLeuAsnGlyGlnSer 88  
DB 472 TTTCAGACTTGATGACAAAGT 495

RESULT 7

AAH78219  
ID AAH78219 standard; DNA: 3213 BP.

XX AAH78219;

XX 26-NOV-2001 (first entry)

DE Nucleotide sequence of a human secreted polypeptide.

XX Human; secreted polypeptide; nervous disease; muscular disease; tumour;

KW gastrointestinal ulceration; spinal cord disease; trachea disease;  
KW thyroid gland disease; ovary disease; prostate disease; heart disease;  
KW renal gland disease; small intestine disease; thymus disease;  
KW lymph node disease; muscular system disease; colon disease;  
KW lipase deficiency; cystic fibrosis; pancreatitis; clot formation;  
KW myocardial infarction; angioplasty; liver disease; coagulation disorder;  
KW microbial disease; immune disorder; inflammation; transplant rejection;  
KW bone thickness; bone density; ferroxidase loss; apoptosis;  
KW vascular smooth cell proliferation; vaccine; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..3213  
FT /\*tag= a  
FT /product= "secreted polypeptide"  
XX  
PN MO20016690-A2.  
XX  
PD 13-SEP-2001.  
XX  
PE 05-MAR-2001; 2001WO-US07143.  
XX  
XX 06-MAR-2000; 2000US-0187107.  
PR 13-MAR-2000; 2000US-0188916.  
PR 03-OCT-2000; 2000US-0236874.  
PR 03-OCT-2000; 2000US-0237846.  
XX  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
XX  
PI Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;  
XX  
DR WPI: 2001-570768/64.  
DR P-PSDB: AAG67527.  
XX  
XX Novel isolated secreted polypeptide useful for treating nervous and  
PT muscular diseases, gastrointestinal ulceration, coagulation and immune  
PT disorders, microbial diseases, inflammation and transplant rejection -  
XX  
XX Claim 2; Page 53-54; 102pp; English.  
XX  
XX The present sequence encodes a human secreted polypeptide. The  
CC secreted polypeptides and polynucleotides are useful for treating  
CC nervous and muscular diseases, for inhibiting tumour formation and  
CC metastasis, for treating gastrointestinal ulceration, for preventing  
CC and treating diseases in spinal cord, thyroid gland, ovary, prostate,  
CC renal gland, small intestine, heart, trachea, thymus, lymph node,  
CC muscular system and colon, for treating lipase deficiency in cystic  
CC fibrosis and pancreatitis, for treating undesirable clot formation  
CC such as myocardial infarction, during angioplasty and all surgical  
CC procedures that require decreased blood clot formation, for treating  
CC liver diseases, coagulation disorders and microbial diseases, for  
CC treating immune disorders, for treating inflammation and transplant  
CC rejection, for enhancing bone thickness and increasing bone density,  
CC for reducing the loss of essential ferroxidases, for suppressing  
CC apoptosis, and for regulating vascular smooth cell proliferation. They  
CC may also be used as vaccines.  
XX  
SQ Sequence 3213 BP; 916 A; 704 C; 756 G; 837 T; 0 other;

Alignment Scores:  
Pred. No.: 3,99e-53 Length: 3213  
Score: 458.00 Matches: 87  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 98.86% Mismatches: 0  
Query Match: 99.35% Indels: 0  
DB: 22 Gaps: 0

US-09-697-089-2\_COPY\_1\_88 (1-88) x AAH78219 (1-3213)  
OY 1 MetasnphelleySaPaSnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20  
:::|||||

Db 139 TTGAATTCATTAAGACATATAGCCGACCCCTTATTCAAAGATGGAGATCTGTATA 198  
OY 21 LysGlnIleThrAspAspLeuPheValIrpAsnValIleAsnArgGluValAsnIle 40  
|||||  
Db 199 AAGCAATACACAGATGACCTATTGTATGAAATTTCTGAATCCGAAAGAACTAAACATC 258  
OY 41 IleCysCysGluIysValGluGlnAspAlaAlaArgGlyIleIleHISmetIleLeuIys 60  
|||||  
Db 259 ATTGCTGCAGAGAGATGGACAGACATGCTCTAGAGGAGATTCACATGATTTTGAAA 318  
OY 61 LysGlySerGluSerCysAsnLeuPheLeuIysSerLeuIysGluTyrPasnTyrProIeu 80  
|||||  
Db 319 AAGGGTTCAGAGTCTCTTAACCTCTTAAATCCCTTAAGAGTGAAGTATCTCTTA 378  
OY 81 PheGlnAspLeuAsnGlyGlnSer 88  
|||||  
Db 379 TTTCAGGACTTGAAATGACAAAGT 402

RESULT 8  
ABK22765  
ID ABK22765 standard; cDNA; 261 BP.  
XX  
AC ABK22765;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Human cDNA encoding CLAN CARD.  
XX  
KW Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;  
KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;  
KW autoimmune disease; inflammation; keratinocyte hyperplasia;  
KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;  
KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;  
KW leukemia; allergy; arthritis; lupus; Schogen's syndrome;  
KW Crohn's disease; graft-versus-host disease; stroke;  
KW myocardial infarction; heart failure; neurodegenerative disease;  
KW Parkinson's disease; Alzheimer's disease; HIV;  
KW human immunodeficiency virus infection.  
XX  
OS Homo sapiens.  
XX  
PN WO200190156-A2.  
XX  
PD 29-NOV-2001.  
XX  
PE 24-MAY-2001; 2001WO-US17158.  
XX  
PR 24-MAY-2000; 2000US-0579240.  
PR 10-OCT-2000; 2000US-0686347.  
PR 14-MAR-2001; 2001US-275980P.  
PR 23-MAY-2001; 2001US-0864921.  
XX  
PA (BURN-) BURNHAM INSE.  
XX  
PI Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;  
PI Oliveira VAM, Hayashi H, Pawlowski K;  
XX  
DR WPI: 2002-083086/11.  
DR P-PSDB: AAU80871.  
XX  
XX New caspase recruitment domain (CARD)-containing polypeptides and  
PT encoding nucleic acids, useful for treating abnormal cell proliferation  
PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,  
XX arthritis or stroke  
XX  
XX Claim 1; Page 199; 216pp; English.  
XX  
XX The invention relates to an isolated caspase recruitment domain (CARD)  
CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain  
CC from it, and the polynucleotides encoding them. Also included are a  
CC recombinant vector comprising the polynucleotide, recombinant cells  
CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian  
CC and insect cells) and an anti-CARD antibody. The CARD-containing

CC polypeptide and CARD-encoding nucleic acid are useful for treating a  
CC pathology characterised by abnormal cell proliferation (e.g. cancer),  
CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In  
CC particular, the polypeptide and nucleic acid are useful for treating  
CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth  
CC muscle cell proliferation in arteries following balloon angioplasty  
CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,  
CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,  
CC graft-versus-host disease, stroke, myocardial infarction, heart failure,  
CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's  
CC disease) or immunodeficiency associated disease (e.g. human  
CC immunodeficiency virus (HIV) infection). The nucleic acids are useful  
CC in a variety of diagnostic applications. The present sequence is a  
CC cDNA encoding a CARD domain containing protein.  
XX  
SO Sequence 261 BP; 86 A; 44 C; 59 G; 72 T; 0 other;

Alignment Scores:  
Pred. No.: 1.82e-54 Length: 261  
Score: 457.00 Matches: 87  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.13% Indels: 0  
DB: Gaps: 0

US-09-697-089-2\_COPY\_1\_88 (1-88) x ABR22765 (1-261)

OY 1 MetanphelelllyAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20  
DB 1 AAGAAATTCATTAAGACAAATAGCCGAGCCCTTATTCAAAGATGGAGATGCTGTATA 60  
OY 21 LysGlnIleThrAspAspLeuPheValITrpaSValIleAsnArgGluValAsnIle 40  
DB 61 AAGCAATACACAGATGACCTATTGTATGAAATGTTCTGAAATCGCGAAGAACTAAACATC 120  
OY 41 IleCysGlyLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60  
DB 121 ATTTCTCGAGAAAGGTGAGACAGATCTGCTAGAGGAGATCATTCACATGATTTTGAAA 180  
OY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerIleLysGluITrpaSntyrProIeu 80  
DB 181 AAGGTTGAGAGTCTGTACCTCTTTCTTAAATCCCTTAAGAGAGTGAACATATCTCTTA 240  
OY 81 PheGlnAspLeuAsnGlyGln 87  
DB 241 TTTCAGGACTTGATGACAA 261

RESULT 9  
AAS03946  
ID AAS03946 standard; DNA; 3615 BP.  
AC AAS03946;  
XX  
DT 12-SEP-2001 (first entry)  
XX  
DE Human caspase recruitment domain 12 (CARD-12) genomic DNA.  
XX  
KW Caspase recruitment domain; CARD-12; apoptosis; stress-related pathway;  
KW cancer; viral infection; poxvirus; adenovirus; autoimmune disorder;  
KW systemic lupus erythematosus; arthritis; neurological disorder; stroke;  
KW Alzheimer's disease; amyotrophic lateral sclerosis; haematologic disease;  
KW aplastic anaemia; myocardial infarction; inflammatory disorder;  
KW Crohn's disease; insulin-dependent diabetes; contact dermatitis;  
KW psoriasis; graft rejection; bacterial infection; lepromatous leprosy;  
KW tuberculosis; ischaemic brain injury; hypoxic brain injury; ds;  
KW kidney ischaemia; reperfusion injury; acute bacterial meningitis;  
KW excitotoxic brain damage; liver disease.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT 1..3615  
FT CDS /\*tag= a

FT /product= "Human CARD-12"  
XX  
XX WO200130971-A2.  
XX  
XX 03-MAY-2001.  
XX  
XX 26-OCT-2000; 2000WO-US29643.  
XX  
XX 27-OCT-1999; 99US-0161822.  
XX  
XX (MILL-) MILLENNIUM PHARM INC.  
XX  
XX Bertin J, Robison KE;  
XX  
XX WPI: 2001-308628/32.  
XX  
XX P-PSDB; AAU02881.  
XX  
XX  
XX Isolated caspase recruitment domain-12 polypeptide and nucleic acids  
XX encoding them, useful for treating and diagnosing disorders associated  
XX with abnormal apoptosis such as cancer, arthritis and Alzheimer's  
XX disease -  
XX  
XX Disclosure: Fig 2; 93pp; English.

The sequence represents a genomic DNA which encodes the human caspase  
recruitment domain 12 (CARD-12) polypeptide. CARD domains are found in a  
number of proteins that transmit signals that activate apoptosis and  
inflammatory pathways in response to stress and other stimuli. Therefore,  
CARD-12 and its corresponding nucleic acid may be used in treatment and  
diagnosis of patients suffering from disorders associated with an  
abnormal level (an increase or a decrease) of apoptotic cell death or  
abnormal activity of stress-related pathways. The disorders include  
cancer, viral infections (e.g. caused by poxviruses, adenoviruses),  
autoimmune disorders (e.g. systemic lupus erythematosus, arthritis),  
neurological disorders (e.g. Alzheimer's disease, amyotrophic lateral  
sclerosis), haematologic diseases (e.g. aplastic anaemia, myocardial  
infarction, stroke), inflammatory and immune system disorders (e.g.  
Crohn's disease, insulin-dependent diabetes, contact dermatitis,  
psoriasis, graft rejection), bacterial infections (e.g. tuberculosis,  
lepromatous leprosy), ischaemic and hypoxic brain injury, kidney  
ischaemia/reperfusion injury, excitotoxic brain damage, acute bacterial  
meningitis and liver disease.

SO Sequence 3615 BP; 1041 A; 811 C; 845 G; 918 T; 0 other;

Alignment Scores:  
Pred. No.: 6.45e-53 Length: 3615  
Score: 457.00 Matches: 87  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 98.86% Mismatches: 0  
Query Match: 99.13% Indels: 0  
DB: Gaps: 0

US-09-697-089-2\_COPY\_1\_88 (1-88) x AAS03946 (1-3615)

OY 1 MetanphelelllyAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20  
DB 418 GTGAATTCATTAAGACAAATAGCCGAGCCCTTATTCAAAGATGGAGATGCTGTATA 477  
OY 21 LysGlnIleThrAspAspLeuPheValITrpaSValIleAsnArgGluValAsnIle 40  
DB 478 AAGCAATACACAGATGACCTATTGTATGAAATGTTCTGAAATCGCGAAGAACTAAACATC 537  
OY 41 IleCysGlyLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60  
DB 538 ATTTCTCGAGAAAGGTGAGACAGATCTGCTAGAGGAGATCATTCACATGATTTTGAAA 597  
OY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerIleLysGluITrpaSntyrProIeu 80  
DB 598 AAGGTTGAGAGTCTGTACCTCTTTCTTAAATCCCTTAAGAGAGTGAACATATCTCTTA 657  
OY 81 PheGlnAspLeuAsnGlyGlnSer 88  
|||||

DB 658 TTTCAGGACTTGAAATGACAAAGT 681

RESULT 10

AAH78218

ID AAH78218 standard; DNA: 2215 BP.

XX

AC AAH78218;

XX

DT 26-NOV-2001 (first entry)

XX

DE Nucleotide sequence of a human secreted polypeptide.

XX

KW Human: secreted polypeptide; nervous disease; muscular disease; tumour;

KW gastrointestinal ulceration; spinal cord disease; trachea disease;

KW thyroid gland disease; ovary disease; prostate disease; heart disease;

KW renal gland disease; small intestine disease; thymus disease;

KW lymph node disease; muscular system disease; colon disease;

KW lipase deficiency; cystic fibrosis; pancreatitis; clot formation;

KW myocardial infarction; angioplasty; liver disease; coagulation disorder;

KW microbial disease; immune disorder; inflammation; transplant rejection;

KW bone thickness; bone density; ferroxidase loss; apoptosis;

KW vascular smooth cell proliferation; vaccine; ss.

XX

OS Homo sapiens.

XX

Key Location/Qualifiers

FT 1..2214

FT CDS /tag= a

FT /product= "secreted polypeptide"

FT /note= "no termination codon given"

XX

PN WO200166690-A2.

PD 13-SEP-2001.

XX

PF 05-MAR-2001; 2001WO-US07143.

XX

PR 06-MAR-2000; 2000US-0187107.

PR 13-MAR-2000; 2000US-0188916.

PR 03-OCT-2000; 2000US-0236874.

PR 03-OCT-2000; 2000US-0237846.

XX

PA (SMIK ) SMITHKLINE BEECHAM CORP.

PA (SMIK ) SMITHKLINE BEECHAM PLC.

XX

PI Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;

XX

DR WPI: 2001-570768/64.

DR P-PSDB: AAG67526.

XX

PT Novel isolated secreted polypeptide useful for treating nervous and

PT muscular diseases, gastrointestinal ulceration, coagulation and immune

PT disorders, microbial diseases, inflammation and transplant rejection -

XX

PS Claim 2; Page 52-53; 102pp; English.

XX

XX The present sequence encodes a human secreted polypeptide. The

CC secreted polypeptides and polynucleotides are useful for treating

CC nervous and muscular diseases, for inhibiting tumour formation and

CC metastasis, for treating gastrointestinal ulceration, for preventing

CC and treating diseases in spinal cord, thyroid gland, ovary, prostate,

CC renal gland, small intestine, heart, trachea, thymus, lymph node,

CC muscular system and colon, for treating lipase deficiency in cystic

CC fibrosis and pancreatitis, for treating undesirable clot formation

CC such as myocardial infarction, during angioplasty and all surgical

CC procedures that require decreased blood clot formation, for treating

CC liver diseases, coagulation disorders and microbial diseases, for

CC treating immune disorders, for treating inflammation and transplant

CC rejection, for enhancing bone thickness and increasing bone density,

CC for reducing the loss of essential ferroxidases, for suppressing

CC apoptosis, and for regulating vascular smooth cell proliferation. They

CC may also be used as vaccines.

XX

SQ Sequence 2215 BP, 621 A; 522 C; 519 G; 553 T; 0 other;

Alignment Scores:

Pred. No.:	3.54e-44	Length:	2215
Score:	392.00	Matches:	74
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	85.03%	Indels:	0
DB:	22	Gaps:	0

US-09-697-089-2\_COPY\_1\_88 (1-88) x AAH78218 (1-2215)

QY 15 MetGlyMetThrValIleLysGlnIleThrAspAspLeuPheValIrrAsnValIleAsn 34

DB 1 ATGGAATGACTGTTTAAAGCAAAATCACAGAGACTATTATGAGATGTTGAAAT 60

QY 35 ArgGluGluValAsnIleIleCysGlnLysValGluGlnAspAlaAArgGlyIle 54

DB 61 CGGAGAAAGTAAACATCATTTGCTGCGAGAAAGTGGAGCAGATGCTGTAAGGGATC 120

QY 55 IleHisMetIleLeuLysLysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLys 74

DB 121 ATTCACTGATTTTGAAGAAAGGGTTGAGACTCCTGTAACCTTTTCTTAATCCCTTAAG 180

QY 75 GluTrpAsnTrpProLeuPheGlnAspLeuAsnGlyGlnSer 88

DB 181 GAGTGAACATATCCTCTATTTCAGGACTTGAAATGACAAAGT 222

RESULT 11

AAAX27725

ID AAAX27725 standard; DNA: 1215 BP.

XX

AC AAAX27725;

XX

DT 02-JUN-1999 (first entry)

XX

DE Canine interleukin-1 beta convertase coding sequence.

XX

KW Canine; interleukin 18; dil18; interleukin 1 beta convertase; ICF; dog;

KW leukocyte; MHC; tumour cell; lymphocyte; Fas ligand; allergy; cancer;

KW immune disorder; infectious disease; skin inflammation; ss.

XX

OS Canis sp.

XX

PN WO9907851-A1.

PD 18-FEB-1999.

XX

PF 07-AUG-1998; 98WO-JP03524.

XX

PR 07-AUG-1997; 97JP-0213754.

XX

PA (TORA ) TORAY IND INC.

XX

PI Okano F;

XX

DR WPI: 1999-167427/14.

DR P-PSDB: AAY01315.

XX

PT Canine interleukin 18 and canine interleukin 1-beta convertase -

PT for treatment of immune disorders of dogs including cancer,

PT allergies and inflammatory diseases.

XX

PS Claim 8; Page 26-29; 44pp; Japanese.

XX

XX The invention relates to a canine interleukin 18 (dil18) and a canine

CC interleukin 1 beta convertase (dICB) which can cleave precursor forms of

CC dil18 and interleukin 1 beta to give the active forms. Host cells

CC transformed by vectors comprising the dil18 DNA (optionally with DNA

CC coding for dICB) are used for the recombinant expression of the protein.

CC The canine interleukin 18 is able to act on canine leukocytes to induce

CC a factor potentiating the expression of class II MHC on canine tumour

CC cells; to promote the proliferation of canine lymphocytes; to potentiate

CC the expression of Fas ligand on canine lymphocytes and tumour cells; to  
CC damage and kill canine tumour cells; to reduce tumour size in the living  
CC dog; and to activate canine leukocytes to inhibit allergies. dril8 in  
CC combination with dril2 can be used for the treatment of immune disorders  
CC of dogs, such as cancer, allergies, infectious diseases or skin  
CC inflammation. The present sequence represents the coding sequence of  
CC drilc.

SQ Sequence 1215 BP; 347 A; 290 C; 284 G; 294 T; 0 other,



XX 07-AUG-1997; 97JP-0213754.  
XX (TORA ) TORAY IND INC.  
XX  
XX  
XX Okano F;  
XX WPI; 1999-167427/14.  
XX P-PSDB; AAY01315.  
XX  
XX Canine interleukin 18 and canine interleukin 1-beta convertase  
XX For treatment of immune disorders of dogs including cancer,  
XX allergies and inflammatory diseases.  
XX  
XX Claim 10; Page 32-35; 44pp; Japanese.  
XX  
XX The invention relates to a canine interleukin 18 (dli18) and a canine  
XX interleukin 1 beta convertase (dice) which can cleave precursor forms of  
XX dli18 and interleukin 1 beta to give the active forms. Host cells  
XX transformed by vectors comprising the dli18 DNA (optionally with DNA  
XX coding for dice) are used for the recombinant expression of the protein.  
XX The canine interleukin 18 is able to act on canine leukocytes to induce  
XX a factor potentiating the expression of class II MHC on canine tumour  
XX cells; to promote the proliferation of canine lymphocytes; to potentiate  
XX the expression of Fas ligand on canine lymphocytes and tumour cells; to  
XX damage and kill canine tumour cells; to reduce tumour size in the living  
XX dog; and to activate canine leukocytes to inhibit allergies. dli18 in  
XX combination with dli12 can be used for the treatment of immune disorders  
XX of dogs, such as cancer, allergies, infectious diseases or skin  
XX inflammation. The present sequence represents the DNA encoding dice.  
XX  
XX  
XX Sequence 1560 BP; 468 A; 365 C; 355 G; 372 T; 0 other;  
XX  
XX  
XX Alignment Scores:  
XX Pred. No.: 2.15e-06 Length: 1560  
XX Score: 118.50 Matches: 26  
XX Percent Similarity: 52.44% Conservative: 17  
XX Best Local Similarity: 31.71% Mismatches: 38  
XX Query Match: 25.70% Indels: 1  
XX DB: Gaps: 1  
XX  
XX US-09-697-089-2\_COPY\_1\_88 (1-88) x AAX27727 (1-1560)  
XX  
XX QY 4 IlelyspasnsenrArgAlaleuileGlnrGmetGlyMetThrValIlelysglnile 23  
XX DB 217 CTGAAGGCAAGAGAGGCTGTGTCGGTCAGACATGGGACCATCAATGCTTTG 276  
XX QY 24 ThrspaspleupheValTrpAsnValleuasnArGluGluVal--AsnIleleCys 42  
XX DB 277 CTGATGTAACCTTTGAGAAAAGAGTGTGTAACCAAGAGAGATGAGAGTGGGTGT 336  
XX QY 43 CysgluysValGluGlnAspAlaAlaArgIlyleIleHsMetIleLeuLysGly 62  
XX DB 337 GCACACTCTACAGTTATGATCAGGCCGAGTCTGATGTGATCGCTTCGGAAGG 396  
XX QY 63 SerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrrProLeuPheGln 82  
XX DB 397 CCAATGATGCCAGATTATTCTAATATTGCAATGAGACATTCACTCGCACAG 456  
XX QY 83 Aspleu 84  
XX DB 457 ACGCTG 462  
XX  
XX RESULT 14  
XX AAA13796  
XX ID AAA13796 standard; cDNA; 1560 BP.  
XX  
XX AC AAA13796;  
XX  
XX XX 27-JUL-2000 (first entry)  
XX  
XX DE Canine Interleukin 1beta conversion enzyme encoding cDNA SEQ ID NO:4.  
XX

KW Canine; dog; interleukin 18; IL-18; interleukin 1beta conversion enzyme;  
KW ICE; Immune disease; tumour; ss.  
XX  
XX OS Canis sp.  
XX  
XX FT Key Location/Qualifiers  
XX CDS 202-1416  
XX FT /\*tag= a  
XX FT /product= "interleukin 1beta conversion enzyme"  
XX  
XX PN JP2000078975-A.  
XX  
XX PD 21-MAR-2000.  
XX  
XX PF 04-AUG-1998; 98JP-0220074.  
XX  
XX PR 07-AUG-1997; 97JP-0213754.  
XX PR 11-DEC-1997; 97JP-0341741.  
XX PR 06-JUL-1998; 98JP-0190594.  
XX  
XX PA (TORA ) TORAY IND INC.  
XX  
XX DR WPI; 2000-342448/30.  
XX DR P-PSDB; AAY82561.  
XX  
XX PS Canine interleukin 18 - useful for treating canine immune diseases  
XX  
XX Claim 10; Page 13-14; 16pp; Japanese.  
XX  
XX CC The present invention describes canine interleukin 18 (IL-18). Canine  
XX IL-18 is capable of inducing an antiviral activity factor and a factor  
XX reinforcing the expression of class II MHC molecules on canine tumour  
XX cells by reacting with canine leukocytes, promoting the growth of  
XX canine lymphocytes, reinforcing the expression of Fas ligand on canine  
XX lymphocytes and canine tumour cells, obstructing and killing canine  
XX tumour cells, reducing the tumour formed in a canine body and preventing  
XX the treatment of canine immune diseases. The present invention also  
XX describes the canine interleukin 1beta conversion enzyme (ICE), which  
XX has the ability of cleaving the precursor proteins of interleukin 1beta  
XX and IL-18 to convert them to their active types. The present sequence  
XX encodes canine ICE.  
XX  
XX  
XX Sequence 1560 BP; 468 A; 365 C; 355 G; 372 T; 0 other;  
XX  
XX  
XX Alignment Scores:  
XX Pred. No.: 2.15e-06 Length: 1560  
XX Score: 118.50 Matches: 26  
XX Percent Similarity: 52.44% Conservative: 17  
XX Best Local Similarity: 31.71% Mismatches: 38  
XX Query Match: 25.70% Indels: 1  
XX DB: Gaps: 1  
XX  
XX US-09-697-089-2\_COPY\_1\_88 (1-88) x AAA13796 (1-1560)  
XX  
XX QY 4 IlelyspasnsenrArgAlaleuileGlnrGmetGlyMetThrValIlelysglnile 23  
XX DB 217 CTGAAGGCAAGAGAGGCTGTGTCGGTCAGACATGGGACCATCAATGCTTTG 276  
XX QY 24 ThrspaspleupheValTrpAsnValleuasnArGluGluVal--AsnIleleCys 42  
XX DB 277 CTGATGTAACCTTTGAGAAAAGAGTGTGTAACCAAGAGAGATGAGAGTGGGTGT 336  
XX QY 43 CysgluysValGluGlnAspAlaAlaArgIlyleIleHsMetIleLeuLysGly 62  
XX DB 337 GCACACTCTACAGTTATGATCAGGCCGAGTCTGATGTGATCGCTTCGGAAGG 396  
XX QY 63 SerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrrProLeuPheGln 82  
XX DB 397 CCAATGATGCCAGATTATTCTAATATTGCAATGAGACATTCACTCGCACAG 456  
XX QY 83 Aspleu 84  
XX DB 457 ACGCTG 462  
XX



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GenCore version 5.1.3  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 31, 2003, 11:50:07 : Search time 719.086 Seconds

(without alignments)  
1981.965 Million cell updates/sec

Title: US-09-697-089-2\_COPY1\_188

Perfect score: 461

Sequence: 1 MNRFKDSRALIQMGWTVI.....FLKSLKRWNPPLFQDLNGQS 88

Scoring table:

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Xgapop 10.0 , Ygapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
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-O=/cgn2\_1/USPPO.spool/US09697089/runat\_29012003\_092754\_19729/app-query.fasta\_1.981  
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-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
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Database :

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8: em\_hlc:\*  
9: gb\_estl:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
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16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vit:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
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26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	441	95.7	741	13 B1824482	B1824482 603038854
3	322	69.8	404	17 A0889169	A0889169 HS_2161_B
4	182	39.5	728	9 AL652549	AL652549 AL652549
5	114.5	24.8	571	12 BF080490	BF080490 231404_MA
6	108	23.4	681	10 B1199526	B1199526 B1199526
7	108	23.4	757	12 BE744578	BE744578 BE744578
8	108	23.4	800	12 BG190354	BG190354 RST9419_A
9	108	23.4	808	12 BG209460	BG209460 RST28980
10	108	23.4	808	12 BG13953	BG13953 RST13094
11	108	23.4	812	12 BG188190	BG188190 RST7203_A
12	108	23.4	963	12 BG287772	BG287772 603384122
13	108	23.4	976	12 BG028431	BG028431 602294338
14	107	23.2	512	14 BQ235318	BQ235318 h456e06.9
15	106	23.0	665	10 AV682308	AV682308 AV682308
16	106	23.0	791	12 BG212560	BG212560 RST32152
17	104	22.6	741	12 BG205749	BG205749 RST25183
18	104	22.6	835	12 BG139532	BG139532 RST13093
19	103.5	22.5	542	12 BF080489	BF080489 231403_MA
20	101	21.9	613	12 BF213554	BF213554 601845353
21	100	21.7	250	10 AW988325	AW988325 u06f04.Y
22	100	21.7	467	10 AW988289	AW988289 u05f04.Y
23	97.5	21.1	663	10 AW958463	AW958463 EST370533
24	97	21.0	588	10 AW372984	AW372984 QVA-BF038
25	97	21.0	801	13 B1830457	B1830457 603073325
26	96	20.8	239	12 BG200554	BG200554 RST19870
27	95.5	20.7	256	9 A1767140	A1767140 w193f12.x
28	95.5	20.7	551	12 BF080849	BF080849 233611_MA
29	95.5	20.7	561	12 BG573534	BG573534 602595339
30	95	20.6	812	12 BG390044	BG390044 602415771
31	93.5	20.3	300	9 A0098419	A0098419 A0098419
32	93.5	20.3	488	10 AV713637	AV713637 AV713637
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34	93.5	20.3	903	13 BM457265	BM457265 AGENCOURT
35	93.5	20.3	1098	12 BG024814	BG024814 602275555
36	93	20.2	583	10 AV654714	AV654714 AV654714
37	92.5	20.1	635	14 BQ021083	BQ021083 UI-H-DH1-
38	91.5	19.8	493	10 AV757470	AV757470 AV757470
39	91.5	19.8	795	12 BG547974	BG547974 602576081
40	91.5	19.8	851	13 B1838827	B1838827 603082641
41	91.5	19.8	1062	14 BM920134	BM920134 AGENCOURT
42	91.5	19.8	1267	14 BM832207	BM832207 K-EST0106
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#### ALIGNMENTS

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LOCUS  
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603066455P1 NIH\_MGC\_118 Homo sapiens cDNA clone IMAGE:521566 5',  
B1908869  
ACCESSION B1908869  
VERSION B1908869.1 GI:16171950  
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SOURCE human  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 748)  
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL  
COMMENT

Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: c9abs-r@mail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
Plate: LHAM1541 row: m column: 14  
High quality sequence start: 744.  
Location/Qualifiers

FEATURES  
source

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/lab\_host="DH10B"  
/note="Vector: pCMV-SPORT6; Site.1: NotI; Site.2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH\_MGC Library."  
BASE COUNT 236 a 148 c 166 g 198 t  
ORIGIN

Alignment Scores:

Pred. No.: 4,06e-54 Length: 748  
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Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 13 Gaps: 0

US-09-697-089-2\_COPY\_1\_88 (1-88) x B1908869 (1-748)

OY 1 Metasnpheilleysaspasnserrargalaleuileglnaragmetglymethrvalle 20  
Db 252 ATGCAATTTCAATAAGACAAATAGCCGAGCCCTATTCAAGAAATGGCAATGACTGTATA 311  
OY 21 Lysglnlethrasspaspheulepthevaltrpansvalleuasnarvglnuvalasni 40  
Db 312 AAGCAATTCACAGATGACCTATTGTATGAGATGTCGAATCGGAAGAAATAAACATC 371  
OY 41 lleCysCysglulysvalgluInaspalaalaaraglyllelleHismetilleuleuys 60  
Db 372 ATTTGCTGCGAGAGAGTGCAGAGATGCTCTAGAGGATCATTCATATTTTGA 431  
OY 61 LysglysergluserCysasnleupheuleysserleuysglutrpasntyrProleu 80  
Db 432 AAGGTTTCAGAGTCTCTTAACCTCTTCTTAATCCCTTAAGAGATGGAACATATCCTCTA 491  
OY 81 PheglInaspLeuasnglyInser 88  
Db 492 TTTTCAGGACTTGAATGACAAAGT 515

RESULT 2

LOCUS B1824482 741 bp mRNA linear EST 04-OCT-2001  
DEFINITION 603038854F1 NIH\_MGC\_115 Homo sapiens cDNA clone IMAGE:5179909 5',  
mRNA sequence.

ACCESSION B1824482  
VERSION B1824482.1 GI:15936032  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE  
1 (bases 1 to 741)  
NIH-MGC <http://mgc.ncl.nih.gov/>  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: c9abs-r@mail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
Plate: LHAM1448 row: k column: 14  
High quality sequence start: 705.  
Location/Qualifiers

FEATURES  
source

1. 741  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5179909"  
/clone\_id="NIH\_MGC\_115"  
/lab\_host="DH10B"  
/note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site.1: NotI; Site.2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH\_MGC Library."  
BASE COUNT 233 a 147 c 164 g 197 t  
ORIGIN

Alignment Scores:

Pred. No.: 2.58e-51 Length: 741  
Score: 441.00 Matches: 88  
Percent Similarity: 97.78% Conservative: 0  
Best Local Similarity: 97.78% Mismatches: 0  
Query Match: 95.66% Indels: 2  
DB: 13 Gaps: 0

US-09-697-089-2\_COPY\_1\_88 (1-88) x B1824482 (1-741)

OY 1 Metasnpheilleysaspasnserrarg--alaleuileglnaragmetglymethrval 20  
Db 228 ATGCAATTTCAATAAGCAATAGCCGAGCCCTATTCAAGAAATGGCAATGACTGTATA 287  
OY 20 lelysglnlethrasspaspheulepthevaltrpansvalleuasnarvglnuvalasni 40  
Db 288 TAAAGCAATTCACAGATGACCTATTGTATGAGATGTCGAATCGGAAGAAATTAACA 347  
OY 40 lleleCysCysglulysvalgluInaspalaalaaraglyllelleHismetilleuleu 60  
Db 348 TCATTGCTGCGAGAGAGTGCAGAGATGCTCTAAGGATCATTCACATGATTTTGA 407  
OY 60 yslYsglysergluserCysasnleupheuleysserleuysglutrpasntyrPro 80  
Db 408 AAAAGGTTTCAGAGTCTCTTAACCTCTTCTTAATCCCTTAAGAGATGGAACATATCCTC 467  
OY 80 eupheglInaspLeuasnglyInser 88  
Db 468 TATTTTCAGGACTTGAATGACAAAGT 493

RESULT 3

LOCUS A0889169/c 404 bp DNA linear GSS 10-NOV-1999  
DEFINITION HS\_2161\_B1\_A01.T7C CIT Approved Human Genomic Sperm Library D Homo  
sapiens genomic clone Plate=2161 Col=1 Row=B, DNA sequence.

ACCESSION A0889169  
VERSION A0889169.1 GI:6345359  
KEYWORDS GSS.  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 404)  
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.  
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)  
MEDLINE 99380589  
COMMENT Contact: Mahairas GG, Wallace JC, Hood L  
High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887  
Email: jwallaceu.washington.edu  
Clones may be purchased from Research Genetics (info@resgen.com).  
BAC end Web Server: http://www.htsc.washington.edu  
Plate: 2161 row: B column: 1  
Seq primer: T7  
Class: BAC ends  
High quality sequence stop: 404.  
FEATURES  
source  
1..404  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="plate-2161 Col-1 Row-B"  
/clone\_1id="C1F Approved Human Genomic Sperm Library D"  
/sex="male"  
/note="Organ: sperm; Vector: pBelOBAC11; BAC clones in E-Coli DH10B"  
BASE COUNT 119 a 93 c 70 g 122 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 4.89e-35 Length: 404  
Score: 322.00 Matches: 69  
Percent Similarity: 88.64% Conservative: 9  
Best Local Similarity: 78.41% Mismatches: 10  
Query Match: 69.85% Indels: 1  
Gaps: 0  
US-09-697-089-2\_COPY\_1\_88 (1-88) x A0889169 (1-404)  
QY 1 MetasnphelieIySAspAsnSerArgAlaLeuIleGlnArgMetGlyMethrValIle 20  
Db 351 GTGAATTTCATAGAGACGATGACCGAGC-CTTATTCAGAAAGATGGGAATGGCTGTATA 293  
QY 21 LysGlnIleTrnAspAspLeuPheValTrpAsnValIleuAsnArgGluValAsnIle 40  
Db 292 GAGCTACTCACAGATGACCTTTGTATGAATGTATGAATCGAAGAAATGAACATC 233  
QY 41 IleCysCysGluIySValGluGlnAspAlaIaAaArgGlyIleIleHisMetIleLeuS 60  
Db 232 ATTTTCGTGGAGAGGTGACAGATGCTGTAGAGGAGCATTCATCATGATTTTGAA 173  
QY 61 LysGlySerGluSerCysAsnLeuPheLeuIySLeuIySLeuIySGluTrpAsnTyPProIeu 80  
Db 172 GAGGGTTTCAGAGTCTCTGAACCTTAAGTAAATCCCTTAAGAGTGAACATATCTCTTA 113  
QY 81 PheGlnAspLeuAsnGlyGln 88  
Db 112 TTTCAGGACTTGAAGGACAAAGT 89  
RESULT 4  
AL652549 728 bp mRNA linear EST 13-DEC-2001  
LOCUS

DEFINITION AL652549 XGC-gastrula silurana tropicalis cDNA clone Tgas028114 5', mRNA sequence.  
ACCESSION AL652549  
VERSION AL652549.1 GI:17663115  
KEYWORDS EST.  
SOURCE western clawed frog.  
ORGANISM Silurana tropicalis  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae; Xenopodinae; Silurana.  
AUTHORS Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J.  
TITLE Sanger Xenopus tropicalis EST project 2001 (10\_2001)  
JOURNAL Unpublished (2001)  
COMMENT Contact: Huckle E  
Sanger Centre  
Hinxton, Cambridgeshire, CB10 1SA, UK  
Email: trop@sanger.ac.uk  
Sanger Xenopus tropicalis EST project 2001  
TROPICALIS\_SEQUENCE\_ID: Tgas028114.sp6  
Sequencing primer: SP6  
This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.  
FEATURES  
source  
1..728  
/organism="Silurana tropicalis"  
/db\_xref="taxon:8364"  
/clone="Tgas028114"  
/clone\_1id="XGC-gastrula"  
/dev\_stage="gastrula (stages 10.5-13 mixed)"  
/lab\_host="Escherichia coli XL1-blue"  
/note="Vector: pCS107; Site\_1: EcoRI; Site\_2: NotI; cDNA was oligo dt primed from 5ug of poly A+ RNA from stages 10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end."  
BASE COUNT 232 a 130 c 168 g 197 t 1 others  
ORIGIN  
Alignment Scores:  
Pred. No.: 6.21e-15 Length: 728  
Score: 182.00 Matches: 39  
Percent Similarity: 65.52% Conservative: 18  
Best Local Similarity: 44.83% Mismatches: 30  
Query Match: 39.48% Indels: 0  
Gaps: 0  
US-09-697-089-2\_COPY\_1\_88 (1-88) x AL652549 (1-728)  
QY 1 MetasnphelieIySAspAsnSerArgAlaLeuIleGlnArgMetGlyMethrValIle 20  
Db 122 ATGATTTTAATTAGAAAACCTATGCAGAGCTGTTCAGAGAAATGGAGGACGATTCT 181  
QY 21 LysGlnIleTrnAspAspLeuPheValTrpAsnValIleuAsnArgGluValAsnIle 40  
Db 182 GTACAGATTAATAAGACTGTTCACAGAAATATCTTTCTATGGGTGACATGAGGAA 241  
QY 41 IleCysCysGluIySValGluGlnAspAlaIaAaArgGlyIleIleHisMetIleLeuS 60  
Db 242 ATTCGTCTCTTAAGGTGACAAAGATCTAACAGAGAAAGCTTAATGTTATTTTAAA 301  
QY 61 LysGlySerGluSerCysAsnLeuPheLeuIySLeuIySLeuIySGluTrpAsnTyPProIeu 80  
Db 302 AAAGGCACAGAGTCTCTGACATCGGTACTTCAGTCTCGAATCAAGATCCTTTTTC 361  
QY 81 PheGlnAspLeuAsnGlyGln 87  
Db 362 TATGAGACTTGTATTGGACAG 382  
RESULT 5  
BF080490 571 bp mRNA linear EST 18-OCT-2000  
LOCUS  
DEFINITION 231404 MARC 2Pig Sus scrofa cDNA 5', mRNA sequence.

ACCESSION BF080490  
 VERSION BF080490.1 GI:10874320  
 KEYWORDS EST.  
 SOURCE pig.  
 ORGANISM Sus scrofa  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.  
 REFERENCE 1 (bases 1 to 571)  
 Fahrénkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.  
 Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine  
 Unpublished (2000)  
 JOURNAL Contact: Smith TPL  
 USDA, ARS, US Meat Animal Research Center  
 PO Box 166, Clay Center, NE 68933-0166, USA  
 Tel: 402 762 4366  
 Fax: 402 762 4390  
 Email: smith@email.marc.usda.gov  
 Single pass sequencing. Bases called and alt-trimmed with phred v0.980904.e. Vector identified by cross\_match with the -minscore 18 and -match 12 options.  
 PCR primers  
 FORWARD: AGGAACACGCTATGACCAT  
 BACKWARD: GTTTCGACGTCACGACG  
 Plate: 52 row: B column: 21  
 Seq primer: ATTTCAGTCGACACTATAG.  
 FEATURES  
 source  
 1..571  
 /organism="Sus scrofa"  
 /db\_xref="taxon:9823"  
 /clone\_lib="MARC 2P1G"  
 /tissue\_type="pooled"  
 /lab\_host="DH10B"  
 /note="Vector: PCMV SPORT6; Site.1: NotI; Site.2: SalI; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, placental, and placenta."  
 BASE COUNT 168 a 142 c 138 g 123 t  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 1.26e-05 Length: 571  
 Score: 114.50 Matches: 22  
 Percent Similarity: 56.34% Conservative: 18  
 Best Local Similarity: 30.99% Mismatches: 30  
 Query Match: 24.84% Indels: 1  
 DB: 12 Gaps: 1  
 US-09-697-089-2\_COPY\_1\_88 (1-88) x BF080490 (1-571)  
 QY 4 11elysaspasensetargalaleuilelnarfmetygmcthrvallellysglnle 23  
 Db 27 CTGAAGGAGAGAGAGAGCGCTTTGCTCGTCACTGCGCATGGGAGCATCAATGCGCTC 86  
 QY 24 ThraspaspaleuphevaltrpaspvalleuasnarglgluvalasnllelleCysCys 43  
 Db 87 TTGGATGAACATTTACACACACAGAGTCTGTACACGAGGAGGATGAGATGATAGATGT 146  
 QY 44 Glulysvalglu---GlnaspAlaAlargllyllelleHsmetilleleulyslysgly 62  
 Db 147 GAACACGCTACAGTATGATAGAGCCCGGAGCTTTGATGATGATGATGATGATGATGATG 206  
 QY 63 SerGuserCysasnleupheleulysserleu 73  
 Db 207 CCCGAGCATGCCAATTTGCATCATCATATAT 239  
 RESULT 6 681 bp mRNA linear EST 31-AUG-2001  
 LOCUS BB199526  
 DEFINITION BB199526 RIKEN full-length enriched, 0 day neonate thymus Mus  
 musculus cDNA clone A430015K19 3', mRNA sequence.  
 ACCESSION BB199526

VERSION BB199526.2 GI:15409668  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 681)  
 Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Haru, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Kono, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Sasaki, Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.  
 RIKEN Mouse ESTs (Arakawa, T., et al. 2001)  
 Unpublished (2001)  
 On Jun 30, 2000 this sequence version replaced gi:8664479.  
 JOURNAL Contact: Yoshihide Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suenho-cho, Tsukuba-shi, Ibaraki, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216  
 Email: genome-res@gsr.riken.go.jp,  
 URL: http://genome.gsc.riken.go.jp/  
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)  
 wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.  
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multichannel sequencer. Genome Res. 10 (11), 1757-1771 (2000)  
 Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.  
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 Yamanaka, T., Kiyosawa, H., Kondo, S., Saito, T., Shinagawa, A., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., Arakawa, T., Ishii, Y. and Hayashizaki, Y.  
 Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct. Func. Genomics 2 pre, 172-186 (2001)  
 Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.  
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
 FEATURES  
 source  
 1..681  
 /organism="Mus musculus"  
 /db\_xref="taxon:10090"  
 /clone\_lib="A430015K19"  
 /clone\_lib="RIKEN full-length enriched, 0 day neonate thymus"  
 /tissue\_type="thymus"  
 /dev\_stage="0 day neonate"  
 /lab\_host="DH10B"  
 /note="Site.1: SalI; Site.2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was







FEATURES	source
ORGANISM	1. 812 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_id="Athersys RAGE Library" /cell_line="HT1080" /note="See 'Creation of Genome-wide Protein Expression' Libraries using Random Activation of Gene Expression', Nature Biotechnology, In press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
BASE COUNT	269 a 113 c 156 g 273 t 1 others
ALIGNMENT SCORES	
PRED. NO.:	0.000187
SCORE:	108.00
PERCENT SIMILARITY:	58.33%
BEST LOCAL SIMILARITY:	34.52%
QUERY MATCH:	23.43%
DB:	12
US-09-697-089-2_COPY_1_88 (1-88) x BG184190 (1-812)	
QY	1 MetanpheiIeIyAspAsnSerIrgAlaIeUleIegInaIrgmEclIymethIvalIle 20
DB	2 TTGTCTATTAATTCGGAAACAGAAATGGCTCTTTCAACA-----TTGACATGTGTG 55
QY	21 LysGluIleItrAspAspLeuPheValITrpAsnValIeAsnArgGluGluValAsnIle 40
DB	56 CTTCCTATTCCTGGATATACCTTTTAAAGGCCATGTAATTAATTAACAGACATGATATT 115
QY	41 IleCySGyGluIySValGluGlnAspAlaAlaArgGlyIleIleIleIleIleIleIyS 60
DB	116 ATTAACAACAAAACACAGATACCTTTACAGAGAGAAAGATGATACCATTTTGGTT 175
QY	61 LysGlySerGluSerCyAsnLeuPheIeUySserIeUySgluITrpAsnTyIProIeu 80
DB	176 AAAGGAAATGCTGGCGGCACATCTTCAAAAAACGTCTAAAGAAATTGACTCTACATTG 235
QY	81 PheGlnAspLeu 84
DB	236 TATTAAGAACTTA 247
RESULT 12	
LOCUS	BG287772 963 bp mRNA linear EST 21-FEB-2001
DEFINITION	602384122P1 NIH_MGC_93 Homo sapiens cDNA clone IMAGE:4513277 5',
ACCESSION	RNA sequence.
VERSION	BG287772
KEYWORDS	BG287772.1 GI:13041938
SOURCE	EST.
ORGANISM	human.
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL	1 (bases 1 to 963)
COMMENT	NIH-MGC http://mgs.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgaabs-remail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMNL at: http://image.llnl.gov Plate: LMNL0399 row: k column: 06 High quality sequence stop: 629. Location/Qualifiers 1. 963

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4513277"
/clone_lib="NIH_MGC_93"
/tissue_type="transitional cell papilloma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: bladder; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

BASE COUNT      325 a      144 c      231 g      262 t      1 others
ORIGIN

Alignment Scores:
Pred. No.:      0.000249      Length:      963
Score:      108.00      Matches:      29
Percent Similarity: 58.33%      Conservative: 20
Best Local Similarity: 34.52%      Mismatches: 33
Query Match:      23.43%      Indels:      2
DB:      12      Gaps:      1

US-09-697-089-2_COPY_1_88 (1-88) x BG287772 (1-963)

QY 1 Metasnpheileysaspasnserrargalaleuileglnargmetglymethrvallile 20
      ::::: ||::: ||| ||||| ||::: ::||| ::
Db 320 TTGTCATTAATTCGGAAGACAGATGGCTCTTTCACAA-----TTGCATGTGTG 373

QY 21 Lysglnlietrraspasleuphevaltrpsavalleuasnarvgglgluvalasnlle 40
      ||| ||::: ||| ||||| ||::: ||::: ||| ::|||
Db 374 CTTCCTATCCGGAATAACTTTTAAAGGCCAATGAATTAATAACAGAACATCATATTT 433

QY 41 Ilecyssgslulysvalgluclnaspalaalaargglylleilehismetilleuys 60
      ||| ::::: ||| ||||| ||||| ||||| |||||
Db 434 ATTAACAAAAAACAACAGATACCTTTACAGCGAGAGACGATGATGATCCATTGGTT 493

QY 61 Lysglserglusercysasnleupheuleysserleuysglutrpasntrproleu 80
      |||||::: ::::: ||::: ||| ||||| ||| ::|||
Db 494 AAAGGAATGCTGGCGCCAAACATCTCTCAAAACGTGCTAAAGAAATTCAGCTCATTG 553

QY 81 Pheglnaspleu 84
      ::::: ||::: |||
Db 554 TATAAGAACTTA 565

RESULT 13
BG028431      976 bp      mRNA      linear      EST 24-JAN-2001
LOCUS      BG028431
DEFINITION      M602294338P1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:4389248 5',
ACCESSION      BG028431
VERSION      BG028431.1 GI:12417525
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 976)
AUTHORS      NIH-MGC http://mgc.ncl.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
      Email: cgapds@email.nih.gov
      Tissue Procurement: ATCC
      cDNA Library Preparation: Life Technologies, Inc.
      DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
      DNA Sequencing by: Incyte Genomics, Inc.
      Clone distribution: MGC clone distribution information can be
      found through the I.M.A.G.E. Consortium/LNL at:
      http://image.lnl.gov
      Plate: L1M10076 row: k column: 09
      High quality sequence stop: 646.
      Location/Qualifiers
      1..976
```

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4389248"
/clone_lib="NIH_MGC_86"
/tissue_type="osteosarcoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: bone; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.53 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

BASE COUNT      368 a      128 c      222 g      258 t
ORIGIN

Alignment Scores:
Pred. No.:      0.000255      Length:      976
Score:      108.00      Matches:      29
Percent Similarity: 58.33%      Conservative: 20
Best Local Similarity: 34.52%      Mismatches: 33
Query Match:      23.43%      Indels:      2
DB:      12      Gaps:      1

US-09-697-089-2_COPY_1_88 (1-88) x BG028431 (1-976)

QY 1 Metasnpheileysaspasnserrargalaleuileglnargmetglymethrvallile 20
      ::::: ||::: ||| ||||| ||::: ::||| ::
Db 146 TTGTCATTAATTCGGAAGACAGATGGCTCTTTCACAA-----TTGCATGTGTG 199

QY 21 Lysglnlietrraspasleuphevaltrpsavalleuasnarvgglgluvalasnlle 40
      ||| ||::: ||| ||||| ||::: ||::: ||| ::|||
Db 200 CTTCCTATCCGGAATAACTTTTAAAGGCCAATGAATTAATAACAGAACATCATATTT 259

QY 41 Ilecyssgslulysvalgluclnaspalaalaargglylleilehismetilleuys 60
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Db 260 ATTAACAAAAAACAACATACCTTTACAGCGAGAGACGATGATGATCCATTGGTT 319

QY 61 Lysglserglusercysasnleupheuleysserleuysglutrpasntrproleu 80
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Db 320 AAAGGAATGCTGGCGCCAAACATCTCTCAAAACGTGCTAAAGAAATTCAGCTCATTG 379

QY 81 Pheglnaspleu 84
      ::::: ||::: |||
Db 380 TATAAGAACTTA 391

RESULT 14
B0235318      512 bp      mRNA      linear      EST 03-MAY-2002
LOCUS      B0235318
DEFINITION      h056e06.g1 Canis Total Brain CDNAS Canis familiaris cDNA clone
ACCESSION      B0235318
VERSION      B0235318.1 GI:20431194
KEYWORDS      EST.
SOURCE      dog.
ORGANISM      Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE      1 (bases 1 to 512)
AUTHORS      O'Shaughnessy,A.L., Palmer,L., McCombie,W.R., Baker,J.P., Bahret,A.
      , Cummins,D., Dedhia,N.N., de la Bastide,M., Katzenberger,F., King
      ,L., Kirchoff,K.A., Miller,B., Muller,S., Nascimento,L.O., Preston
      ,R.R., Shah,R.S., Spiegel,L.A., Zuttervern,T., Santos,L. and Hannon
      ,G.J.
      Expressed sequence tags from Canis familiaris (dog) (5_2002)
      Unpublished (2002)
      Contact: W. Richard McCombie
      Lita Annenberg Hazen Genome Sequencing Center
      Cold Spring Harbor Laboratory
      PO Box 100, Cold Spring Harbor, NY 11724, USA
      Tel: 516 367 8884
      Fax: 516 367 8874
      Email: mcombie@cshl.org
      Plate: h056 row: e column: 06
      Seq primer: -21M130n1vrev
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High quality sequence stop: 512.

FEATURES  
sourceLocation/Qualifiers  
1. 512/organism="Canis familiaris"  
/db\_xref="taxon:9615"/clone="hd56e06"  
/note="Vector: Lambda Zap II: The library was provided by

Greg Hannon and Lee Santos (Cold Spring Harbor Laboratory). This library is oligo(dT) primed using stratagene zap cDNA synthesis kit. It was made from dog whole brain cells. Please contact Greg Hannon (hannon@cshl.org) with any library related inquiries."

BASE COUNT  
ORIGIN

177 a 80 c 121 g 134 t

## Alignment Scores:

Pred. No.:	0.000119	Length:	512
Score:	107.00	Matches:	28
Percent Similarity:	58.33%	Conservative:	21
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Query Match:	23.21%	Indels:	2
DB:	14	Gaps:	1

US-09-697-089-2\_COPY\_1\_88 (1-88) x BQ235318 (1-512)

QY 1 MetanphelelySASPasnSerrArgAlaleuileGlnArgMetGlyMetThrValIle 20

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QY 21 LysGlnIleThrAspAspleuPheValITrpAsnValIleuAsnArgGluValAsnIle 40

Db 179 CTTCCTATCCGCGATTAATCTTTAAAGCCCAATGTAATTAATTAACAGACATGATATC 238

QY 41 IleCysGluIysValGluGlnAspAlaIaArgGlyIleIleHisMetIleLeuLys 60

Db 229 ATTAACAAAACACACATACCTTTCAGACGAGAGAAAGATGATGATGATCTTACTT 298

QY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerIleLysGluITPAsnTyProLeu 80

Db 299 AAGGAAACCTCGCGCCACATCTTCAAAAGTTGTTAAAGAAATGACACTCTACATTA 358

QY 81 PheGlnAspleu 84

Db 359 TATAAGACTTA 370

RESULT 15  
AV682308 665 bp mRNA linear EST 16-JAN-2002

LOCUS AV682308 GKB Homo sapiens cDNA clone GKBAC11 5', mRNA sequence.

ACCESSION AV682308  
VERSION AV682308.1 GI:10284171

KEYWORDS EST.

SOURCE human.  
ORGANISM Homo sapiensEukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.REFERENCE 1 (bases 1 to 665)  
AUTHORS Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,Xiao,H., Ou,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,  
Hu,G., Gu,J., Chen,F., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,Hu,G., Gu,J., Chen,F., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,  
TITLE Insight into hepatocellular carcinogenesis at transcriptome levelby comparing gene expression profiles of hepatocellular carcinoma  
with those of corresponding noncancerous liverJOURNAL MEDLINE  
COMMENT Contact: Zeguang Han

Chinese National Human Genome Center at Shanghai

351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai

201203, P. R. China  
Tel: 86-21-50801919(ex.45)  
Fax: 86-21-50801922Email: hanzg@chgc.sh.cn  
This clone is available at CHGC in Shanghai.FEATURES  
sourceLocation/Qualifiers  
1. 665/organism="Homo sapiens"  
/db\_xref="taxon:9606"/clone="GKBAC11"  
/note="Vector: Lambda Zap II: The library was provided by  
Greg Hannon and Lee Santos (Cold Spring Harbor Laboratory). This library is oligo(dT) primed using stratagene zap cDNA synthesis kit. It was made from dog whole brain cells. Please contact Greg Hannon (hannon@cshl.org) with any library related inquiries."BASE COUNT  
ORIGIN

223 a 98 c 129 g 213 t 2 others

## Alignment Scores:

Pred. No.:	0.000255	Length:	665
Score:	106.00	Matches:	29
Percent Similarity:	57.83%	Conservative:	19
Best Local Similarity:	34.94%	Mismatches:	33
Query Match:	22.99%	Indels:	2
DB:	10	Gaps:	1

US-09-697-089-2\_COPY\_1\_88 (1-88) x AV682308 (1-665)

QY 2 AsnPhelIeLySASPasnSerrArgAlaleuileGlnArgMetGlyMetThrValIleLys 21

Db 1 TCATTAAATTCGAGAAACGAAATGCGCTCTTTTCACAA-----TTGACATGTGTGTG 54

QY 22 GlnIleThrAspAspleuPheValITrpAsnValIleuAsnArgGluValAsnIleIle 41

Db 55 CCTATCTCGATTAATCTTTAAAGCCCAATGTAATTAATTAACAGACATGATATC 114

QY 42 CysCysGluIysValGluGlnAspAlaIaArgGlyIleIleHisMetIleLeuLys 61

Db 115 AAGGAAACCTCGCGCCACATCTTCAAAAGTTGTTAAAGAAATGACACTCTACATTA 174

QY 62 GlySerGluSerCysAsnLeuPheLeuLysSerIleLysGluITPAsnTyProLeu 81

Db 175 GGAATGCTCGCGCCACATCTTCAAAAGTTGTTAAAGAAATGACACTCTACATTA 234

QY 82 GlnAspleu 84

Db 235 AAGAACTTA 243

Search completed: January 31, 2003, 16:18:48  
Job time : 723.086 secs



GenCore version 5.1.3  
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OM protein - nucleic search, using frame\_plus.p2n model

Run on: January 31, 2003, 11:43:51 ; Search time 19.9209 Seconds  
(without alignments)  
1354.737 Million cell updates/sec

Title: US-09-697-089-2\_COPY\_1\_88  
Perfect score: 461  
Sequence: 1 MNFIKDSRALIQRMGWTI.....FLSKIKMNPPLFDLNGQS 88

Scoring table:  
BIOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-O-/cgn2\_1/USPTO.spool/US09697089/runat\_29012003\_092754\_19735/app-query.fasta\_1.981  
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-LOOPEXT=0 -UNITS-bits -START-1 -END-1 -MATRIX-biosum62 -TRANS-human40.cdl  
-LIST=45 -DOCALIGN=200 -THR SCORE-pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
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-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued\_Patents\_NA.\*  
1: /cgn2\_6/ptodata/2/ina/5A.COMB.seq.\*  
2: /cgn2\_6/ptodata/2/ina/5B.COMB.seq.\*  
3: /cgn2\_6/ptodata/2/ina/6A.COMB.seq.\*  
4: /cgn2\_6/ptodata/2/ina/6B.COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/PCTUS.COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfile1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	108	23.4	1435	5	PCT-US95-05922A-1
2	108	23.4	2589	5	PCT-US95-749-1
3	108	23.4	2589	5	PCT-US96-12860-1
4	108	23.4	3532	2	US-09-205-204-1
5	108	23.4	3732	2	US-09-212-971-7
6	108	23.4	3732	3	US-08-800-929A-7
7	108	23.4	3732	4	US-09-617-053A-7
8	102	22.1	2580	2	US-08-511-485-7
9	100	21.7	2862	4	US-08-569-749-13
10	100	21.7	2862	5	PCT-US96-12860-13
11	100	21.7	3151	3	US-09-212-971-13
12	100	21.7	3151	3	US-08-800-929A-13

13	100	21.7	3151	4	US-09-617-053A-13	Sequence 13, Appl
14	95	20.6	1215	1	US-08-242-663A-1	Sequence 1, Appl
15	95	20.6	1215	3	US-08-954-536-17	Sequence 17, Appl
16	95	20.6	1215	4	US-08-748-547-1	Sequence 1, Appl
17	95	20.6	1215	4	US-09-561-756-4	Sequence 4, Appl
18	95	20.6	1215	4	US-09-227-721-4	Sequence 4, Appl
19	95	20.6	1215	5	PCT-US95-06132-1	Sequence 1, Appl
20	95	20.6	1216	2	US-08-573-880-1	Sequence 1, Appl
21	95	20.6	1216	4	US-09-248-179-1	Sequence 1, Appl
22	95	20.6	1248	2	US-08-391-916A-1	Sequence 1, Appl
23	95	20.6	1373	3	US-08-394-189B-3	Sequence 3, Appl
24	95	20.6	1373	5	PCT-US93-05705-3	Sequence 3, Appl
25	93.5	20.3	1185	2	US-08-391-916A-3	Sequence 3, Appl
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27	86	18.7	2601	5	PCT-US96-12860-3	Sequence 3, Appl
28	86	18.7	2676	2	US-08-511-485-5	Sequence 3, Appl
29	86	18.7	3076	2	US-09-205-144-1	Sequence 5, Appl
30	86	18.7	6669	3	US-09-212-971-5	Sequence 1, Appl
31	86	18.7	6669	3	US-08-800-929A-5	Sequence 5, Appl
32	86	18.7	6669	4	US-09-617-053A-5	Sequence 5, Appl
33	75	16.3	1400	4	US-09-245-281-9	Sequence 40, Appl
34	75	16.3	1400	4	US-09-207-359B-40	Sequence 9, Appl
35	75	16.3	2859	4	US-09-099-041A-9	Sequence 9, Appl
36	75	16.3	2859	4	US-09-245-281-9	Sequence 9, Appl
37	75	16.3	2859	4	US-09-207-359B-9	Sequence 9, Appl
38	75	16.3	3382	4	US-09-099-041A-7	Sequence 7, Appl
39	75	16.3	3382	4	US-09-245-281-7	Sequence 7, Appl
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41	75	16.3	4302	4	US-09-245-281-38	Sequence 38, Appl
42	75	16.3	4302	4	US-09-207-359B-38	Sequence 38, Appl
43	69	15.0	4141	4	US-09-245-281-42	Sequence 42, Appl
44	69	15.0	4141	4	US-09-207-359B-42	Sequence 42, Appl
45	68.5	14.9	1333	3	US-08-954-536-15	Sequence 15, Appl

#### ALIGNMENTS

RESULT 1  
PCT-US95-05922A-1  
Sequence 1, Application PC/TUS9505922A  
GENERAL INFORMATION:  
APPLICANT: HE, ET AL.  
TITLE OF INVENTION: Human Inhibitor of Apoptosis Gene 1  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
ADDRESSSEE: CECCHI, STEWART & OLSTEIN  
STREET: 6 BECKER FARM ROAD  
CITY: ROSELAND  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WORD PERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/05922A  
FILING DATE: 11 MAY 1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: FERRARO, GREGORY D.  
REGISTRATION NUMBER: 36,134  
REFERENCE/DOCKET NUMBER: 325800-292  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:



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; LENGTH: 1435 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: CDNA
PCT-US95-05922A-1

Alignment Scores:
Pred. No.: 2.81e-06 Length: 1435
Score: 108.00 Matches: 29
Percent Similarity: 58.33% Conservative: 20
Best Local Similarity: 34.52% Mismatches: 33
Query Match: 23.43% Indels: 2
DB: Gaps: 1

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DB 1015 AAAGGAATGCTGGCCACATCTTCAAAAACGTCTTAAGAAATGACTTACATTG 1074
QY 81 Pheglinspleu 84
DB 1075 TATAAGACTTA 1086

RESULT 2
US-08-569-749-1
; Sequence 1, Application us/08569749
; Patent No. 6187557
; GENERAL INFORMATION:
; APPLICANT: Rothe, Mike
; APPLICANT: Goedel, David V
; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/08/569,749
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brezner, David J.
; REGISTRATION NUMBER: 24,774
; REFERENCE/DOCKET NUMBER: A-62464/DJB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)781-1989
; TELEFAX: (415)398-3249
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2589 base pairs
; TYPE: nucleic acid
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-569-749-1

Alignment Scores:
Pred. No.: 6.49e-06 Length: 2589
Score: 108.00 Matches: 29
Percent Similarity: 58.33% Conservative: 20
Best Local Similarity: 34.52% Mismatches: 33
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DB: Gaps: 1

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DB 1680 ATTAACAAAACACAGATACCTTTACAAAGCAGACAGACATGATGATTTGGTT 1739
QY 61 LysglYsergluSerCysAsnleupheleuLysSerleuLysgluTrpAsnTyProleu 80
DB 1740 AAAGGAATGCTGGCCACATCTTCAAAAACGTCTTAAGAAATGACTTACATTG 1799
QY 81 Pheglinspleu 84
DB 1800 TATAAGACTTA 1811

RESULT 3
PCT-US96-12860-1
; Sequence 1, Application PC/TUS9612860
; GENERAL INFORMATION:
; APPLICANT: TULARIK, INC.
; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/12860
; FILING DATE: 06 AUG 1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brezner, David J.
; REGISTRATION NUMBER: 24,774
; REFERENCE/DOCKET NUMBER: A-62464/DJB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)781-1989
; TELEFAX: (415)398-3249
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2589 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
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; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; PCT-US96-12860-1

Alignment Scores:
Pred. No.: 6.49e-06 Length: 2589
Score: 108.00 Matches: 29
Percent Similarity: 58.33% Conservative: 20
Best Local Similarity: 34.52% Mismatches: 33
Query Match: 23.43% Indels: 2
DB: 5 Gaps: 1

US-09-697-089-2_COPY_1_88 (1-88) x PCT-US96-12860-1 (1-2589)

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Oy 21 LysGlnIleThrAspAspLeuPheValIrrpAsnValIleAsnArgGluGluValAsnIle 40
Db 1620 CTTCCTATCCCGAATACCTTTTAAAGGCCAATGTAATTAATTAACAGAACATGATATT 1679

Oy 41 IleCysGluIlyValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
Db 1680 ATTAACAACAAAACACAGATACCTTTACACGACAGAGAACTGATGATACCATTTTGGTT 1739

Oy 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrrProleu 80
Db 1740 AAAGGAATGCTGCGGCCACACATCTTCAAAAACGTGTCTAAAGAAATGACTCTACATTG 1799

Oy 81 PheGlnAspLeu 84
Db 1800 TATAAGAACTTA 1811

RESULT 4
US-09-205-204-1
; Sequence 1, Application US/09205204
; Patent No. 5958772
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF CELLULAR INHIBITOR OF APOPTOSIS-1 EXPRES
; FILE REFERENCE: PFS-0020
; CURRENT APPLICATION NUMBER: US/09/205, 204
; CURRENT FILING DATE: 1998-12-03
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 3532
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1160)..(3016)
US-09-205-204-1

Alignment Scores:
Pred. No.: 1.01e-05 Length: 3532
Score: 108.00 Matches: 29
Percent Similarity: 58.33% Conservative: 20
Best Local Similarity: 34.52% Mismatches: 33
Query Match: 23.43% Indels: 2
DB: 2 Gaps: 1

US-09-697-089-2_COPY_1_88 (1-88) x US-09-205-204-1 (1-3532)

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Oy 21 LysGlnIleThrAspAspLeuPheValIrrpAsnValIleAsnArgGluGluValAsnIle 40
Db 2585 CTTCCTATCCCGAATACCTTTTAAAGGCCAATGTAATTAATTAACAGAACATGATATT 2644
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Oy 41 IleCysGluIlyValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
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Oy 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrrProleu 80
Db 2705 AAAGGAATGCTGCGGCCACACATCTTCAAAAACGTGTCTAAAGAAATGACTCTACATTG 2764

Oy 81 PheGlnAspLeu 84
Db 2765 TATAAGAACTTA 2776

RESULT 5
US-09-212-971-7
; Sequence 7, Application US/09212971B
; Patent No. 6107041
; GENERAL INFORMATION:
; APPLICANT: Korneljuk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 07891/009002
; CURRENT APPLICATION NUMBER: US/09/212, 971B
; EARLIER FILING DATE: 1998-12-16
; EARLIER APPLICATION NUMBER: 60/017, 354
; EARLIER FILING DATE: 1996-04-26
; EARLIER APPLICATION NUMBER: 60/030, 590
; EARLIER FILING DATE: 1996-11-14
; EARLIER APPLICATION NUMBER: 08/800, 929
; EARLIER FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 3732
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-212-971-7

Alignment Scores:
Pred. No.: 1.09e-05 Length: 3732
Score: 108.00 Matches: 29
Percent Similarity: 58.33% Conservative: 20
Best Local Similarity: 34.52% Mismatches: 33
Query Match: 23.43% Indels: 2
DB: 3 Gaps: 1

US-09-697-089-2_COPY_1_88 (1-88) x US-09-212-971-7 (1-3732)

Oy 1 MetasphelileysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20
Db 2751 TTGTCATTAAATTCGGAGAAACGATGCTCTCTTCAACAA-----TTGACATGTGTG 2804

Oy 21 LysGlnIleThrAspAspLeuPheValIrrpAsnValIleAsnArgGluGluValAsnIle 40
Db 2805 CTTCCTATCCCGAATACCTTTTAAAGGCCAATGTAATTAATTAACAGAACATGATATT 2864

Oy 41 IleCysGluIlyValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
Db 2865 ATTAACAACAAAACACAGATACCTTTACACGACGAGAACTGATGATACCATTTTGGTT 2924

Oy 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrrProleu 80
Db 2925 AAAGGAATGCTGCGGCCACACATCTTCAAAAACGTGTCTAAAGAAATGACTCTACATTG 2984

Oy 81 PheGlnAspLeu 84
Db 2985 TATAAGAACTTA 2996
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RESULT 6
US-08-800-929A-7
; Sequence 7, Application US/08800929A
; Patent No. 6133437
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF
; TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/800,929A
; FILING DATE: 13-FEB-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/030,590
; FILING DATE: 14-NOV-1996
; APPLICATION NUMBER: 60/017,354
; FILING DATE: 26-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bleker-Brady, Kristina
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 07891/009001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3732 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-800-929A-7

Alignment Scores:
Pred. No.: 1.09e-05 Length: 3732
Score: 108.00 Matches: 29
Percent Similarity: 58.33% Conservative: 20
Best Local Similarity: 34.52% Mismatches: 33
Query Match: 23.43% Indels: 2
Gaps: 1

US-09-697-089-2_COPY_1_88 (1-88) x US-08-800-929A-7 (1-3732)
Oy 1 MetasnpheilelyaspsasnserrargAlaleuileglnargmetglymetThValille 20
Db 2751 TTGTCATTAAATTCGGAAGACAGATGCTCTTTCAACA-----TTGACATGTGTG 2804
Oy 21 LysGlnIleThrasPaspIeuPheValITrpAsnValIeuAsnArgGluGluValAsnIle 40
Db 2805 CTTCCTATCCGGAATATCTTTAAAGGCCAATGTAATTAATAACAGGACATGATATT 2864
Oy 41 IleCysCysGluIysValGluGlnAspAlaIaIaarglyIleIleHISmetIleuIys 60
Db 41 IleCysCysGluIysValGluGlnAspAlaIaIaarglyIleIleHISmetIleuIys 60
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Db 2865 ATTAACAAAAACACAGATACCTTTACAAAGCAGAGACATGATGTATACATTTCGT 2924
Oy 61 LysGlySerGluSerCysAsnIeuPheLeuIysSerIeuIysGluITrPasnITrProIeu 80
Db 2925 AAAGAAATGCTGCGCCACATCTTCAAAAACGTCTAAGAAATGACTCTACATTG 2984
Oy 81 PheGlnAspIeu 84
Db 2985 TATAAGAACTTA 2996

RESULT 7
US-09-617-053A-7
; Sequence 7, Application US/09617053A
; Patent No. 6300492
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 07891/009003
; CURRENT APPLICATION NUMBER: US/09/617,053A
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 3732
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-617-053A-7

Alignment Scores:
Pred. No.: 1.09e-05 Length: 3732
Score: 108.00 Matches: 29
Percent Similarity: 58.33% Conservative: 20
Best Local Similarity: 34.52% Mismatches: 33
Query Match: 23.43% Indels: 2
Gaps: 1

US-09-697-089-2_COPY_1_88 (1-88) x US-09-617-053A-7 (1-3732)
Oy 1 MetasnpheilelyaspsasnserrargAlaleuileglnargmetglymetThValille 20
Db 2751 TTGTCATTAAATTCGGAAGACAGATGCTCTTTCAACA-----TTGACATGTGTG 2804
Oy 21 LysGlnIleThrasPaspIeuPheValITrpAsnValIeuAsnArgGluGluValAsnIle 40
Db 2805 CTTCCTATCCGGAATATCTTTAAAGGCCAATGTAATTAATAACAGGACATGATATT 2864
Oy 41 IleCysCysGluIysValGluGlnAspAlaIaIaarglyIleIleHISmetIleuIys 60
Db 2865 ATTAACAAAAACACAGATACCTTTCAAAAGCAGAGACATGATGTATACATTTCGT 2924
Oy 61 LysGlySerGluSerCysAsnIeuPheLeuIysSerIeuIysGluITrPasnITrProIeu 80
Db 2925 AAAGAAATGCTGCGCCACATCTTCAAAAACGTCTAAGAAATGACTCTACATTG 2984
Oy 81 PheGlnAspIeu 84
Db 2985 TATAAGAACTTA 2996

RESULT 8
US-08-511-485-7
; Sequence 7, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
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:
: APPLICANT: Korneluk, Robert G.
: APPLICANT: Mackenzie, Alexander E.
: APPLICANT: Baird, Stephen
: TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
: NUMBER OF SEQUENCES: 38
: PROBES, AND DETECTION METHODS
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fish & Richardson P.C.
: STREET: 225 Franklin Street
: CITY: Boston
: STATE: MA
: COUNTRY: USA
: ZIP: 02110-2804
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/511,485
: FILING DATE: 04-AUG-1995
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Clark, Paul T.
: REGISTRATION NUMBER: 30,162
: REFERENCE/DOCKET NUMBER: 07540/002001
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617/542-5070
: TELEFAX: 617/542-8906
: TELEX: 200154
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2580 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: both
: TOPOLOGY: both
: MOLECULE TYPE: DNA (genomic)
:
: US-08-511-485-7
:
: Alignment Scores:
: Pred. No.: 4.88e-05 Length: 2580
: Score: 102.00 Matches: 28
: Percent Similarity: 57.14% Conservative: 20
: Best Local Similarity: 33.33% Mismatches: 34
: Query Match: 22.13% Indels: 2
: DB: Gaps: 1
:
: US-09-697-089-2_COPY_1_88 (1-88) x US-08-511-485-7 (1-2580)
:
: QY 1 MetAspHeIleIySAsPAsnSerArgAlaLeuIleGlnArgMetGlyMethrValIle 20
:      :      :      :      :      :      :      :      :      :      :
: Db 1609 TTGCTATTAAATCGGAGAACAGATGGCTCTCTTCAACA-----TTGACATGTGTG 1662
:
: QY 21 LysGlnIleThrAspAspLeuPheValITrpAsnValIleuAsnArgGluGluValAsnIle 40
:      :      :      :      :      :      :      :      :      :      :
: Db 1663 CTCTCATCTCCGATTAATCTTTAAAGGCCAATGTAATTAATAACAGAACATATATT 1722
:
: QY 41 IleCysGlyValIleGlnAspAlaIleArgGlyIleIleHisMetIleuLys 60
:      :      :      :      :      :      :      :      :      :      :
: Db 1723 ATTAACAACAAAACACAGATACCTTTACAGCGAGAGAACTGATGATTCATTTGGGTT 1782
:
: QY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerIleuLysGluITrpAsnITyrProLeu 80
:      :      :      :      :      :      :      :      :      :      :
: Db 1783 AAGGAAATGCTGCGCCACACATCTTCAAAAACCTGTAAAGAAATTGACTCTACATTG 1842
:
: QY 81 PheGlnAspLeu 84
:      :      :      :      :      :      :      :      :      :      :
: Db 1843 TATAGAACTTA 1854
:
: RESULT 9
: US-08-569-749-13
: Sequence 13, Application US/08569749
: APPLICANT: TULARIK, INC.
: TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
```

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:
: GENERAL INFORMATION:
: APPLICANT: Rothe, Mike
: APPLICANT: Goeddel, David V
: TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
: STREET: 4 Embarcadero Center, Suite 3400
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/569,749
: FILING DATE:
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Brezner, David J.
: REGISTRATION NUMBER: 24,774
: REFERENCE/DOCKET NUMBER: A-62464/DJB
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415)781-1989
: TELEFAX: (415)398-3249
: INFORMATION FOR SEQ ID NO: 13:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2862 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
:
: US-08-569-749-13
:
: Alignment Scores:
: Pred. No.: 0.000111 Length: 2862
: Score: 100.00 Matches: 27
: Percent Similarity: 58.33% Conservative: 22
: Best Local Similarity: 32.14% Mismatches: 33
: Query Match: 21.69% Indels: 2
: DB: Gaps: 1
:
: US-09-697-089-2_COPY_1_88 (1-88) x US-08-569-749-13 (1-2862)
:
: QY 1 MetAspHeIleIySAsPAsnSerArgAlaLeuIleGlnArgMetGlyMethrValIle 20
:      :      :      :      :      :      :      :      :      :      :
: Db 1836 TTATACGTGATTCGGAGAAATGAGATGGCCCTTTCAACAG-----TTGACACATGTG 1879
:
: QY 21 LysGlnIleThrAspAspLeuPheValITrpAsnValIleuAsnArgGluGluValAsnIle 40
:      :      :      :      :      :      :      :      :      :      :
: Db 1880 CTCTCATCTCCGATTAATCTTTGAGGCCAATGTAATTAACAACAGAACATATATT 1939
:
: QY 41 IleCysGlyValIleGlnAspAlaIleArgGlyIleIleHisMetIleuLys 60
:      :      :      :      :      :      :      :      :      :      :
: Db 1940 ATTAGACGAAACACACAGATACCTTACAGCAGACAGAGCTTATGACACCTTTAGTC 1999
:
: QY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerIleuLysGluITrpAsnITyrProLeu 80
:      :      :      :      :      :      :      :      :      :      :
: Db 2000 AAGGAAATGCTGCGCCACACATCTTCAAAAACCTGTGAAGAAATTGACTCCACGTTA 2059
:
: QY 81 PheGlnAspLeu 84
:      :      :      :      :      :      :      :      :      :      :
: Db 2060 TATGAAACTTA 2071
:
: RESULT 10
: PCT-US96-12860-13
: Sequence 13, Application PC/TUS9612860
: GENERAL INFORMATION:
: APPLICANT: TULARIK, INC.
: TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
```

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      : NUMBER OF SEQUENCES:    14
      : CORRESPONDENCE ADDRESS:
      : ADDRESSEE: FLEHR, HONBACH, TEST, ALBRITTON & HERBERT
      : STREET:   4 Embarcadero Center, Suite 3400
      : CITY:     San Francisco
      : STATE:    California
      : COUNTRY:  USA
      : ZIP:       94111
      : COMPUTER READABLE FORM:
      : MEDIUM TYPE: Floppy disk
      : COMPUTER: IBM PC compatible
      : OPERATING SYSTEM: PC-DOS/MS-DOS
      : SOFTWARE: PatentIn Release #1.0, Version #1.30
      : CURRENT APPLICATION DATA:
      : APPLICATION NUMBER: PCT-US96/12860
      : FILING DATE: 06 AUG 1996
      : CLASSIFICATION:
      : PRIOR APPLICATION DATA:
      : APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749
      : CLASSIFICATION:
      : ATTORNEY/AGENT INFORMATION:
      : NAME: Brezner, David J.
      : REGISTRATION NUMBER: 24,774
      : REFERENCE/DOCKET NUMBER: A-62464/DJB
      : TELECOMMUNICATION INFORMATION:
      : TELEPHONE: (415)781-1989
      : TELEFAX: (415)398-3249
      : INFORMATION FOR SEQ ID NO: 13:
      : SEQUENCE CHARACTERISTICS:
      : LENGTH: 2862 base pairs
      : TYPE: nucleic acid
      : STRANDEDNESS: single
      : TOPOLOGY: linear
      : MOLECULE TYPE: cDNA
      : PCT-US96-12860-13

Alignment Scores:
Pred. No.:              0.000111          Length:           2862
Score:                100.00             Matches:            27
Percent Similarity:    58.33%             Conservative:       22
Best Local Similarity: 32.14%             Mismatches:         3
Query Match:           21.69%             Indels:              3
DB:                    5                  Gaps:                1

US-09-697-089-2_COPY_1_-88 (1-88) x PCT-US96-12860-13 (1-2862)
OY      1 MetcnsphlellysaspsnserarqalaleuIlcglnargmetclymethrvallle 20
Db      1826 TTATCATCGATTTCGGAAGAATAAATAGGCCCTTTCAACAG-----TTGCACATGTCC 1879
OY      21 LysglnllcthraspaaplauphevalitTPAsVValLeuaSnArgslgnluValasnlie 40
Db      1880 CTTCCTATTCGGTAATCTTCTTGAGGCCAGTGTAATTACAACAAGCACATGATATATT 1939
OY      41 IllecycsgylusValgluglnaspalaAlaIArglylleIIshismetlleuleuls 60
Db      1940 ATTAGACAGAAACACAGATACCCTTACAAAGCAGAGACTTAATTGACACCGCTTTATATC 1999
OY      61 LyselgyserclussercySaaNleupheleulsSerleuluyslguTrPAsntTyProleu 80
Db      2000 AAGGAAAATGCTGCAGCCAACATCTTCAAAMAActtCTGaaggaAAttgactccAcgttta 2059
OY      81 Phcglnasplau 84
Db      2060 TATGAAAACTTA 2071

RESULT 11
US-09-212-971-13
: Sequence 13, Application us/09212971B
: Patent No. 6107041
: GENERAL INFORMATION:
: APPLICANT: Kornelius, Robert G
: APPLICANT: Mackenzie, Alexander E
```

```

: APPLICANT: Bairston, Peter
: APPLICANT: Bairston, Stephen
: APPLICANT: Tsang, Benjamin K
: APPLICANT: Pratt, Christine
: TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
: TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
: FILE REFERENCE: 07891/009002
: CURRENT APPLICATION NUMBER: US/09/212,971B
: CURRENT FILING DATE: 1998-12-16
: EARLIER APPLICATION NUMBER: 60/017,354
: EARLIER FILING DATE: 1996-04-26
: EARLIER APPLICATION NUMBER: 60/030,590
: EARLIER FILING DATE: 1996-11-14
: EARLIER APPLICATION NUMBER: 08//800,929
: EARLIER FILING DATE: 1997-02-13
: NUMBER OF SEQ ID NOS: 17
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 13
: LENGTH: 3151
: TYPE: DNA
: ORGANISM: Mus musculus
US-09-212-971-13

Alignment Scores:
Pred. No.: 0.000127 Length: 3151
Score: 100.00 Matches: 27
Percent Similarity: 58.33% Conservative: 22
Best Local Similarity: 32.14% Mismatches: 33
Query Match: 21.69% Indels: 2
DB: 3 Gaps: 1

US-09-697-089-2_COPY_1_88 (1-88) x US-09-212-971-13 (1-3151)
OY 1 MetAsnpHeilelYsAsPnsSerArGAlaLeuIleGlnArgMetGlYmetThrValIle 20
Db 2132 TTATACAGCATTCGGAAACAATAGAATGCCTCTTTCACAG-----TTACACATGTC 2185
OY 21 LysGInIleThrAspAsPleuPhueValTrpAsnValIeuAsnArGluGluValasnlle 40
Db 2186 CTTCCTATCCGTGGAAATCTCTTGAGGCCAGGTGAATTACAAAACAGAACATGATTA 2245
OY 41 IleCysGlyLuLyVaIGluGlnAspAlaIalAArgGlyIlelleHIsMeIleuLyS 60
Db 2246 ATTACACGAAAAACACACATACCCTTACACAGCAAGAGCTTATTGACACCGTTTAGTC 2305
OY 61 LysGlySerGluSerCysAsnLeuPheluYserLeuLySGluTrpAsnTyPrProleu 80
Db 2306 AAGGGAATGCTGCAGCACACATCTCAAAAACCTCTGAAGGAAATGACTCCACGTTA 2365
OY 81 pHeGlnAspleu 84
Db 2366 TATGAAAACTTA 2377

RESULT 12
US-08-800-929A-13
: Sequence 13, Application US/08800929A
: Patent No. 6133437
: GENERAL INFORMATION:
: APPLICANT: Korneluk, Robert G
: APPLICANT: Mackenzie, Alexander E
: APPLICANT: Liston, Peter
: APPLICANT: Baird, Stephen
: APPLICANT: Tsang, Benjamin K
: APPLICANT: Pratt, Christine
: TITLE OF INVENTION: DETECTION AND MODULATION OF
: TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERAT
: TITLE OF INVENTION: DISEASE
: NUMBER OF SEQUENCES: 17
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Clark & Elbing LLP
: STREET: 176 Federal Street
: CITY: Boston

```

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STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,929A
FILING DATE: 13-FEB-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,590
FILING DATE: 14-NOV-1996
APPLICATION NUMBER: 60/017,354
FILING DATE: 26-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bieker-Brady, Kristina
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 07891/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
TELEX:
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 3151 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-800-929A-13

Alignment Scores:
Pred. No.: 0.000127 Length: 3151
Score: 100.00 Matches: 27
Percent Similarity: 58.33% Conservative: 22
Best Local Similarity: 32.14% Mismatches: 33
Query Match: 21.69% Indels: 2
Gaps: 1

US-09-697-089-2_COPY_1_88 (1-88) x US-08-800-929A-13 (1-3151)

QY 1 MetasnpheilleysaspasnserrarglaleuileglnargmetglymetrthValille 20
Db 2132 TTATCAGTCGATTCGGAAGAAATGAGATGCCCCCTCTTCACAG-----TTGACACATGTC 2185
QY 21 LysglnlthrpsaspbleuphevaltrpsnvalleuasnararglgluValasnlle 40
Db 2186 CTTCCTATCCGATTAATCTTCTTGAGGCCAGTGTATTTACAAACAGGACATGATATT 2245
QY 41 IleCysCysgluysValgluGlnaspAlaIlaarglylelleHismetIleleuyls 60
Db 2246 ATTAGACAGAAACACAGATACCTTACACAGAGAGAGCTTATTTGACACCGTTTAACTC 2305
QY 61 LysglYsergluserCysAsnleupheleuylsSerleuylsglUtrPasnTyFProleu 80
Db 2306 AAGGGAATGCTGCAGCCACATCTTCAAAAACCTCTGGAAGAAATTGACTCCACGTTA 2365
QY 81 PheGlnAspleu 84
Db 2366 TATGAAAACCTTA 2377

RESULT 13
; Sequence 13, Application US/09617053A
; Patent No. 6300492
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
```

```
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IABs AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
DISEASE
FILE REFERENCE: 07891/009003
CURRENT APPLICATION NUMBER: US/09/617,053A
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/800,929
PRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 3151
TYPE: DNA
ORGANISM: Mus musculus
US-09-617-053A-13

Alignment Scores:
Pred. No.: 0.000127 Length: 3151
Score: 100.00 Matches: 27
Percent Similarity: 58.33% Conservative: 22
Best Local Similarity: 32.14% Mismatches: 33
Query Match: 21.69% Indels: 2
Gaps: 1

US-09-697-089-2_COPY_1_88 (1-88) x US-09-617-053A-13 (1-3151)

QY 1 MetasnpheilleysaspasnserrarglaleuileglnargmetglymetrthValille 20
Db 2132 TTATCAGTCGATTCGGAAGAAATGAGATGCCCCCTCTTCACAG-----TTGACACATGTC 2185
QY 21 LysglnlthrpsaspbleuphevaltrpsnvalleuasnararglgluValasnlle 40
Db 2186 CTTCCTATCCGATTAATCTTCTTGAGGCCAGTGTATTTACAAACAGGACATGATATT 2245
QY 41 IleCysCysgluysValgluGlnaspAlaIlaarglylelleHismetIleleuyls 60
Db 2246 ATTAGACAGAAACACAGATACCTTACACAGAGAGAGCTTATTTGACACCGTTTAACTC 2305
QY 61 LysglYsergluserCysAsnleupheleuylsSerleuylsglUtrPasnTyFProleu 80
Db 2306 AAGGGAATGCTGCAGCCACATCTTCAAAAACCTCTGGAAGAAATTGACTCCACGTTA 2365
QY 81 PheGlnAspleu 84
Db 2366 TATGAAAACCTTA 2377

RESULT 14
; Sequence 14, Application US/08242663A
; Patent No. 5492824
; GENERAL INFORMATION:
; APPLICANT: Talianian, Robert V.
; APPLICANT: Dang, Leonard Luan Cao
; APPLICANT: Walker, Nigel Pelham Clinton
; APPLICANT: Chayur, Tatig
; TITLE OF INVENTION: ICE AND ICE-LIKE COMPOSITIONS AND
; TITLE OF INVENTION: METHODS OF MAKING SAME
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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Mon Feb 3 14:11:41 2003

us-09-697-089-2\_copy\_1\_88.p2n.rni

Page 9

Search completed: January 31, 2003, 15:16:34  
Job time : 22.9209 secs

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GenCore version 5.1.3  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 31, 2003, 15:16:37 ; Search time 24.3692 Seconds  
(without alignments)  
1622.345 Million cell updates/sec

Title: US-09-697-089-2\_COPY\_1\_88

Perfect score: 461

Sequence: 1 MRFKDSRALRIQRMGTVI.....FLSKREMYNPLFDLNGQS 88

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 396772 seqs, 224632407 residues

Total number of hits satisfying chosen parameters: 793544

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database: Published Applications\_NA:

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14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	461	100.0	768	9	US-09-864-921-102
3	461	100.0	1395	9	US-09-864-921-98
4	461	100.0	3072	10	US-09-841-739-3

5	461	100.0	3133	10	US-09-841-739-1	Sequence 1, App1
6	461	100.0	3396	9	US-09-864-921-96	Sequence 96, App1
7	457	99.1	261	9	US-09-864-921-177	Sequence 177, App1
8	457	99.1	3612	10	US-09-841-739-6	Sequence 6, App1
9	457	99.1	3615	10	US-09-841-739-12	Sequence 12, App1
10	457	99.1	3615	10	US-09-841-739-12	Sequence 12, App1
11	126.5	27.4	1233	10	US-09-917-265-14	Sequence 14, App1
12	126.5	27.4	1233	10	US-09-917-265-14	Sequence 14, App1
13	123.5	26.8	526	10	US-09-917-265-17	Sequence 17, App1
14	123.5	26.8	526	10	US-09-917-265-19	Sequence 19, App1
15	123.5	26.8	1230	10	US-09-917-265-23	Sequence 23, App1
16	123.5	26.8	1230	10	US-09-917-265-25	Sequence 25, App1
17	108	23.4	3532	10	US-09-880-107-3354	Sequence 3354, App1
18	108	23.4	3732	9	US-09-974-592-7	Sequence 7, App1
19	102.5	22.2	3321	9	US-09-864-921-69	Sequence 69, App1
20	102.5	22.2	2580	9	US-09-201-936-7	Sequence 7, App1
21	100	21.7	3151	10	US-09-974-592-13	Sequence 13, App1
22	97	21.0	1293	10	US-09-996-617-6	Sequence 6, App1
23	97	21.0	1293	10	US-09-931-071-6	Sequence 6, App1
24	97	21.0	1487	9	US-09-388-221-7	Sequence 7, App1
25	97	21.0	4466	9	US-09-388-221-11	Sequence 11, App1
26	97	21.0	4556	9	US-09-388-221-9	Sequence 9, App1
27	97	21.0	5059	10	US-09-996-617-3	Sequence 3, App1
28	97	21.0	5059	10	US-09-931-071-3	Sequence 3, App1
29	95	20.6	1215	10	US-09-954-697-4	Sequence 4, App1
30	95	20.6	1216	10	US-09-827-7084-1	Sequence 1, App1
31	95	20.6	1373	10	US-09-888-243-3	Sequence 3, App1
32	93	20.2	2416	9	US-09-201-936-41	Sequence 41, App1
33	91.5	19.8	510	9	US-09-864-921-85	Sequence 85, App1
34	86	18.7	2676	9	US-09-201-936-5	Sequence 5, App1
35	86	18.7	3076	9	US-09-954-531-16	Sequence 16, App1
36	86	18.7	3076	10	US-09-954-456-1635	Sequence 1635, App1
37	86	18.7	6669	10	US-09-974-592-5	Sequence 5, App1
38	82.5	17.9	328	10	US-09-867-701-3	Sequence 3, App1
39	77	16.7	460	10	US-09-960-352-8049	Sequence 8049, App1
40	75	16.3	1400	9	US-10-118-984-40	Sequence 40, App1
41	75	16.3	1400	10	US-09-728-721-40	Sequence 40, App1
42	75	16.3	2859	9	US-10-118-984-9	Sequence 9, App1
43	75	16.3	2859	10	US-09-728-721-9	Sequence 9, App1
44	75	16.3	2859	12	US-10-105-931-9	Sequence 9, App1
45	75	16.3	3382	9	US-10-118-984-7	Sequence 7, App1

#### ALIGNMENTS

RESULT 1  
US-09-864-921-100  
: Sequence 100, Application US/09864921  
: Patent No. US20020176853A1  
GENERAL INFORMATION:  
APPLICANT: Reed, John C.  
APPLICANT: Pio, Frederick F.  
APPLICANT: Godzik, Adam  
APPLICANT: Stehlik, Christian  
APPLICANT: Damiano, Jason S.  
APPLICANT: Lee, Sung-Hyung  
APPLICANT: Oliveira, Vasco A.  
APPLICANT: Pawlowski, Hideki  
APPLICANT: Pawlowski, Krzysztof  
TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing  
FILE REFERENCE: P-1J 4757  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US/09/864, 921  
PRIOR FILING DATE: 2000-05-24  
PRIOR APPLICATION NUMBER: US 09/686, 347  
PRIOR FILING DATE: 2000-10-10  
PRIOR APPLICATION NUMBER: US 60/275, 980  
NUMBER OF SEQ ID NOS: 195  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 100

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; LENGTH: 578
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (277)...(552)
US-09-864-921-100

Alignment Scores:
Pred. No.: 2,3e-59      Length: 578
Score: 461.00          Matches: 88
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
DB: 9                  Caps: 0

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QY 21 LysGlnIleThrAspAspLeuPheValITrPAsnValLeuAsnArgGluGluValAsnIle 40
Db 337 AAGCAAAATCACAGATGACCTATTGTGTGATGTGTAATCCCGAAGAAGTAACATC 396
QY 41 IleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
Db 397 ATTGCTGCCGAGAAAGTGAGACAGATGCTGCTAGAGGATCATTCATGATTTTGAA 456
QY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeu 80
Db 457 AAGGTTTCAGAGTCTCTTAACCTCTTCTTAATAATCCCTTAAGAGTGAATCATCTCTA 516
QY 81 PheGlnAspLeuAsnGlyGlnSer 88
Db 517 TTTCAGAGCTTGAATGACAAAGT 540

RESULT 2
US-09-864-921-102
; Sequence 102, Application US/09864921
; Patent No. US20020176853A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Pio, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sung-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing
; TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods of Use
; FILE REFERENCE: P-LJ 4752
; CURRENT APPLICATION NUMBER: US/09/864,921
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102
; LENGTH: 768
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (277)...(744)
US-09-864-921-102
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Alignment Scores:
Pred. No.: 3,47e-59      Length: 768
Score: 461.00          Matches: 88
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
DB: 9                  Caps: 0

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QY 21 LysGlnIleThrAspAspLeuPheValITrPAsnValLeuAsnArgGluGluValAsnIle 40
Db 337 AAGCAAAATCACAGATGACCTATTGTGTGATGTGTAATCCCGAAGAAGTAACATC 396
QY 41 IleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
Db 397 ATTGCTGCCGAGAAAGTGAGACAGATGCTGCTAGAGGATCATTCATGATTTTGAA 456
QY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeu 80
Db 457 AAGGTTTCAGAGTCTCTTAACCTCTTCTTAATAATCCCTTAAGAGTGAATCATCTCTA 516
QY 81 PheGlnAspLeuAsnGlyGlnSer 88
Db 517 TTTCAGAGCTTGAATGACAAAGT 540

RESULT 3
US-09-864-921-98
; Sequence 98, Application US/09864921
; Patent No. US20020176853A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Pio, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sung-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing
; TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods of Use
; FILE REFERENCE: P-LJ 4752
; CURRENT APPLICATION NUMBER: US/09/864,921
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 98
; LENGTH: 1395
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (277)...(1353)
US-09-864-921-98

Alignment Scores:
Pred. No.: 8,27e-59      Length: 1395
Score: 461.00          Matches: 88
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
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QY 21 Lysglniethrpsasppluepheyalttrpasnvalileuasnarnglucnuvalasnnile 40
DB 337 AAGCAAAATCACAGATGACCTATTGTATGGAATGTTCTAAATCGCGAAGAGATTAACATC 396
QY 41 IleCysCysGluLysValGluGlnaspalaalargglylleilehismetilleuLys 60
DB 397 ATTTCCTCGAAGAGATGGAGCAGATGCTGCTAGAGGATCATTCACATGATTTTGAAA 456
QY 61 LysgIysSerGluSerCysAsnleuPheleuLysSerleuLysGluTrpasnTyProleu 80
DB 457 AAGGGTTGAGAGTCCCTGTAACTCTTCTTAATCCCTTAAGAGAGTGAATATCCTCTTA 516
QY 81 PheGlnaspLeuansnglyInser 88
DB 517 TTTCAGGACTTGATGAGCAAAAGT 540

RESULT 4
US-09-841-739-3
; Sequence 3, Application US/09841739
; Patent No. US20020034784A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-329001
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3072
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-841-739-3

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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 10

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QY 21 Lysglniethrpsasppluepheyalttrpasnvalileuasnarnglucnuvalasnnile 40
DB 61 AAGCAAAATCACAGATGACCTATTGTATGGAATGTTCTAAATCGCGAAGAGATTAACATC 120
QY 41 IleCysCysGluLysValGluGlnaspalaalargglylleilehismetilleuLys 60
DB 121 ATTTCCTCGAAGAGATGGAGCAGATGCTGCTAGAGGATCATTCACATGATTTTGAAA 180
QY 61 LysgIysSerGluSerCysAsnleuPheleuLysSerleuLysGluTrpasnTyProleu 80
DB 181 AAGGGTTGAGAGTCCCTGTAACTCTTCTTAATCCCTTAAGAGAGTGAATATCCTCTTA 240
QY 81 PheGlnaspLeuansnglyInser 88
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DB 241 TTTCAGGACTTGATGAGCAAAAGT 264

RESULT 5
US-09-841-739-1
; Sequence 1, Application US/09841739
; Patent No. US20020034784A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES TH
; FILE REFERENCE: 07334-329001
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3133
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (36)...(3107)
US-09-841-739-1

Alignment Scores:
Pred. No.: 2,68e-58 Length: 3133
Score: 461.00 Matches: 88
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10

US-09-697-089-2_copy_1_88 (1-88) x US-09-841-739-1 (1-3133)
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DB 36 ATGAATTTTCATTAAGACAAATAGCCGAGCCCTTATTCAAAGATGGAAATGACTGTATA 95
QY 21 Lysglniethrpsasppluepheyalttrpasnvalileuasnarnglucnuvalasnnile 40
DB 96 AAGCAAAATCACAGATGACCTATTGTATGGAATGTTCTAAATCGCGAAGAGATTAACATC 155
QY 41 IleCysCysGluLysValGluGlnaspalaalargglylleilehismetilleuLys 60
DB 156 ATTTCCTCGAAGAGATGGAGCAGATGCTGCTAGAGGATCATTCACATGATTTTGAAA 215
QY 61 LysgIysSerGluSerCysAsnleuPheleuLysSerleuLysGluTrpasnTyProleu 80
DB 216 AAGGGTTGAGAGTCCCTGTAACTCTTCTTAATCCCTTAAGAGAGTGAATATCCTCTTA 275
QY 81 PheGlnaspLeuansnglyInser 88
DB 276 TTTCAGGACTTGATGAGCAAAAGT 299

RESULT 6
US-09-864-921-96
; Sequence 96, Application US/09864921
; Patent No. US20020176853A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Plo, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sung-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing
```

;; TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods of Use  
;; FILE REFERENCE: P-LJ 4752  
;; CURRENT APPLICATION NUMBER: US/09/864,921  
;; CURRENT FILING DATE: 2001-05-23  
;; PRIOR APPLICATION NUMBER: US 09/579,240  
;; PRIOR FILING DATE: 2000-05-24  
;; PRIOR APPLICATION NUMBER: US 09/686,347  
;; PRIOR FILING DATE: 2000-10-10  
;; PRIOR APPLICATION NUMBER: US 60/275,980  
;; PRIOR FILING DATE: 2001-03-14  
;; NUMBER OF SEQ ID NOS: 195  
;; SOFTWARE: FASTSEQ for Windows Version 4.0  
;; SEQ ID NO 96  
;; LENGTH: 3396  
;; TYPE: DNA  
;; ORGANISM: Homo sapien  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: (277)...(3348)  
US-09-864-921-96

## Alignment Scores:

Pred. No.:	3,01e-58	Length:	3396
Score:	461.00	Matches:	88
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-697-089-2\_COPY\_1\_88 (1-88) x US-09-864-921-96 (1-3396)

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OY 21 Lysglnilethrappaspaleuphevaltrpansvalileuananargluclvalasnlle 40  
Db 337 AAGCAATACAGATGACCTATTGTATGATGAAATGTCGAATCGGAGAAAGTAAACATC 396  
OY 41 IlecyCsylulysvalgluGlnaspalaalaarglylelleHLSmetilleuyls 60  
Db 397 ATTGCTCGGAGAGGTGACAGATGCTGCTAGAGGATCATTCACATGATTTTGAA 456  
OY 61 LysglYsergluSerCysasnleupheleuylsSerleuylsGluTrpAsnTyrrProleu 80  
Db 457 AAGGTTTCAGAGTCCTGTAACTCTTCTTAATCCCTTAAGAGATGGAATATCCTCTA 516  
OY 81 PheGlnAspLeuAsnGlyGlnSer 88  
Db 517 TTTCAGACTTGAATGACAAAGT 540

## RESULT 7

US-09-864-921-177  
;; Sequence 177, Application US/09864921  
;; Patent No. US20020176853A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Reed, John C.  
;; APPLICANT: Pio, Frederick F.  
;; APPLICANT: Godzik, Adam  
;; APPLICANT: Stehlik, Christian  
;; APPLICANT: Damiano, Jason S.  
;; APPLICANT: Lee, Sug-Hyung  
;; APPLICANT: Oliveira, Vasco A.  
;; APPLICANT: Hayashi, Hideki  
;; APPLICANT: Pawlowski, Krzysztof  
;; TITLE OF INVENTION: No. US20020176853A1e1 Card Domain Containing  
;; FILE REFERENCE: P-LJ 4752  
;; CURRENT APPLICATION NUMBER: US/09/864,921  
;; PRIOR APPLICATION NUMBER: US 09/579,240  
;; PRIOR FILING DATE: 2000-05-24  
;; PRIOR APPLICATION NUMBER: US 09/686,347

;; PRIOR FILING DATE: 2000-10-10  
;; PRIOR APPLICATION NUMBER: US 60/275,980  
;; PRIOR FILING DATE: 2001-03-14  
;; NUMBER OF SEQ ID NOS: 195  
;; SOFTWARE: FASTSEQ for Windows Version 4.0  
;; SEQ ID NO 177  
;; LENGTH: 261  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: (1)...(261)  
US-09-864-921-177

## Alignment Scores:

Pred. No.:	2,84e-59	Length:	261
Score:	457.00	Matches:	87
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	99.13%	Indels:	0
DB:	9	Gaps:	0

US-09-697-089-2\_COPY\_1\_88 (1-88) x US-09-864-921-177 (1-261)

OY 1 Metasnphelllelysaspasnserarghaleuileglnarqmetglymethrvalille 20  
Db 1 ATGATTTTCATAAAGGACAAATAGCCGAGCCCTTATTCAAAAGATGGAAATGACTGTATA 60  
OY 21 Lysglnilethrappaspaleuphevaltrpansvalileuananargluclvalasnlle 40  
Db 61 AAGCAATACAGATGACCTATTGTATGATGAAATGTCGAATCGGAGAAAGTAAACATC 120  
OY 41 IlecyCsylulysvalgluGlnaspalaalaarglylelleHLSmetilleuyls 60  
Db 121 ATTGCTCGGAGAGGTGACAGATGCTGCTAGAGGATCATTCACATGATTTTGAA 180  
OY 61 LysglYsergluSerCysasnleupheleuylsSerleuylsGluTrpAsnTyrrProleu 80  
Db 181 AAGGTTTCAGAGTCCTGTAACTCTTCTTAATCCCTTAAGAGATGGAATATCCTCTA 240  
OY 81 PheGlnAspLeuAsnGlyGln 87  
Db 241 TTTCAGACTTGAATGACAA 261

## RESULT 8

US-09-841-739-6  
;; Sequence 6, Application US/09841739  
;; Patent No. US20020034784A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Bertlin, John  
;; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES TH  
;; FILE REFERENCE: 07334-329001  
;; CURRENT APPLICATION NUMBER: US/09/841,739  
;; CURRENT FILING DATE: 2001-08-29  
;; PRIOR APPLICATION NUMBER: US 09/697,089  
;; PRIOR FILING DATE: 2000-10-26  
;; PRIOR APPLICATION NUMBER: US 60/161,822  
;; PRIOR FILING DATE: 1999-10-27  
;; NUMBER OF SEQ ID NOS: 16  
;; SOFTWARE: FASTSEQ for Windows Version 4.0  
;; SEQ ID NO 6  
;; LENGTH: 3612  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-09-841-739-6

## Alignment Scores:

Pred. No.:	1,29e-57	Length:	3612
Score:	457.00	Matches:	87
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	98.86%	Mismatches:	0
Query Match:	99.13%	Indels:	0
DB:	10	Gaps:	0

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QY 21 Lysglnlethrpsaspheuphevaltrpasnvalleusnaargglugluvalasnlle 40
Db 478 AAGCAAAATCACAGATGACATATTGTGTGGAATGTTCTGGAATCGCGAAGAACTAAACATC 537
QY 41 IleCysCysgluylsValgluGlnaspAlaalaarglyleileileHsmetileleuyls 60
Db 538 ATTTCGTCGCGAAGAGGTGAGCAGATGCTGCTAGAGGATCATTCACATGATTTTGAAA 597
QY 61 LysglYsergluSerCysasnleupheleuylsSerleuylsGluTrpAsnTyr-Proleu 80
Db 598 AAGGTTTCAGAGTCTGTAACCTCTTCTTAATAATCCCTTAAGAGGTGGAAGTAACTATCCTCTA 657
QY 81 PheGlnaspLeuasnGlyGlnSer 88
Db 658 TTTCAGGACTTGAAATGGACAAAGT 681

RESULT 9
; Sequence 4, Application US/09841739
; Patent No. US20020034784A1
; GENERAL INFORMATION:
; APPLICANT: Bertlin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-329001
; CURRENT APPLICATION NUMBER: US/09/841,739
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 3615
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3612)
; US-09-841-739-4

Alignment Scores:
Pred. No.: 1,29e-57 Length: 3615
Score: 457.00 Matches: 87
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 98.86% Mismatches: 0
Query Match: 99.13% Indels: 0
Gaps: 0

US-09-697-089-2_COPY_1_88 (1-88) x US-09-841-739-4 (1-3615)
QY 1 Metasnpheilelysaspasnserrargalaleuileglnargmetglymetrhvalille 20
Db 418 GTGAATTTCAATAAGACAAATAGCCGACCCCTTATTCAAAAGAAATGGAAATGACGTGTATA 477
QY 21 Lysglnlethrpsaspheuphevaltrpasnvalleusnaargglugluvalasnlle 40
Db 478 AAGCAAAATCACAGATGACATATTGTGTGGAATGTTCTGGAATCGCGAAGAACTAAACATC 537
QY 41 IleCysCysgluylsValgluGlnaspAlaalaarglyleileileHsmetileleuyls 60
Db 538 ATTTCGTCGCGAAGAGGTGAGCAGATGCTGCTAGAGGATCATTCACATGATTTTGAAA 597
QY 61 LysglYsergluSerCysasnleupheleuylsSerleuylsGluTrpAsnTyr-Proleu 80
Db 598 AAGGTTTCAGAGTCTGTAACCTCTTCTTAATAATCCCTTAAGAGGTGGAAGTAACTATCCTCTA 657
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QY 81 PheGlnaspLeuasnGlyGlnSer 88
Db 658 TTTCAGGACTTGAAATGGACAAAGT 681

RESULT 10
; Sequence 12, Application US/09841739
; Patent No. US20020034784A1
; GENERAL INFORMATION:
; APPLICANT: Bertlin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-329001
; CURRENT APPLICATION NUMBER: US/09/841,739
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 3615
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-841-739-12

Alignment Scores:
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Score: 457.00 Matches: 87
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 98.86% Mismatches: 0
Query Match: 99.13% Indels: 0
Gaps: 0

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QY 1 Metasnpheilelysaspasnserrargalaleuileglnargmetglymetrhvalille 20
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QY 21 Lysglnlethrpsaspheuphevaltrpasnvalleusnaargglugluvalasnlle 40
Db 3138 AAGCAAAATCACAGATGACATTTGTGTATGATGATTTTCGATCCGGAAGAACTAAACATC 3079
QY 41 IleCysCysgluylsValgluGlnaspAlaalaarglyleileileHsmetileleuyls 60
Db 3078 ATTTCGTCGCGAAGAGGTGAGCAGATGCTGCTAGAGGATCATTCACATGATTTTGAAA 3019
QY 61 LysglYsergluSerCysasnleupheleuylsSerleuylsGluTrpAsnTyr-Proleu 80
Db 3018 AAGGTTTCAGAGTCTGTAACCTCTTCTTAATAATCCCTTAAGAGGTGGAAGTAACTATCCTCTA 2959
QY 81 PheGlnaspLeuasnGlyGlnSer 88
Db 2958 TTTCAGGACTTGAAATGGACAAAGT 2935

RESULT 11
; Sequence 14, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Borouhns, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREIN
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
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Db 1218 CTGAAGGAGAGAGGAGCAGTTCATCAACTCAGTCGGCATGGGGACCGGTCAACGGCTTG 1159

## RESULT 14

## RESULT 14

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US-09-917-265-19/c
; Sequence 19, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Borroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 526
; TYPE: DNA
; ORGANISM: Felis catus
US-09-917-265-19

Alignment Scores:
Pred. No.: 2,27e-09 Length: 526
Score: 123.50 Matches: 27
Percent Similarity: 54.88% Conservative: 18
Best Local Similarity: 32.93% Mismatches: 36
Query Match: 26,79% Indels: 1
DB: 10 Gaps: 1

US-09-697-089-2_COPY_1_88 (1-88) x US-09-917-265-19 (1-526)

QY 4 ILeYsAspAsnSerArGAlaLeuIlleGlnArgMetGlyMetThrValIleYsGlnIle 23
Db 494 CTGAAGGGCAAGAGGAGCACTTCATCACTCACTGCGCATGGGAGCGTCAACGGCTTG 435
QY 24 ThrAspAspLeuPheValITrpAsnValIleuAsnArgGluGluValAsnIleIleCysCys 43
Db 434 CTGATGAACTCTTTGAGAAAAACGTCTGACACGAGAGAGATGAGAGATAAATGT 375
QY 44 GluLySValGlu--GlnAspAlaAlaArgGlyIleIleHisMetIleLeuYsLySgly 62
Db 374 GAAACGCTACCGTTATGACAAGCCCGAGCTGTGATCGACAGCGCTCGCGGAAAGGG 315
QY 63 SerGluSerCysAsnLeuPheLeuYsSerLeuYsGluTrpAsnTrpProLeuPheGln 82
Db 314 CCACGGCGGTGCGAGATCTTTATCTGTACATCTGTGAGAGAACCCACCTTGAGAG 255
QY 83 Aspleu 84
Db 254 ACGCTG 249

RESULT 15
US-09-917-265-23
; Sequence 23, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Borroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 1230
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1230)
; OTHER INFORMATION:
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US-09-917-265-23

Alignment Scores:
Pred. No.: 7.8e-09 Length: 1230
Score: 123.50 Matches: 27
Percent Similarity: 54.88% Conservative: 18
Best Local Similarity: 32.93% Mismatches: 36
Query Match: 26,79% Indels: 1
DB: 10 Gaps: 1

US-09-697-089-2_COPY_1_88 (1-88) x US-09-917-265-23 (1-1230)

QY 4 ILeYsAspAsnSerArGAlaLeuIlleGlnArgMetGlyMetThrValIleYsGlnIle 23
Db 16 CTGAAGGGCAAGAGGAGCACTTCATCACTCACTGCGCATGGGAGCGTCAACGGCTTG 75
QY 24 ThrAspAspLeuPheValITrpAsnValIleuAsnArgGluGluValAsnIleIleCysCys 43
Db 76 CTGATGAACTCTTTGAGAAAAACGTCTGACACGAGAGAGATGAGAGATAAATGT 135
QY 44 GluLySValGlu--GlnAspAlaAlaArgGlyIleIleHisMetIleLeuYsLySgly 62
Db 136 GAAACGCTACCGTTATGACAAGCCCGAGCTGTGATCGACAGCGCTCGCGGAAAGGG 195
QY 63 SerGluSerCysAsnLeuPheLeuYsSerLeuYsGluTrpAsnTrpProLeuPheGln 82
Db 196 CCACGGCGGTGCGAGATCTTTATCTGTACATCTGTGAGAGAACCCACCTTGAGAG 255
QY 83 Aspleu 84
Db 256 ACGCTG 261

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Job time : 26.3692 secs
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GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

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Listing first 45 summaries

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72: /cgn2\_6/ptodata/2/pna/US6028\_COMB.seq: \*  
73: /cgn2\_6/ptodata/2/pna/US6029\_COMB.seq: \*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	461	100.0	3072	PCT-US00-29643-3	Sequence 3, App1
5	461	100.0	3072	US-09-697-089-3	Sequence 3, App1
6	461	100.0	3072	US-09-841-739-3	Sequence 3, App1

7	461	100.0	3075	41	US-10-156-733-1	Sequence 1, Appl1
8	461	100.0	3133	1	PCT-US00-29643-8	Sequence 1, Appl1
9	461	100.0	3133	27	US-09-697-089-1	Sequence 1, Appl1
10	461	100.0	3133	32	US-09-841-739-1	Sequence 1, Appl1
11	461	100.0	3219	41	US-10-156-733-14	Sequence 14, Appl1
12	461	100.0	3396	33	US-09-864-921-.96	Sequence 96, Appl1
13	461	100.0	3545	18	US-09-491-404-1319	Sequence 1319, Appl1
14	461	100.0	3545	34	US-09-922-279-1319	Sequence 1319, Appl1
15	461	100.0	3545	34	US-09-922-279-1319	Sequence 1319, Appl1
16	461	100.0	6012	22	US-09-557-676-911	Sequence 911, Appl1
17	461	100.0	6012	22	US-09-557-676-911	Sequence 911, Appl1
18	461	100.0	6012	38	US-10-042-938-911	Sequence 911, Appl1
19	461	100.0	6012	38	US-10-042-938-917	Sequence 917, Appl1
20	458	99.3	3018	22	US-09-577-408-3077	Sequence 3077, Appl1
21	458	99.3	3213	1	PCT-US01-07143-23	Sequence 23, Appl1
22	458	99.3	3213	42	US-10-221-097-23	Sequence 23, Appl1
23	457	99.1	261	33	US-09-864-921-177	Sequence 177, Appl1
24	457	99.1	2343	22	US-09-578-789-15	Sequence 15, Appl1
25	457	99.1	2343	22	US-09-578-789-15	Sequence 15, Appl1
26	457	99.1	2415	22	US-09-578-789-17	Sequence 17, Appl1
27	457	99.1	2415	22	US-09-578-789-17	Sequence 17, Appl1
28	457	99.1	3260	1	PCT-US01-14826-66	Sequence 66, Appl1
29	457	99.1	3260	26	US-09-667-998-66	Sequence 66, Appl1
30	457	99.1	3612	27	US-09-697-089-6	Sequence 6, Appl1
31	457	99.1	3612	32	US-09-841-739-6	Sequence 6, Appl1
32	457	99.1	3615	1	PCT-US00-29643-4	Sequence 4, Appl1
33	457	99.1	3615	1	PCT-US00-29643-6	Sequence 6, Appl1
34	457	99.1	3615	27	US-09-697-089-4	Sequence 4, Appl1
35	457	99.1	3615	27	US-09-697-089-12	Sequence 12, Appl1
36	457	99.1	3615	32	US-09-841-739-4	Sequence 4, Appl1
37	457	99.1	3615	32	US-09-841-739-12	Sequence 12, Appl1
38	457	99.1	3890	22	US-09-578-789-3078	Sequence 3078, Appl1
39	457	99.1	6900	22	US-09-578-789-73	Sequence 73, Appl1
40	457	99.1	6900	22	US-09-578-789-73	Sequence 73, Appl1
41	457	99.1	6900	27	US-09-666-347-100	Sequence 100, Appl1
42	445	96.5	578	27	US-09-666-347-100	Sequence 100, Appl1
43	445	96.5	768	27	US-09-666-347-98	Sequence 98, Appl1
44	445	96.5	1395	27	US-09-666-347-98	Sequence 98, Appl1
45	445	96.5	3396	27	US-09-666-347-96	Sequence 96, Appl1

## ALIGNMENTS

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1 RESULT 1
2 US-09-864-921-100
3 ; Sequence 100, Application US/09864921
4 ; GENERAL INFORMATION:
5 ; APPLICANT: Reed, John C.
6 ; APPLICANT: Plo, Frederick F.
7 ; APPLICANT: Godzik, Adam
8 ; APPLICANT: Stehlik, Christian
9 ; APPLICANT: Damiano, Jason S.
10 ; APPLICANT: Lee, Sug-Hyung
11 ; APPLICANT: Oliveira, Vasco A.
12 ; APPLICANT: Hayashi, Hideki
13 ; APPLICANT: Pawlowski, Krzysztof
14 ; TITLE OF INVENTION: Novel Card Domain Containing
15 ; TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods of Use
16 ; FILE REFERENCE: P-IJ 4752
17 ; CURRENT APPLICATION NUMBER: US/09/864,921
18 ; CURRENT FILING DATE: 2001-05-23
19 ; PRIOR APPLICATION NUMBER: US 09/579,240
20 ; PRIOR FILING DATE: 2000-05-24
21 ; PRIOR APPLICATION NUMBER: US 09/686,347
22 ; PRIOR FILING DATE: 2000-10-10
23 ; PRIOR APPLICATION NUMBER: US 60/275,980
24 ; PRIOR FILING DATE: 2001-03-14
25 ; NUMBER OF SEQ ID NOS: 195
26 ; SOFTWARE: FastSeq for Windows Version 4.0
27 ; SEQ ID NO 100
28 ; LENGTH: 578
29 ; TYPE: DNA
30 ; ORGANISM: Homo sapien

```

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (277)...(552)
US-09-864-921-100

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### Alignment S

Pred. No.:	1,29e-51	length:	578
Score:	461.00	Matches:	88
Percent Similarity:	100.00%	Conservative:	0
Best local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	33	Gaps:	0

US-09-697-089-2\_COPY\_1\_88 (1-88) x US-09-864-921-100 (1-578)

QY 1 Metasnpheillelyspasnserrargalaleuileglnargmetglymethrvalile 20

Db 277 ATGAATTTCATAAAGGACATAGCCGAGCCCTTATTCAAGAATGGGAATGACTGTTATA 33

21 LysGlnIleThrAspPleuPheValTrrPasnValLeuAsnArgLugluValAsnIle 40

DB 33 / AAGCAATTCACAGATGACCTATTGTATGGAAATGTCAGAAATCCGAAAGTAGTAAACATC 330

41 Necyscyssoidus variuosinsepianianigoly lccicmshacccccccc

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PRODUCT

US-09-864-921-102  
Sequence 102 Amplification US/09864921

```

; GENERAL INFORMATION:
: APPLICANT: Reed, John C

```

APPLICANT: Godzik, Adam

APPLICANT: Damiano, Jason S.

APPLICANT: Oliveira, Vasco A.

APPLICANT: Pawlowski, Krzysztof

1. TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods of Use

; CURRENT APPLICATION NUMBER: US/09/864,921

PRIOR APPLICATION NUMBER: US 09/579,240

PRIOR APPLICATION NUMBER: US 09/686,347  
PRIORITY DATE: 2000-10-10

PRIOR APPLICATION NUMBER: US 60/275,980  
PRIOR FILING DATE: 2001-03-14

```

; NUMBER OF SEQ ID NOS: 195
SOFTWARE: FastSeq for Windows Version 4.0

```

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: : SEQ ID NO 102
: :
: : LENGTH: 768

```

ORGANISM: *Homo sapiens*

NAME/KEY: CDS

US-09-864-921-102

### Alignment Scores:

Score:	461.00	Matches:
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768  
88

Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
DB: 33  
Gaps: 0

US-09-697-089-2\_COPY\_1\_88 (1-88) x US-09-864-921-102 (1-768)

OY 1 MetasphelelyAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20  
DB 277 ATGAATTTTCATTAAGACAAATAGCCGAGCCCTTATTCAAGAGATGGATGACTCTTATA 336  
OY 21 LysGlnIleThrAspAspLeuPheValITrpAsnValIleAsnArgGluGluValAsnIle 40  
DB 337 AAGCAATACACAGATGACCTATTGTATGAGATGTTCGAATCGCGAAGATAACATC 396  
OY 41 IleCysCysGluLysValGluGlnAspAlaIleArgGlyIleIleHisMetIleLeuLys 60  
DB 397 ATTTGCTCGAGAAAGTGGAGAGATGCTGCTTAAGAGATCATTCACATGATTTTGA 456  
OY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluITrpAsnTyrProLeu 80  
DB 457 AAGGTTTCAGAGTCCCTGTAACTCTTTCTTAATCCCTTAAGAGATGGAATATCTCTTA 516  
OY 81 PheGlnAspLeuAsnGlyGlnSer 88  
DB 517 TTTCAGAGCTTGAATGACAAAGT 540

### RESULT 3

US-09-864-921-98  
Sequence 98, Application US/09864921  
GENERAL INFORMATION:

APPLICANT: Reed, John C.  
APPLICANT: Plo, Frederick F.  
APPLICANT: Godzik, Adam  
APPLICANT: Stehlik, Christian  
APPLICANT: Damiano, Jason S.  
APPLICANT: Lee, Sung-Hyung  
APPLICANT: Oliveira, Vasco A.  
APPLICANT: Pawlowski, Krzysztof  
TITLE OF INVENTION: Novel Card Domain Containing  
FILE REFERENCE: P-LJ 4752  
CURRENT FILING DATE: 2001-05-23  
CURRENT APPLICATION NUMBER: US/09/864,921  
PRIOR FILING DATE: 2000-05-24  
PRIOR APPLICATION NUMBER: US 09/686,347  
PRIOR FILING DATE: 2000-10-10  
PRIOR APPLICATION NUMBER: US 60/275,980  
NUMBER OF SEQ ID NOS: 195  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 98  
LENGTH: 1395  
TYPE: DNA  
ORGANISM: Homo sapien  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (277)...(1353)  
US-09-864-921-98

### Alignment Scores:

Pred. No.: 4,02e-51 Length: 1395  
Score: 461.00 Matches: 88  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 33 Gaps: 0

US-09-697-089-2\_COPY\_1\_88 (1-88) x US-09-864-921-98 (1-1395)

OY 1 MetasphelelyAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20

DB 277 ATGAATTTTCATTAAGACAAATAGCCGAGCCCTTATTCAAGAGATGGATGACTCTTATA 336  
OY 21 LysGlnIleThrAspAspLeuPheValITrpAsnValIleAsnArgGluGluValAsnIle 40  
DB 337 AAGCAATACACAGATGACCTATTGTATGAGATGTTCGAATCGCGAAGATAACATC 396  
OY 41 IleCysCysGluLysValGluGlnAspAlaIleArgGlyIleIleHisMetIleLeuLys 60  
DB 397 ATTTGCTCGAGAAAGTGGAGAGATGCTGCTTAAGAGATCATTCACATGATTTTGA 456  
OY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluITrpAsnTyrProLeu 80  
DB 457 AAGGTTTCAGAGTCCCTGTAACTCTTTCTTAATCCCTTAAGAGATGGAATATCTCTTA 516  
OY 81 PheGlnAspLeuAsnGlyGlnSer 88  
DB 517 TTTCAGAGCTTGAATGACAAAGT 540

### RESULT 4

PCT-US00-29643-3  
Sequence 3, Application PC/TUS0029643  
GENERAL INFORMATION:

APPLICANT: Millennium Pharmaceuticals, Inc.  
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
FILE REFERENCE: 0734-136W01  
CURRENT FILING DATE: 2000-10-26  
CURRENT APPLICATION NUMBER: PCT/US00/29643  
PRIOR FILING DATE: 1999-10-27  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 3072  
TYPE: DNA  
ORGANISM: Homo sapiens  
PCT-US00-29643-3

### Alignment Scores:

Pred. No.: 1.11e-50 Length: 3072  
Score: 461.00 Matches: 88  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 1 Gaps: 0

US-09-697-089-2\_COPY\_1\_88 (1-88) x PCT-US00-29643-3 (1-3072)

OY 1 MetasphelelyAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20  
DB 1 ATGAATTTTCATTAAGACAAATAGCCGAGCCCTTATTCAAGAGATGGATGACTCTTATA 60  
OY 21 LysGlnIleThrAspAspLeuPheValITrpAsnValIleAsnArgGluGluValAsnIle 40  
DB 61 AAGCAATACACAGATGACCTATTGTATGAGATGTTCGAATCGCGAAGATAACATC 120  
OY 41 IleCysCysGluLysValGluGlnAspAlaIleArgGlyIleIleHisMetIleLeuLys 60  
DB 121 ATTTGCTCGAGAAAGTGGAGAGATGCTGCTTAAGAGATCATTCACATGATTTTGA 180  
OY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluITrpAsnTyrProLeu 80  
DB 181 AAGGTTTCAGAGTCCCTGTAACTCTTTCTTAATCCCTTAAGAGATGGAATATCTCTTA 240  
OY 81 PheGlnAspLeuAsnGlyGlnSer 88  
DB 241 TTTCAGAGCTTGAATGACAAAGT 264

### RESULT 5

US-09-697-089-3  
Sequence 3, Application US/09697089  
GENERAL INFORMATION:

APPLICANT: Bertin, John  
APPLICANT: Robison, Keith E.  
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
FILE REFERENCE: 07334-136001  
CURRENT APPLICATION NUMBER: US/09/697,089  
CURRENT FILING DATE: 2000-10-26  
PRIOR APPLICATION NUMBER: US 60/161,822  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 3072  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-697-089-3

Alignment Scores:  
Pred. No.: 1,11e-50 Length: 3072  
Score: 461.00 Matches: 88  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 27 Gaps: 0

US-09-697-089-2\_COPY\_1\_88 (1-88) x US-09-697-089-3 (1-3072)

QY 1 Metasphelleyaspasnserrargalaleuileglnarqmetglmetthrvalille 20  
DB 1 ATGAATTTCAATAAGCAATAGCCGAGCCCTTTTCAAAATAGGGAATACGTATATA 60  
QY 21 Lysglnlethrpsaspplleuphewa1trpsanvalleuasnarglgluvalasnlle 40  
DB 61 AAGCAATACACAGATGACCTTTTGTATGAAATGTTCTGATCCGGAAGATTAACATC 120  
QY 41 IlecyScysglulysvalgluglnaspalaalargyllelleHsmetlleleulys 60  
DB 121 ATTGCTGCGAAGAGGTGACAGAGATGCTCTAGAGGATCATTCATGATTTTGAAA 180  
QY 61 LysglYsergluSerCysAsnleuphelauleysSerleuylsGIUTrpsanTyrProleu 80  
DB 181 AAGGTTTCAGAGTCTCTTAACCTTTCTTAAATCCCTTAAGAGTGAATATCCTCTA 240  
QY 81 PheglinspleuasnnglylnSer 88  
DB 241 TTTCAGACTTGAATGACAAAGT 264

RESULT 6  
US-09-841-739-3  
Sequence 3, Application US/09841739  
GENERAL INFORMATION:  
APPLICANT: Bertin, John  
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
FILE REFERENCE: 07334-1329001  
CURRENT APPLICATION NUMBER: US/09/841,739  
CURRENT FILING DATE: 2001-08-29  
PRIOR APPLICATION NUMBER: US 09/697,089  
PRIOR FILING DATE: 2000-10-26  
PRIOR APPLICATION NUMBER: US 60/161,822  
PRIOR FILING DATE: 1999-10-27  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 3072  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-841-739-3

Alignment Scores:  
Pred. No.: 1,11e-50 Length: 3072  
Score: 461.00 Matches: 88  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0  
DB: 32 Gaps: 0  
US-09-697-089-2\_COPY\_1\_88 (1-88) x US-09-841-739-3 (1-3072)

QY 1 Metasphelleyaspasnserrargalaleuileglnarqmetglmetthrvalille 20  
DB 1 ATGAATTTCAATAAGCAATAGCCGAGCCCTTTTCAAAATAGGGAATACGTATATA 60  
QY 21 Lysglnlethrpsaspplleuphewa1trpsanvalleuasnarglgluvalasnlle 40  
DB 61 AAGCAATACACAGATGACCTTTTGTATGAAATGTTCTGATCCGGAAGATTAACATC 120  
QY 41 IlecyScysglulysvalgluglnaspalaalargyllelleHsmetlleleulys 60  
DB 121 ATTGCTGCGAAGAGGTGACAGAGATGCTCTAGAGGATCATTCATGATTTTGAAA 180  
QY 61 LysglYsergluSerCysAsnleuphelauleysSerleuylsGIUTrpsanTyrProleu 80  
DB 181 AAGGTTTCAGAGTCTCTTAACCTTTCTTAAATCCCTTAAGAGTGAATATCCTCTA 240  
QY 81 PheglinspleuasnnglylnSer 88  
DB 241 TTTCAGACTTGAATGACAAAGT 264

RESULT 7  
US-10-156-733-1  
Sequence 1, Application US/10156733  
GENERAL INFORMATION:  
APPLICANT: Alnemri, Emdad S.  
TITLE OF INVENTION: IPAF, AN ICE-PROTEASE ACTIVATING  
FILE REFERENCE: 480140.477  
CURRENT APPLICATION NUMBER: US/10/156,733  
CURRENT FILING DATE: 2002-05-24  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 3075  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(3075)  
US-10-156-733-1

Alignment Scores:  
Pred. No.: 1,12e-50 Length: 3075  
Score: 461.00 Matches: 88  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 41 Gaps: 0

US-09-697-089-2\_COPY\_1\_88 (1-88) x US-10-156-733-1 (1-3075)  
QY 1 Metasphelleyaspasnserrargalaleuileglnarqmetglmetthrvalille 20  
DB 1 ATGAATTTCAATAAGCAATAGCCGAGCCCTTTTCAAAATAGGGAATACGTATATA 60  
QY 21 Lysglnlethrpsaspplleuphewa1trpsanvalleuasnarglgluvalasnlle 40  
DB 61 AAGCAATACACAGATGACCTTTTGTATGAAATGTTCTGATCCGGAAGATTAACATC 120  
QY 41 IlecyScysglulysvalgluglnaspalaalargyllelleHsmetlleleulys 60  
DB 121 ATTGCTGCGAAGAGGTGACAGAGATGCTCTAGAGGATCATTCATGATTTTGAAA 180  
QY 61 LysglYsergluSerCysAsnleuphelauleysSerleuylsGIUTrpsanTyrProleu 80  
DB 181 AAGGTTTCAGAGTCTCTTAACCTTTCTTAAATCCCTTAAGAGTGAATATCCTCTA 240  
QY 81 PheglinspleuasnnglylnSer 88

```
Db 241 TTTCAGAGCTGATGACAAAGT 264
|||||
PCT-US00-29643-1
; Sequence 1, Application PC/TUS0029643
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-136W01
; CURRENT APPLICATION NUMBER: PCT/US00/29643
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3133
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (36)...(3107)
PCT-US00-29643-1

Alignment Scores:
Pred. No.: 1.14e-50 Length: 3133
Score: 461.00 Matches: 88
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-697-089-2_COPY_1_88 (1-88) x PCT-US00-29643-1 (1-3133)
Qy 1 Metasphelilelyspasnserrgalauleuileglnargmetglymethrvallie 20
|||||
Db 36 ATGAATTTTCATTAAGGACAAATAGCCGAGCCCTTATTCAAAGATGGATGACTGTATTA 95
|||||
Qy 21 Lysglnilerhraspaspleuphevaltrpasnvalleuasnaragluciluvalasnile 40
|||||
Db 96 AAGCAATACACAGATGACCTATTGTATGAGATGTTCTGAATCGCGAAGAATAACATC 155
|||||
Qy 41 IleCysCysglulysvalgluinspalaalaarglylleihismetlleuleuls 60
|||||
Db 156 ATTTCCTCGAGAAAGCTGAGCAGATCTCTAGAGGATCATTCACATGATTTTGAAA 215
|||||
Qy 61 Lysglsersglusercysasnleupheuleuysserleuylsglutrpasntyrproleu 80
|||||
Db 216 AAGGTTAGAGTCTCTGTACCTCTTTCTTAATCCCTTAAGAGTGGACTATCTCTTA 275
|||||
Qy 81 Pheglnaspleuasnglylnser 88
|||||
Db 276 TTTCAGAGCTGATGACAAAGT 299
|||||

RESULT 9
US-09-697-089-1
; Sequence 1, Application US/09697089
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-136001
; CURRENT APPLICATION NUMBER: US/09/697,089
; CURRENT FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3133
```

```
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (36)...(3107)
US-09-697-089-1

Alignment Scores:
Pred. No.: 1.14e-50 Length: 3133
Score: 461.00 Matches: 88
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 27 Gaps: 0

US-09-697-089-2_COPY_1_88 (1-88) x US-09-697-089-1 (1-3133)
Qy 1 Metasphelilelyspasnserrgalauleuileglnargmetglymethrvallie 20
|||||
Db 36 ATGAATTTTCATTAAGGACAAATAGCCGAGCCCTTATTCAAAGATGGATGACTGTATTA 95
|||||
Qy 21 Lysglnilerhraspaspleuphevaltrpasnvalleuasnaragluciluvalasnile 40
|||||
Db 96 AAGCAATACACAGATGACCTATTGTATGAGATGTTCTGAATCGCGAAGAATAACATC 155
|||||
Qy 41 IleCysCysglulysvalgluinspalaalaarglylleihismetlleuleuls 60
|||||
Db 156 ATTTCCTCGAGAAAGCTGAGCAGATCTCTAGAGGATCATTCACATGATTTTGAAA 215
|||||
Qy 61 Lysglsersglusercysasnleupheuleuysserleuylsglutrpasntyrproleu 80
|||||
Db 216 AAGGTTAGAGTCTCTGTACCTCTTTCTTAATCCCTTAAGAGTGGACTATCTCTTA 275
|||||
Qy 81 Pheglnaspleuasnglylnser 88
|||||
Db 276 TTTCAGAGCTGATGACAAAGT 299
|||||

RESULT 10
US-09-841-739-1
; Sequence 1, Application US/09841739
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-322001
; CURRENT APPLICATION NUMBER: US/09/841,739
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3133
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (36)...(3107)
US-09-841-739-1

Alignment Scores:
Pred. No.: 1.14e-50 Length: 3133
Score: 461.00 Matches: 88
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 32 Gaps: 0

US-09-697-089-2_COPY_1_88 (1-88) x US-09-841-739-1 (1-3133)
Qy 1 Metasphelilelyspasnserrgalauleuileglnargmetglymethrvallie 20
|||||
```



```
Db 36 ATGAATTCATTAAGACATAGCCGACCCCTTATTCATAAGATGGAGTACTGTTATA 95
Qy 21 LysGlnIleThrAspAspLeuPheValTrpAsnValIleAsnArgGluValAsnIle 40
Db 96 AAGCAAAATCAGATGACCTTATTTGTATGATGTCGAAATCGGAGAAAGTAAACATC 155
Qy 41 IleCysCysGluValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
Db 156 ATTGCTGCGAGAGGTGAGCAGAGATGCTGTAGAGGATCATTCACATGATTTTGAAA 215
Qy 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerIleLysGluTrpAsnTyrProleu 80
Db 216 AAGGTTTACAGAGTCTGTACCTCTTTCTTAATCCCTTAAGAGTGGAGTACTCTCTA 275
Qy 81 PheGlnAspLeuAsnGlyGlnSer 88
Db 276 TTTCAGGACTTGATGACAAAGT 299

RESULT 11
US-10-156-733-14
; Sequence 14, Application US/10156733
; GENERAL INFORMATION:
; APPLICANT: Alnemrl, Emad S.
; TITLE OF INVENTION: IPAF, AN ICE-PROTEASE ACTIVATING
; FILE REFERENCE: 480140.477
; CURRENT APPLICATION NUMBER: US/10/156,733
; CURRENT FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 3219
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-156-733-14

Alignment Scores:
Pred. No.: 1,18e-50 Length: 3219
Score: 461.00 Matches: 88
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 41 Gaps: 0

US-09-697-089-2_COPY_1_88 (1-88) x US-10-156-733-14 (1-3219)
Qy 1 MetAsnPhelIeLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20
Db 145 ATGAATTTTCATTAAGACAAATAGCCGACCCCTTATTCATAAGATGGAGTACTGTTATA 204
Qy 21 LysGlnIleThrAspAspLeuPheValTrpAsnValIleAsnArgGluValAsnIle 40
Db 205 AAGCAAAATCAGATGACCTTATTTGTATGATGTCGAAATCGGAGAAAGTAAACATC 264
Qy 41 IleCysCysGluValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
Db 265 ATTGCTGCGAGAGGTGAGCAGAGATGCTGTAGAGGATCATTCACATGATTTTGAAA 324
Qy 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerIleLysGluTrpAsnTyrProleu 80
Db 325 AAGGTTTACAGAGTCTGTACCTCTTTCTTAATCCCTTAAGAGTGGAGTACTCTCTA 384
Qy 81 PheGlnAspLeuAsnGlyGlnSer 88
Db 385 TTTCAGGACTTGATGACAAAGT 408

RESULT 12
US-09-864-921-96
; Sequence 96, Application US/09864921
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Pio, Frederick F.
; APPLICANT: Godzik, Adam
```

```
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sung-Hyun
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: Novel Card Domain Containing
; FILE REFERENCE: P-1J 4752
; CURRENT APPLICATION NUMBER: US/09/864,921
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 3396
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (277)...(3348)
US-09-864-921-96

Alignment Scores:
Pred. No.: 1,27e-50 Length: 3396
Score: 461.00 Matches: 88
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 33 Gaps: 0

US-09-697-089-2_COPY_1_88 (1-88) x US-09-864-921-96 (1-3396)
Qy 1 MetAsnPhelIeLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20
Db 277 ATGAATTTTCATTAAGACAAATAGCCGACCCCTTATTCATAAGATGGAGTACTGTTATA 336
Qy 21 LysGlnIleThrAspAspLeuPheValTrpAsnValIleAsnArgGluValAsnIle 40
Db 337 AAGCAAAATCAGATGACCTTATTTGTATGATGTCGAAATCGGAGAAAGTAAACATC 396
Qy 41 IleCysCysGluValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLys 60
Db 397 ATTGCTGCGAGAGGTGAGCAGAGATGCTGTAGAGGATCATTCACATGATTTTGAAA 456
Qy 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerIleLysGluTrpAsnTyrProleu 80
Db 457 AAGGTTTACAGAGTCTGTACCTCTTTCTTAATCCCTTAAGAGTGGAGTACTCTCTA 516
Qy 81 PheGlnAspLeuAsnGlyGlnSer 88
Db 517 TTTCAGGACTTGATGACAAAGT 540

RESULT 13
US-09-491-404-1319
; Sequence 1319, Application US/09491404
; GENERAL INFORMATION:
; APPLICANT: Tang, Yuanhua T.
; APPLICANT: Tillinghast, John
; APPLICANT: Slinku, Ankura
; APPLICANT: Liu, Chenghua
; APPLICANT: Dirmanc, Radoje T.
; TITLE OF INVENTION: Novel Contigs Obtained
; FILE REFERENCE: 785
; CURRENT APPLICATION NUMBER: US/09/491,404
; CURRENT FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 3796
```

```
SOFTWARE: PL_SP_genes Version 1.0
; SEQ ID NO 1319
; LENGTH: 3545
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (781)...(916)
; OTHER INFORMATION: this location contains the signal peptide sequence,
; OTHER INFORMATION: MLMGSGKALTKRFVFFRLRSRAOGGLFTLCDLIDIPETIR, Run with SignalP
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (679)...(3279)
; OTHER INFORMATION: similar to g13688110 in the genepept database release 114,
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
US-09-491-404-1319

Alignment Scores:
Pred. No.: 1.34e-50 Length: 3545
Score: 461.00 Matches: 88
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-09-697-089-2_COPY_1_88 (1-88) x US-09-491-404-1319 (1-3545)

OY 1 MetAspHeIleLySAsPAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20
DB 232 ATGATTTTCATTAAGACAAATAGCCGACCTTATTCAAGAAATGGAGATGACTGTTATA 291
OY 21 LysGlnIleThrAspAspLeuPheValITrpAsnValIleuAsnArgGluGluValAsnIle 40
DB 292 AAGCAATACACAGATGACCTATTGTATGAGATGTTCTGAATCCGGAAGAACTAACATC 351
OY 41 IleCysGlyIuLySValGluGlnAspAlaIaArgGlyIleIleHisMetIleuLyS 60
DB 352 ATTGCTCGAAGAGATGAGATGCTGCTAGAGGATCATTCACATGATTTTGA 411
OY 61 LysGlySerGluSerCysAsnLeuPheuLySserLeuLySGluTrpAsnTyrProLeu 80
DB 412 AAGGTTTCAGAGTCTCTGTAACCTCTTCTTAATCCCTTAAGAGATGGAATATCTCTA 471
OY 81 PheGlnAspLeuAsnGlyGlnSer 88
DB 472 TTTCAGGACTTGATGACAAAGT 495

RESULT 14
US-09-922-279-1319
; Sequence 1319, Application US/09922279
; GENERAL INFORMATION:
; APPLICANT: Tang, Yuanhua T.
; APPLICANT: Tillinghast, John
; APPLICANT: Sinku, Ankura
; APPLICANT: Liu, Chenghua
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Contigs Obtained
; TITLE OF INVENTION: From Various Libraries
; FILE REFERENCE: 785
; CURRENT APPLICATION NUMBER: US/09/922.279
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 3796
; SOFTWARE: PL_SP_genes Version 1.0
; SEQ ID NO 1319
; LENGTH: 3545
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (781)...(916)
; OTHER INFORMATION: this location contains the signal peptide sequence,
```

```
OTHER INFORMATION: MLMGSGKALTKRFVFFRLRSRAOGGLFTLCDLIDIPETIR, Run with SignalP
; NAME/KEY: misc_feature
; LOCATION: (679)...(3279)
; OTHER INFORMATION: similar to g13688110 in the genepept database release 114,
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
US-09-922-279-1319

Alignment Scores:
Pred. No.: 1.34e-50 Length: 3545
Score: 461.00 Matches: 88
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 34 Gaps: 0

US-09-697-089-2_COPY_1_88 (1-88) x US-09-922-279-1319 (1-3545)

OY 1 MetAspHeIleLySAsPAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20
DB 232 ATGATTTTCATTAAGACAAATAGCCGACCTTATTCAAGAAATGGAGATGACTGTTATA 291
OY 21 LysGlnIleThrAspAspLeuPheValITrpAsnValIleuAsnArgGluGluValAsnIle 40
DB 292 AAGCAATACACAGATGACCTATTGTATGAGATGTTCTGAATCCGGAAGAACTAACATC 351
OY 41 IleCysGlyIuLySValGluGlnAspAlaIaArgGlyIleIleHisMetIleuLyS 60
DB 352 ATTGCTCGAAGAGATGAGATGCTGCTAGAGGATCATTCACATGATTTTGA 411
OY 61 LysGlySerGluSerCysAsnLeuPheuLySserLeuLySGluTrpAsnTyrProLeu 80
DB 412 AAGGTTTCAGAGTCTCTGTAACCTCTTCTTAATCCCTTAAGAGATGGAATATCTCTA 471
OY 81 PheGlnAspLeuAsnGlyGlnSer 88
DB 472 TTTCAGGACTTGATGACAAAGT 495

RESULT 15
US-09-922-279A-1319
; Sequence 1319, Application US/09922279A
; GENERAL INFORMATION:
; APPLICANT: Tang, Yuanhua T.
; APPLICANT: Tillinghast, John
; APPLICANT: Sinku, Ankura
; APPLICANT: Liu, Chenghua
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Contigs Obtained
; TITLE OF INVENTION: From Various Libraries
; FILE REFERENCE: 785
; CURRENT APPLICATION NUMBER: US/09/922.279A
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; NUMBER OF SEQ ID NOS: 3796
; SOFTWARE: PL_SP_genes Version 1.0
; SEQ ID NO 1319
; LENGTH: 3545
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (781)...(916)
; OTHER INFORMATION: this location contains the signal peptide sequence,
; OTHER INFORMATION: MLMGSGKALTKRFVFFRLRSRAOGGLFTLCDLIDIPETIR, Run with SignalP
; OTHER INFORMATION: similar to g13688110 in the genepept database release 114,
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
US-09-922-279A-1319

Alignment Scores:
Pred. No.: 1.34e-50 Length: 3545
Score: 461.00 Matches: 88
```

Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
DB: 34

Conservative: 0  
Mismatches: 0  
Indels: 0  
Gaps: 0

US-09-697-089-2\_COPY\_1\_88 (1-88) x US-09-922-279A-1319 (1-3545)

QY 1 MetAspPheIleLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMetThrValIle 20  
|||||  
DB 232 ATGAATTTCATAAAGCAATAGCCGAGCCCTTATTCAAAGATGGGATGACTGTATA 291  
QY 21 LysGlnIleThrAspAspLeuPheValITrpAsnValLeuAsnArgGluGluValAsnIle 40  
|||||  
DB 292 AAGCAAAATCACAGATGACCTATTGTATGGAATGTCTGAATCCGAAAGATAACATC 351  
QY 41 IleCysCysGluLysValGluGlnAspAlaIleArgGlyIleIleHisMetIleLeuLys 60  
|||||  
DB 352 ATTTGCTGCGAAGAGGTGAGCAGATGCTGTAGAGGATCATTCACATGATTTTGAA 411  
QY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluITrpAsnTyrProLeu 80  
|||||  
DB 412 AAGGCTTCAGAGTCTCTTAACCTTCTTAATCCCTTAAGAGATGGAATATCTCTTA 471  
QY 81 PheGlnAspLeuAsnGlyGlnSer 88  
|||||  
DB 472 TTTCAGGACTTGATGACAAAGT 495

Search completed: January 31, 2003, 17:55:28  
Job time : 1122.24 secs

GenCore version 5.1.3  
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## OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 31, 2003, 13:24:32 ; Search time 82.778 Seconds

(without alignments)  
1295.994 Million cell updates/sec

Title: US-09-697-089-2\_COPY\_1\_88

Perfect score: 461

Sequence: 1 MFNFKDSRALIQHMGMTVL.....FLKSLKEMWYPLFODLNGQS 88

## Scoring table:

BIOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 2500250 seqs, 609544256 residues

Total number of hits satisfying chosen parameters: 5000500

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Command line parameters:

-MODEL=frame+P2n.model -DEV=xlh  
-O/cgcn2\_1/USPFO.spool/US050967089/runat\_29012003\_092755\_19775/app.query.fasta.1.981  
-DB=Pending\_Patents\_NA\_New -QFMT=fastap -SUFFIX=P2n.rnpd -MINMATCH=0.1  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=Dlosum62  
-TRANS-human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTPMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US09697089.eccn\_1\_1\_91\_etrunat\_29012003\_092755\_19775  
-NCPU=6 -ICPU=3 -NO\_XLPMX -NO\_MAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -LONELIOP  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

## Database :

1: Pending\_Patents\_NA\_New.\*  
2: /cgcn2\_6/ptodata/2/pna/PCT\_NEW\_COMB.seq.\*  
3: /cgcn2\_6/ptodata/2/pna/US06\_NEW\_COMB.seq.\*  
4: /cgcn2\_6/ptodata/2/pna/US07\_NEW\_COMB.seq.\*  
5: /cgcn2\_6/ptodata/2/pna/US08\_NEW\_COMB.seq.\*  
6: /cgcn2\_6/ptodata/2/pna/US09\_NEW\_COMB.seq.\*  
7: /cgcn2\_6/ptodata/2/pna/US60\_NEW\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Length	ID	Description
1	461	100.0	3075	1 PCT-US02-21946A-1
2	461	100.0	3219	1 PCT-US02-21946A-14
3	461	100.0	3545	6 US-10-276-781-111
4	108	23.4	1435	6 US-10-323-643-1
5	103.5	22.5	429	6 US-10-276-774-1303
6	97	21.0	5059	1 PCT-US02-04915-82
7	96.5	20.9	549	6 US-10-311-035-36
8	93	20.2	542	5 US-09-724-676-11471
9	93	20.2	542	5 US-09-724-676-11471
10	91.5	19.8	358	5 US-09-724-676-11469
11	91.5	19.8	358	5 US-09-724-676-11469

12	91.5	19.8	362	5	US-09-513-999C-1335	Sequence 1335, Ap
13	91.5	19.8	479	5	US-09-724-676-11470	Sequence 11470, A
14	91.5	19.8	479	5	US-09-724-676A-11470	Sequence 11470, A
15	86	18.7	2563	6	US-10-305-720-1076	Sequence 1076, Ap
16	86	18.7	2916	6	US-09-814-915A-31	Sequence 31, Appl
17	86	18.7	2916	6	US-10-240-425-1436	Sequence 1436, Ap
18	86	18.7	3076	6	US-09-814-915A-11	Sequence 11, Appl
19	75.5	16.4	8201	6	US-10-240-452-27	Sequence 27, Appl
20	75.5	16.4	8201	6	US-10-311-455-29	Sequence 29, App
21	75	16.3	1400	1	PCT-US02-38606-96	Sequence 96, Appl
22	75	16.3	1400	6	US-10-295-981-40	Sequence 40, Appl
23	75	16.3	2859	6	US-10-295-981-9	Sequence 9, Appl1
24	75	16.3	3382	6	US-10-295-981-7	Sequence 7, Appl1
25	75	16.3	4302	1	PCT-US02-38606-95	Sequence 95, Appl
26	75	16.3	4302	6	US-10-295-981-38	Sequence 38, Appl
27	75	16.3	4344	5	US-09-724-676-6860	Sequence 6860, Ap
28	75	16.3	4344	5	US-09-724-676A-6860	Sequence 6860, Ap
29	75	16.3	4373	5	US-09-724-676-6859	Sequence 6859, Ap
30	75	16.3	4373	5	US-09-724-676A-6859	Sequence 6859, Ap
31	75	16.3	4384	5	US-09-949-002-238	Sequence 238, App
32	75	16.3	4390	5	PCT-US02-38606-3	Sequence 3, Appl1
33	75	16.3	4390	5	US-09-949-002-101	Sequence 101, App
34	75	16.3	4570	5	US-09-598-075-169	Sequence 169, App
35	75	16.3	4610	1	PCT-US02-38606-11	Sequence 11, Appl
36	69.5	15.1	1320	6	US-10-123-529-3	Sequence 3, Appl1
37	69.5	15.1	1320	6	US-10-123-529-5	Sequence 5, Appl1
38	69.5	15.1	75033	6	US-10-319-915-18	Sequence 18, Appl
39	69	15.0	4141	6	US-10-295-981-42	Sequence 42, Appl
40	66	14.3	276	5	US-09-531-113-14339	Sequence 14339, A
41	66	14.3	585	5	US-09-531-113-4197	Sequence 4197, Ap
42	65.5	14.2	1209	6	US-10-203-138A-2564	Sequence 2564, Ap
43	65.5	14.2	1209	6	US-10-152-319A-1537	Sequence 1537, Ap
44	65	14.1	1470	6	US-10-295-981-27	Sequence 27, Appl
45	65	14.1	3080	1	PCT-US02-38606-94	Sequence 94, Appl

## ALIGNMENTS

RESULT 1  
PCT-US02-21946A-1  
; Sequence 1, Application PC/TUS0221946A  
; GENERAL INFORMATION:  
; APPLICANT: Thomas Jefferson University  
; APPLICANT: Alnemir, Emdad S.  
; TITLE OF INVENTION: IRAF, AN ICE-PROTEASE ACTIVATING  
; FILE OF INVENTION: FACTOR  
; FILE REFERENCE: 480140.477PC  
; CURRENT APPLICATION NUMBER: PCT/US02/21946A  
; CURRENT FILING DATE: 2002-05-24  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 3075  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(3075)  
PCT-US02-21946A-1

## Alignment Scores:

Pred. No.:	3.72e-54	Length:	3075
Score:	461.00	Matches:	88
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	1	Gaps:	0

US-09-697-089-2\_COPY\_1\_88 (1-88) x PCT-US02-21946A-1 (1-3075)

QY 1 MetaspherielyAspansSerajalaleuileginargmetc1yMetThyValite 20  
|||||  
DB 1 ATGATTTTCATTAAGACATATGCGAGCCCTTATTTCAGAGATGGAATGACTTTATA 60

Oy	21	LysGlnIleTrrAspAspLeuPheValTrrPsnValIleuAsnArgGluGluValAsnIle	40
Db	61	AAGCAAAACACAGATGACCTATTGTATGGAATGTTCTTGATTCGCCGAAGAACTAAACATC	120
Oy	41	IleCysCysGluIysValGluGlnAspAlaIleArgGlyIleIleHisMetIleLeuIys	60
Db	121	ATTTCCTCCGAGAAAGGTGGACAGAGATGCTGTGAGAGGATCATTCATCATGATTTTGAAA	180
Oy	61	LysGlySerGluSerCysAsnLeuPheLeuIysSerLeuIysGluTrrPsnTyrProIeu	80
Db	181	AAGGTTTCAGAGTCCCTGTAACTCTTCTTAAATCCCTTAAGAGAGTGAACATATCCTCTA	240
Oy	81	PheGlnAspLeuAsnGlyGlnSer	88
Db	241	TTTCAGACCTGGAATGGACAAGT	264
RESULT 2			
PCT-US02-21946A-14			
; Sequence 14, Application PC/TUS0221946A			
; GENERAL INFORMATION:			
; APPLICANT: Thomas Jefferson University			
; APPLICANT: Alnemrl, Emad S.			
; TITLE OF INVENTION: IPAF, AN ICE-PROTEASE ACTIVATING			
; TITLE OF INVENTION: FACTOR			
; FILE REFERENCE: 480140.477PC			
; CURRENT APPLICATION NUMBER: PCT/US02/21946A			
; CURRENT FILING DATE: 2002-05-24			
; NUMBER OF SEQ ID NOS: 14			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 14			
; LENGTH: 3219			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
PCT-US02-21946A-14			
Alignment Scores:			
Pred. NO.:			
Score: 3,95e-54			
Percent Similarity: 461.00			
Best Local Similarity: 100.00%			
Query Match: 100.00%			
DB: 1			
Gaps: 0			
US-09-697-089-2_COPY_1_88 (1-88) x PCT-US02-21946A-14 (1-3219)			
Oy	1	MetsnPhelIeliYsAspAsnSerArAlaIleuIleGlnArgMetGlyMetThrValIle	20
Db	145	ATGATTTTCATTAAGGAAATTAAGCCGAGCCCTTATTCAGAAAGGGAATGACGTATATA	204
Oy	21	LysGlnIleTrrAspAspLeuPheValTrrPsnValIleuAsnArgGluGluValAsnIle	40
Db	205	AAGCAAAACACAGATGACCTATTGTATGGAATGTTCTTGATTCGCCGAAGAACTAAACATC	264
Oy	41	IleCysCysGluIysValGluGlnAspAlaIleArgGlyIleIleHisMetIleLeuIys	60
Db	265	ATTTCCTCCGAGAAAGGTGGACAGAGATGCTGTGAGAGGATCATTCATCATGATTTTGAAA	324
Oy	61	LysGlySerGluSerCysAsnLeuPheLeuIysSerLeuIysGluTrrPsnTyrProIeu	80
Db	325	AAGGTTTCAGAGTCCCTGTAACTCTTCTTAAATCCCTTAAGAGAGTGAACATATCCTCTA	384
Oy	81	PheGlnAspLeuAsnGlyGlnSer	88
Db	385	TTTCAGACCTGGAATGGACAAGT	408
RESULT 3			
US-10-276-781-111			
; Sequence 111, Application US/10276781			
; GENERAL INFORMATION:			
; APPLICANT: Hyseq, Inc.			
; APPLICANT: Tang et al.			
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides			

```

; FILE REFERENCE: 21272-018 (785 contig)
; CURRENT APPLICATION NUMBER: US/10/276,781
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; NUMBER OF SEQ ID NOS: 2018
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 111
; LENGTH: 3545
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-276-781-111

Alignment Scores:
Pred. No.: 4,47e-54 Length: 3545
Score: 461.00 Matches: 88
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-697-089-2_COPY_1_88 (1-88) x US-10-276-781-111 (1-3545)
QY 1 MetanpheielluYAspAsnserARgAlaleuileglnaYmetgYmethYvaliile 20
Db 232 AAGAAATTCATTAAGGAACAATAGCCGAGCCCTTATTCAAAGAAAGGGAATGACTGTATA 299
QY 21 LysGlniIeThrAspAspLeuPheValTrpAsnValIeuAsnArGluGluValAsnIle 40
Db 292 AAGCAAAATCACAGATGACCTTTTGTATGAAATGTCTGAAATCGCAAGAAAGTAAACATC 355
QY 41 IleCyScyGluLysValGluGlnAspAlaIaArGlyIleIleHsMetIleuLys 60
Db 352 ATTTCTCGCGAAGAGGTGAGCAGAGATCTGCTAGAGGAAATCAATCATATTTGAAA 411
QY 61 LysGlySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTrpProLeu 80
Db 412 AAGGGTTAGAGTCTCTGTAACCTCTTTCTTAAATCCCTTAAGAGGTGAACTATCTCTTA 471
QY 81 PheGlnAspLeuAsnGlyGlnSer 88
Db 472 TTTCAGGACTTGAATGACAAAGT 495

RESULT 4
US-10-323-643-1
; Sequence 1, Application US/10323643
; GENERAL INFORMATION:
; APPLICANT: He, et al.
; TITLE OF INVENTION: Human Inhibitor of Apoptosis Gene 1
; FILE REFERENCE: PFI65P1D1
; CURRENT APPLICATION NUMBER: US/10/323,643
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 08/464,588
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: PCT/US95/05922
; PRIOR FILING DATE: 1995-05-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1435
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (10)..(1326)
; OTHER INFORMATION:
US-10-323-643-1

Alignment Scores:
Pred. No.: 4.19e-05 Length: 1435
Score: 108.00 Matches: 29
Percent Similarity: 58.33% Conservative: 20
Best Local Similarity: 34.52% Mismatches: 33

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Query Match: 23.43% Indels: 2
DB: 6 Gaps: 1
US-09-697-089-2_COPY_1_88 (1-88) x US-10-323-643-1 (1-1435)
QY 1 Metanphelelyaspasnserrgalaaleuileglnargmetglymethrvalille 20
DB 841 TTGTCATTAATTCGGAAGACAGATGCGCTCTCTTCAACA-----TTGACATGTGTG 894
QY 21 Lysglnilethrpsaspheleuvalitrrpsavalleuasnauglgluvalasnille 40
DB 895 CTCTCATCCGATTAACCTTTTAAAGCCCACTTAATTAATAACAGACACATGATAT 954
QY 41 Illecysgylulysvalgluglnaspalaalaargglyllelelshmetlleuys 60
DB 955 ATTAACAAAACACACACATACCTTTACACGAGAGACATGATGATPACCATTTTGGTT 1014
QY 61 Lysglserglusercysasnleupheleuylsserleuylsglutrpsantyrproleu 80
DB 1015 AAAGAAATGCTGGGCGCAACATCTTCAAAAACGTCTAATAAGAAATGACTCTACATTG 1074
QY 81 Pheglinspleu 84
DB 1075 TATAAGAACTTA 1086

RESULT 5
US-10-276-774-1303
; Sequence 1303, Application US/10276774
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; PRIOR FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 1303
; LENGTH: 429
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-276-774-1303

Alignment Scores:
Pred. No.: 3,78e-05 Length: 429
Score: 103.50 Matches: 21
Percent Similarity: 59.02% Conservative: 15
Best Local Similarity: 34.43% Mismatches: 24
Query Match: 22.45% Indels: 1
Gaps: 1

US-09-697-089-2_COPY_1_88 (1-88) x US-10-276-774-1303 (1-429)
QY 9 Argalaleuileglnargmetglymethrvalillelsglnilethrpsaspheleu 28
DB 230 CGGCTGCTTATCAATTCATTTGGTGAAGGTACAATAATGCTTACTGATGATTAATG 289
QY 29 Valtrpsavalleuasnauglgluvalasnillelellecysgylulysvalglu 48
DB 290 GAGACAAATGCTGAGCCAGAACACAGACATAGTAATAATGGAATAATGACACTT 349
QY 49 ---Aspalaalaargglyllelelshmetlleuylsglserglusercysasn 67
DB 350 ATCATTAAGGCCGAGATTTGCTGACTCGTTATTCGAAAGGGGCGAGGCGCATGTAA 409
QY 68 Leu 68
DB 410 ATT 412
```

```
RESULT 6
PCT-US02-04915-82
; Sequence 82, Application PC/TUS0204915
; GENERAL INFORMATION:
; APPLICANT: Murray, Richard
; APPLICANT: Glynn, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Aziz, Natasha
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and
; FILE REFERENCE: 018501-006200PC
; CURRENT APPLICATION NUMBER: PCT/US02/04915
; CURRENT FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 09/784,356
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/791,390
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: US 60/285,475
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/310,025
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/334,244
; PRIOR FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 230
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
; LENGTH: 5059
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-04915-82

Alignment Scores:
Pred. No.: 0.00738 Length: 5059
Score: 97.00 Matches: 24
Percent Similarity: 52.05% Conservative: 14
Best Local Similarity: 32.88% Mismatches: 33
Query Match: 21.04% Indels: 2
Gaps: 1

US-09-697-089-2_COPY_1_88 (1-88) x PCT-US02-04915-82 (1-5059)
QY 3 Pheillelyaspasnserrgalaaleuileglnargmetglymethrvalillelsgln 22
DB 1352 TTTGTGAAGAGAAACCACTCCAAAGCCAGATGGG-----GACCTGAAGAGG 1405
QY 23 Ilettrpsaspheleuvalitrrpsavalleuasnauglgluvalasnillelel 42
DB 1406 GTGCTGATGATCTCCAGACATGAGGTCTTACTGAGATGAGAGAGAGCTGTGGAG 1465
QY 43 Cysglulysvalgluglnaspalaalaargglyllelelshmetlleuylsgly 62
DB 1466 CAGGAAAAGACGCGCAGACAGAAATGAGCGCTTGTGAGCATGTGGAAGAAAGGG 1525
QY 63 Serglusercysasnleupheleuylsserleuylsglu 75
DB 1526 GACCTGGCCCTGGAGCTGCTCTTCAAGAACATTAAGTAA 1564

RESULT 7
US-10-311-035-36
; Sequence 36, Application US/10311035
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: YUE, Henry
; APPLICANT: ELLIOTT, Vicki
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: LAI, Preeti
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: DELEGEANE, Angelo M.
; APPLICANT: BAUGHN, Mariah R.
```



```
Oy 4 IlelysaPasnSerArgAlaLeuIleGlnArgMetGlyMetThrValIleLysGlnIle 23
Db 63 CTGAAGGAGAAAGAAACCTGTTTATCCATTCATGGGTGAAGGACATATAATGCGCTTA 122
Oy 24 ThrAspAspLeuPheValITrPAsnValLeuAsnArgGluGluValAsnIleIleCysCys 43
Db 123 CTGATGTAATTAATTAACACAAAGGGTCTGAACCAAGAAAGAGATG----- 167
Oy 44 GluLysValGluGln-----AspAlaIleArgGlyIleIleHisMet 57
Db 168 GAGAAAGTAAACGTAAGAAATGCTACAGTATGATTAAGACCCGAGCTTGTGATGACTCC 227
Oy 58 IleLeuLysGlySerGlySerGlySerCysAsnLeuPheLeuLysSerLeuLysGlu----- 75
Db 228 GTTATTCGAAAGGGGACACAGGATGCCAAATTGCAATCACAATTTGCAAGAACAGAC 287
Oy 76 -----TrpAsnTyrProLeu 80
Db 288 AGTTACCTGGCAGGACCGCTGGACTCTCAGCAGATCAACATCTGGAATTAACCTTAAT 347
Oy 81 PheGlnAspLeuAsnGly 86
Db 348 ATGCAAGACTCTCAAGGA 365

RESULT 10
US-09-724-676-11469
; Sequence 11469, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724.676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11469
; LENGTH: 358
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: n is a,c,g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (324)..(324)
; OTHER INFORMATION: n is a,c,g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (333)..(333)
; OTHER INFORMATION: n is a,c,g, or t
US-09-724-676-11469

Alignment Scores:
Pred. No.: 0.00144 Length: 358
Score: 91.50 Matches: 22
Percent Similarity: 51.28% Conserved: 18
Best Local Similarity: 28.21% Mismatches: 27
Query Match: 19.85% Indels: 11
Gaps: 2

US-09-697-089-2_COPY_1_88 (1-88) x US-09-724-676-11469 (1-358)
Oy 4 IlelysaPasnSerArgAlaLeuIleGlnArgMetGlyMetThrValIleLysGlnIle 23
Db 63 CTGAAGGAGAAAGAAACCTGTTTATCCATTCATGGGTGAAGGACATATAATGCGCTTA 122
Oy 24 ThrAspAspLeuPheValITrPAsnValLeuAsnArgGluGluValAsnIleIleCysCys 43
Db 123 CTGATGTAATTAATTAACACAAAGGGTCTGAACCAAGAAAGAGATG----- 167
Oy 44 GluLysValGluGln-----AspAlaIleArgGlyIleIleHisMet 57
Db 168 GAGAAAGTAAACGTAAGAAATGCTACAGTATGATTAAGACCCGAGCTTGTGATGACTCC 227
Oy 58 IleLeuLysGlySerGlySerGlySerCysAsnLeuPheLeuLysSerLeuLysGlu----- 75
Db 228 GTTATTCGAAAGGGGACACAGGATGCCAAATTGCAATCACAATTTGCAAGAACAGAC 287
Oy 76 -----TrpAsnTyrProLeu 80
Db 288 AGTTACCTGGCAGGACCGCTGGACTCTCAGCAGATCAACATCTGGAATTAACCTTAAT 347
Oy 81 PheGlnAspLeuAsnGly 86
Db 348 ATGCAAGACTCTCAAGGA 365

RESULT 10
US-09-724-676-11469
; Sequence 11469, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724.676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11469
; LENGTH: 358
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: n is a,c,g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (324)..(324)
; OTHER INFORMATION: n is a,c,g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (333)..(333)
; OTHER INFORMATION: n is a,c,g, or t
US-09-724-676-11469

Alignment Scores:
Pred. No.: 0.00144 Length: 358
Score: 91.50 Matches: 22
Percent Similarity: 51.28% Conserved: 18
Best Local Similarity: 28.21% Mismatches: 27
Query Match: 19.85% Indels: 11
Gaps: 2

US-09-697-089-2_COPY_1_88 (1-88) x US-09-724-676-11469 (1-358)
Oy 4 IlelysaPasnSerArgAlaLeuIleGlnArgMetGlyMetThrValIleLysGlnIle 23
Db 63 CTGAAGGAGAAAGAAACCTGTTTATCCATTCATGGGTGAAGGACATATAATGCGCTTA 122
Oy 24 ThrAspAspLeuPheValITrPAsnValLeuAsnArgGluGluValAsnIleIleCysCys 43
Db 123 CTGATGTAATTAATTAACACAAAGGGTCTGAACCAAGAAAGAGATG----- 167
Oy 44 GluLysValGluGln-----AspAlaIleArgGlyIleIleHisMet 57
Db 168 GAGAAAGTAAACGTAAGAAATGCTACAGTATGATTAAGACCCGAGCTTGTGATGACTCC 227
Oy 58 IleLeuLysGlySerGlySerGlySerCysAsnLeuPheLeuLysSerLeuLysGlu----- 75
Db 228 GTTATTCGAAAGGGGACACAGGATGCCAAATTGCAATCACAATTTGCAAGAACAGAC 281
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Db 168 GAGAAAGTAAACGTAAGAAATGCTACAGTATGATTAAGACCCGAGCTTGTGATGACTCC 227
Oy 58 IleLeuLysGlySerGlySerGlySerCysAsnLeuPheLysSerLeuLysGlu 75
Db 228 GTTATTCGAAAGGGGACACAGGATGCCAAATTGCAATCACAATTTGCAAGAACAGAC 281

RESULT 11
US-09-724-676A-11469
; Sequence 11469, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724.676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11469
; LENGTH: 358
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: n is a,c,g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (324)..(324)
; OTHER INFORMATION: n is a,c,g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (333)..(333)
; OTHER INFORMATION: n is a,c,g, or t
US-09-724-676A-11469

Alignment Scores:
Pred. No.: 0.00144 Length: 358
Score: 91.50 Matches: 22
Percent Similarity: 51.28% Conserved: 18
Best Local Similarity: 28.21% Mismatches: 27
Query Match: 19.85% Indels: 11
Gaps: 2

US-09-697-089-2_COPY_1_88 (1-88) x US-09-724-676A-11469 (1-358)
Oy 4 IlelysaPasnSerArgAlaLeuIleGlnArgMetGlyMetThrValIleLysGlnIle 23
Db 63 CTGAAGGAGAAAGAAACCTGTTTATCCATTCATGGGTGAAGGACATATAATGCGCTTA 122
Oy 24 ThrAspAspLeuPheValITrPAsnValLeuAsnArgGluGluValAsnIleIleCysCys 43
Db 123 CTGATGTAATTAATTAACACAAAGGGTCTGAACCAAGAAAGAGATG----- 167
Oy 44 GluLysValGluGln-----AspAlaIleArgGlyIleIleHisMet 57
Db 168 GAGAAAGTAAACGTAAGAAATGCTACAGTATGATTAAGACCCGAGCTTGTGATGACTCC 227
Oy 58 IleLeuLysGlySerGlySerGlySerCysAsnLeuPheLysSerLeuLysGlu 75
Db 228 GTTATTCGAAAGGGGACACAGGATGCCAAATTGCAATCACAATTTGCAAGAACAGAC 281

RESULT 12
US-09-513-999C-1335
; Sequence 1335, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J. B.
; APPLICANT: Ductert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.052.RG
; CURRENT APPLICATION NUMBER: US/09/513.999C
; CURRENT FILING DATE: 2000-02-24
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PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 1335
LENGTH: 362
TYPE: DNA
ORGANISM: Homo sapiens
NAME/KEY: CDS
LOCATION: 45..362
US-09-513-999C-1335

Alignment Scores:
Pred. NO.: 0.00146 Length: 362
Score: 91.50 Matches: 22
Percent Similarity: 51.28% Conservative: 18
Best Local Similarity: 28.21% Mismatches: 27
Query Match: 19.85% Indels: 11
DB: 5 Gaps: 2

US-09-697-089-2_COPY_1-88 (1-88) x US-09-513-999C-1335 (1-362)
Oy 4 IlelysaSpasnsrArGAlaLeuIlleGlAargmetGlymethrValIlelysgInIle 23
    ::::::::::: :: ||| ||||| ::| ::|
Db 60 CTGAAGGAGAGAGAAAGCTGTTATTCATTCATGGGTAAAGTACAAATAAATGGCTTA 119
    ::::::::::: ||| ||||| ||||| |||||
Oy 24 ThrAspAsplepheValITPAsnValLeuAsnArgGluValAsnIleIleCysCys 43
    ::::::::::: ||||| ||||| ||||| |||||
Db 120 CTGATGCAATTATTAACAGACAGAGCTGCTGACACAGAGAGATG----- 164
    ::::::::::: ||||| ||||| ||||| |||||
Oy 44 GlulysValGluIn-----AspAlaIlaArgGlyIleIleHisMet 57
    ||||| ||||| ||||| ||||| |||||
Db 165 GAGAAAGTAAACCTGAAATGCTACAGATTATGATTAAGACCCGAGCTTTGATTGACTCC 224
    ||||| ||||| ||||| ||||| |||||
Oy 58 IleleuylsYsgIserGlnserCysAsnLeupheulysSerleuYsgIu 75
    ::::::::::: ||||| ||||| ||||| |||||
Db 225 GTTATTCGAAAGGGGCGACAGCATGCCAAATTGTGCATCAATACATTTGTGA 278
    ::::::::::: ||||| ||||| ||||| |||||

RESULT 13
US-09-724-676-11470
: Sequence 11470, Application US/09724676
: GENERAL INFORMATION:
: APPLICANT: Compugen LTD
: TITLE OF INVENTION: Variants of alternative splicing
: FILE REFERENCE: 129181.4 Compugen
: CURRENT APPLICATION NUMBER: US/09/724,676
: NUMBER OF SEQ ID NOS: 97222
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 11470
: LENGTH: 479
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (20)..(20)
: OTHER INFORMATION: n is a,c,g, or t
US-09-724-676-11470

Alignment Scores:
Pred. NO.: 0.0021 Length: 479
Score: 91.50 Matches: 22
Percent Similarity: 51.28% Conservative: 18
Best Local Similarity: 28.21% Mismatches: 27
Query Match: 19.85% Indels: 11
DB: 5 Gaps: 2

US-09-697-089-2_COPY_1-88 (1-88) x US-09-724-676-11470 (1-479)
Oy 4 IlelysaSpasnsrArGAlaLeuIlleGlAargmetGlymethrValIlelysgInIle 23
    ::::::::::: ||||| ||||| ||||| |||||
Db 63 CTGAAGGAGAGAGAAAGCTGTTATTCATTCATTCATGGGTAAAGTACAAATAAATGGCTTA 1228
    ::::::::::: ||||| ||||| ||||| |||||

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Oy      24  ThrAspAspIleuPheValITrpAsnValIleuAsnArgIleuGluIleValIleAsnIleIleCysCys 43
          |||||
Db      123  CTGATGTAATTAATTATACAGACAAAGGCTGCTACACCGAAGAGATG----- 167

Oy      44  GluIysValIgluGln-----AspAlaIlaArgGlyIleIleHisMet 57
          |||||
Db      168  GAGAAATTAAGCTGAAATCTGTACAGTTATGATATAGCATTAAGACCGAGCTTTGATTGACTCC 227

Oy      58  IleIeuIysIsgIySerGluSerCysAsnIleuPheIleuIysSerIleuIysGlu 75
          :::::
Db      228  GTTATTCGGAAGGGCCACAGCAGCATGCCAATTGTGCATCATCATCATTTGTGGAA 281

RESULT 14
US-09-724-676A-11470
? Sequence 11470, Application US/09724676A
? GENERAL INFORMATION:
? APPLICANT: Compugen LTD
? TITLE OF INVENTION: Variants of alternative splicing
? FILE REFERENCE: 129181.4 Compugen
? CURRENT APPLICATION NUMBER: US/09/724,676A
? NUMBER OF SEQ ID NOS: 97222
? SOFTWARE: PatentIn version 3.2
? SEQ ID NO 11470
? LENGTH: 479
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (20)..(20)
? OTHER INFORMATION: n is a,c,g, or t
US-09-724-676A-11470

Alignment Scores:
Pred. No.: 0.0021 Length: 479
Score: 91.50 Matches: 22
Percent Similarity: 51.28% Conservative: 18
Best local Similarity: 28.21% Mismatches: 27
Query Match: 19.85% Indels: 11
DB: 5 Gaps: 2

US-09-697-089-2_COPY_1_88 (1-88) x US-09-724-676A-11470 (1-479)
Oy      4  IleYsAspAsnSerArgAlaIleuIleGlnArgMetGlyMetTrpValIleIysGlnIle 23
          ::|||
Db      63  CTGAAGGGAAGAGAGAAACCTGTTATCCATTCCTAGGCTGAAGGTACATTAAGCGCTTA 122

Oy      24  ThrAspAspIleuPheValITrpAsnValIleuAsnArgIleuGluIleValIleIleCysCys 43
          |||||
Db      123  CTGATGTAATTAATTATACAGACAAAGGCTGCTGAACCGAAGAGATG----- 167

Oy      44  GluIysValIgluGln-----AspAlaIlaArgGlyIleIleHisMet 57
          |||||
Db      168  GAGAAATTAAGCTGAAATCTGTACAGTTATGATATAGCATTAAGACCGAGCTTTGATTGACTCC 227

Oy      58  IleIeuIysIsgIySerGluSerCysAsnIleuPheIleuIysSerIleuIysGlu 75
          :::::
Db      228  GTTATTCGGAAGGGCCACAGCAGCATGCCAATTGTGCATCATCATCATTTGTGGAA 281

RESULT 15
US-10-305-720-1076
? Sequence 1076, Application US/10305720
? GENERAL INFORMATION:
? APPLICANT: Au-Young, Janice K.; Sellhmer, Jeffrey J.
? TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Express
? FILE REFERENCE: PA-0002-1 CON
? CURRENT APPLICATION NUMBER: US/10/305,720
? CURRENT FILING DATE: 2002-11-26
? PRIOR APPLICATION NUMBER: 09/016,434
? PRIOR FILING DATE: 1998-01-30
? NUMBER OF SEQ ID NOS: 1490
? SOFTWARE: PERL Program

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SEQ ID NO 1076  
LENGTH: 2563  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
OTHER INFORMATION: GenBank ID No: g1160974  
US-10-305-720-1076

Alignment Scores:  
Pred. No.: 0.107 Length: 2563  
Score: 86.00 Matches: 25  
Percent Similarity: 50.62% Conservative: 16  
Best Local Similarity: 30.86% Mismatches: 38  
Query Match: 18.66% Indels: 2  
DB: 6 Gaps: 1

US-09-697-089-2\_COPY\_1\_88 (1-88) x US-10-305-720-1076 (1-2563)

QY 4 ILeIysaspnsenSerArgAlaLeuIIeGlnArgMetGlyMetThrValIIeLysGlnIle 23  
Db 1461 ATCCGAGAATAGATGCGACTTTTCAACAT-----TTGACTGTGTATATTCACATC 1514  
QY 24 ThrAspAspLeuPheValITrpAsnValLeuAsnArgGluGluValAsnIIeIleCysCys 43  
Db 1515 CTGATAGTCTACTACTGCGCGAATTTATATGACACAGAACATGATTTATTAACAG 1574  
QY 44 GluLysValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLysLysGlySer 63  
Db 1575 AAGACACAGACGCTCTTACAAGCAAGAACTGATGTATGATCGATTTTAAAGAAAT 1634  
QY 64 GluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeuPheGlnAsp 83  
Db 1635 ATGCAAGCCACTGATTCAAGAACTCTGCAAGAGCTGAAGCTGTGTATATGAGCAT 1694  
QY 84 Leu 84  
Db 1695 TTA 1697

Search completed: January 31, 2003, 18:02:50  
Job time : 85.778 secs



GenCore version 5.1.3  
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OM protein - nucleic search, using frame\_plus.p2n model

Run on: January 31, 2003, 11:41:11 ; Search time 2366.19 Seconds  
(without alignments)  
2004.811 Million cell updates/sec

Title: US-09-697-089-2\_COPY\_161\_323  
Sequence: 1 LOSPCITEGSGKSKSLLO.....SAQALIREVLKELAEGLL 163

Scoring table:  
BIOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model DEV=rlh  
-Q=/cgn2\_1/USPTO.spool/US09697089/runat\_29012003\_092753\_19716/app\_query.fasta\_1.981  
-DB=GenEmbl -OFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPC=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=D10sum62 -TRANS=human40.cdi -LIST=45  
-DOCLLEN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09697089\_6CGN\_1\_1\_3568\_etunat\_29012003\_092753\_19716 -NCPU=6 -ICPU=3  
-NO\_XLPHY -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_hc:\*  
3: gb\_in:\*  
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5: gb\_ov:\*  
6: gb\_dat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*

29: em\_vl:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htg\_mus:\*  
34: em\_htg\_pln:\*  
35: em\_htg\_rod:\*  
36: em\_htg\_man:\*  
37: em\_htg\_vrt:\*  
38: em\_sy:\*  
39: em\_htgo\_hum:\*  
40: em\_htgo\_mus:\*  
41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	829	100.0	891	6 AX318174	AX318174 Sequence
2	829	100.0	3133	9 AY032589	AY032589 Homo sapi
3	829	100.0	3219	9 AY035391	AY035391 Homo sapi
4	829	100.0	3355	9 AK095467	AK095467 Homo sapi
5	829	100.0	3360	9 BC031555	BC031555 Homo sapi
6	829	100.0	3396	6 AX318091	AX318091 Sequence
7	829	100.0	3396	9 AY027787	AY027787 Homo sapi
8	829	100.0	3581	9 AF376061	AF376061 Homo sapi
9	829	100.0	138909	9 CNS01DS3	AL121653 BAC seque
10	829	100.0	160583	2 AC010968	AC010968 Homo sapi
11	623	75.2	185469	2 AC101793	AC101793 Mus muscu
12	236.5	28.5	4013	9 AB048534	AB048534 Homo sapi
13	236.5	28.5	5366	6 E23944	E23944 Excessive o
14	236.5	28.5	5366	6 E24990	E24990 Apoptosis-1
15	236.5	28.5	5502	6 A64509	A64509 Sequence 1
16	236.5	28.5	5984	6 E23943	E23943 Excessive o
17	236.5	28.5	5984	6 E24989	E24989 Apoptosis-1
18	236.5	28.5	5984	6 E38321	E38321 Monoclonal
19	236.5	28.5	6124	6 A64529	A64529 Sequence 21
20	236.5	28.5	6124	6 AX335820	AX335820 Sequence
21	236.5	28.5	6124	9 HSU19251	U19251 Homo sapien
22	236.5	28.5	6133	6 A64510	A64510 Sequence 2
23	236.5	28.5	6228	6 A64531	A64531 Sequence 23
24	236.5	28.5	82976	9 AC005031	AC005031 Homo sapi
25	236.5	28.5	131078	9 HSU80017	U80017 Homo sapien
26	236.5	28.5	155306	2 AC010272	AC010272 Homo sapi
27	236.5	28.5	155308	2 AC109487	AC109487 Homo sapi
28	236.5	28.5	155809	2 AC012369	AC012369 Homo sapi
29	236.5	28.5	155974	9 AC022119	AC022119 Homo sapi
30	236.5	28.5	168814	9 AC010237	AC010237 Homo sapi
31	235.5	28.4	190871	9 AC0044797	AC0044797 Homo sapi
32	225.5	27.2	716	9 HSNAP1	U1913 Homo sapien
33	220.5	26.6	6829	10 AF135494	AF135494 Mus muscu
34	220.5	26.6	117791	10 AF242431S1	AF242431 Mus muscu
35	220.5	26.6	168388	2 AC114378	AC114378 Rattus no
36	220.5	26.6	206808	2 AC093971	AC093971 Rattus no
37	219.5	26.5	41613	10 AF242433S1	AF242433 Mus muscu
38	216.5	26.1	4752	10 AF135490	AF135490 Mus muscu
39	216.5	26.1	4815	10 AF102871	AF102871 Mus muscu
40	216.5	26.1	4823	10 AF135489	AF135489 Mus muscu
41	216	26.1	5497	10 AF007769	AF007769 Mus muscu
42	216	26.1	90650	10 AF242432	AF242432 Mus muscu
43	216	26.0	196486	2 AC116741	AC116741 Mus muscu
44	215.5	26.0	1554	10 AF361881	AF361881 Rattus no
45	215.5	26.0	179252	10 AF131205	AF131205 Mus muscu

RESULT 1

#### ALIGNMENTS

AX318174  
LOCUS AX318174 891 bp DNA linear PAT 14-DEC-2001  
DEFINITION Sequence 179 from Patent WO0190156.  
ACCESSION AX318174  
VERSION AX318174.1 GI:17900865  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS 1 Reed,J.C., Pio,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H.,  
Oliveira,V.A., Hayashi,H. and Pawlowski,K.  
TITLE Card domain containing polypeptides, encoding nucleic acids, and  
methods of use  
JOURNAL Patent: WO 0190156-A 179-29-NOV-2001;  
The Burnham Institute (US)  
FEATURES  
source  
1. 891  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
<1..>891  
/note="unnamed protein product"  
/codon\_start=1  
/protein\_id="CAD19350.1"  
/translation="IQSPCIIEGSGSGKSTLLQRIAMLGSGKALTKKFFVFLR  
LSRAOGGLFETLDCDLIDPGRIRKOTPMAMILKFORVFLIDGNEFPONCPLE  
ALIKENHRRKNWYIVTTTECLRHITROFALITREVDMDPDSQALIREVLEIELAG  
LLIQIQRKSLNLMKTPLEVVITCAIQWESFESHSTOTTLHTYDLIQNKHKH  
KGVASDPIKSLDHRGDLALIEGVFSHKFDELQDVSSVMDVLLTTLGLCKYARQFK  
PKYKFFHKSQOETAGRRLS"

BASE COUNT 237 a 228 c 217 g 209 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 1.87e-92 Length: 891  
Score: 829.00 Matches: 163  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-09-697-089-2\_COPY\_161\_323 (1-163) x AX318174 (1-891)

QY 1 leuGlnSerProCysIleIleGluGlyGlnSerGlyLysSerThrLeuGln 20  
|||||  
Db 1 CTTGAGAGCCCTGCATCATTTGAAGGGGAATCTGGCAAGGCAAGTCCACTGCTGAG 60  
QY 21 ArgIleAlaMetLeuThrGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40  
|||||  
Db 61 CGCATTCGCATGCTCTGGGGGCTCCGGAAGATGCAAGGCTCTGACCAAGTTCAAAATTCGTC 120  
QY 41 PhePheLeuArgLeuSerArgAlaGlnGlyLysLeuPheGluThrLysCysAspGlnLeu 60  
|||||  
Db 121 TTTCTTCTCCCTCCAGAGGGGCCAGGGGTGACTTTTGAACCCCTGTGATCAACTTC 180  
QY 61 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 80  
|||||  
Db 181 CTGATATACCTGGCACAATAGAGACAGACATTCATGGCCATGCGTCTGAACCTGGG 240  
QY 81 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGlnPheLysProGlnAsnCysProGln 100  
|||||  
Db 241 CAGAGGGTCTTTCTTCCTTCATGAGGCTACAAATGAATTCAGCCCAAGAACTGCCAGAA 300  
QY 101 IleGluAlaLeuLeuLysGlnAsnHisArgPheLysAsnMetValIleValThrThrThr 120  
|||||  
Db 301 ATCGAAGCCCTGATTAAGGAAGAACCCAGGCTTCAAGAACATGTCATCGTACCACTACC 360  
QY 121 ThrGlnCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 140  
|||||  
Db 361 ACTGATGTCCTGAGGACACATACGGCAGTTTGTGCTGACTGCTGAGGTGGGGATATG 420

QY 141 ThrGlnSerAlaGlnAlaLeuIleArgGluValLeuIleLysGlnLeuAlaGluGly 160  
|||||  
Db 421 ACAGAAGACAGCCGCCAGGCTCTCATCCGAGAGTGTGTCAAGAGCTTGCTGAAGGC 480  
QY 161 LeuLeuLeu 163  
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Db 481 TTGTGTGCTC 489

RESULT 2  
LOCUS AY032589 3133 bp mRNA linear PRI 25-MAY-2001  
DEFINITION Homo sapiens caspase recruitment domain protein 12 mRNA, complete  
ACCESSION AY032589  
VERSION AY032589.1 GI:13899172  
KEYWORDS  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS 1 Geddes,B.J., Wang,L., Huang,W.-J., Lavellee,M., Manji,G.A.,  
Brown,M., Jurman,M., Morganstern,J., Merlam,S., Glucksmann,A.,  
Distefano,P.S. and Bertin,J.  
TITLE Human CARD12 is a novel CED4/Apaf-1 family member that induces  
apoptosis  
JOURNAL Blochem. Biophys. Res. Commun. 284 (1), 77-82 (2001)  
MEDLINE 21268963  
PUBMED 11374873  
REFERENCE 2 (bases 1 to 3133)  
AUTHORS Bertin,J.  
TITLE Direct Submission  
JOURNAL Submitted (15-APR-2001) Neurobiology, Millennium Pharmaceuticals  
Inc., 640 Memorial Drive, Cambridge, MA 02139, USA

FEATURES  
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/db\_xref="taxon:9606"  
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/product="caspase recruitment domain protein 12"  
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QLIDPGRIRKOTPMAMILKFORVFLIDGNEFPONCPREIALIKNNHRRKNWYIV  
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/note="LRR; Region: leucine-rich repeats"

BASE COUNT 903 a 691 c 729 g 810 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 9e-92 Length: 3133

Score: 829.00 Matches: 163  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-697-089-2\_COPY\_161\_323 (1-163) x AY032589 (1-3133)

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DB 516 CTTGAGAGCCCTGCATCATATTGAGGGGAATCTGGCAAGCAAGTCCACTCTGCTGCAG 575
QY 21 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40
DB 576 CGCATTTGCATGCTCTGGGGCTCCGGAAAGTCAAGGCTCGACCAATTCAAATTCCTC 635
QY 41 PhePheLeuArgLeuSerArgAlaGlnGlyLysLeuPheGluThrLeuCysAspGlnLeu 60
DB 636 TTCTTCCCTCCCTCAGAGGGCCAGGGGTGACTTTTGAACCTCTGATCACTCACTC 695
QY 61 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLysLeuArg 80
DB 696 CTGATATACCTGGCACATATCAGAGACACATTCATGCCATGCTGCTGAAGCTGGCG 755
QY 81 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 100
DB 756 CAGAGGGTCTTTTCCCTTCTTGATGGCTACATGATTAATCAAGCCCAAGTCCAGAA 815
QY 101 IleguAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValIleThrThr 120
DB 816 ATCGAAGCCCTGATTAAGAAACACCGCTTCAAGAACATGATGTCACCGCTACG 875
QY 121 ThrGluCysLeuArgHisIleArgGlnPheGlyValaLeuThrAlaGluValAspMet 140
DB 876 ACTGATGCTCTGAGGACATATGAGGAGATTGTGGCTCGACTGCTGAGAGTGGGGATATG 935
QY 141 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 160
DB 936 ACAGAAGACAGCGCCAGGCTCTCATCGAAGATGCTGATCAAGAGACTTGTCAAGGC 995
QY 161 LeuLeuLeu 163
DB 996 TTGTTGCTC 1004

RESULT 3
LOCUS AY035391 3219 bp mRNA linear PRI 24-JUL-2001
DEFINITION Homo sapiens ICE-protease activating factor mRNA, complete cds.
ACCESSION AY035391
VERSION AY035391.1 GI:14334214
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Poyet,J.L., Srinivasula,S.M., Tiani,M., Razmaza,M.,
Fernandes-Alnemri,T. and Alnemri,E.S.
TITLE Identification of Ipa1, a human caspase-1-activating protein
related to Araf-1
JOURNAL J. Biol. Chem. 276 (30), 28309-28313 (2001)
MEDLINE 21359454
PUBMED 11390368
REFERENCE
AUTHORS Poyet,J.-L., Srinivasula,S.M., Fernandes-Alnemri,T. and
Alnemri,E.S.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2001) Microbiology and Immunology, Thomas
Jefferson University, 233 S. 10th Street, Philadelphia, PA 19107,
USA

FEATURES
source location/Qualifiers
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/organism="Homo sapiens"
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BASE COUNT 934 a 696 c 748 g 841 t
ORIGIN
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Pred. No.: 9 31e-92 Length: 3219  
Score: 829.00 Matches: 163  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-697-089-2\_COPY\_161\_323 (1-163) x AY035391 (1-3219)

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QY 21 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40
DB 685 CGAATTTGCCATGCTCTGGGGCTCCGGAAAGTCAAGGCTCGACCAATTCAAATTCCTC 744
QY 41 PhePheLeuArgLeuSerArgAlaGlnGlyLysLeuPheGluThrLeuCysAspGlnLeu 60
DB 745 TTCTTCCCTCCCTCAGAGGGCCAGGGGTGACTTTTGAACCTCTGATCACTCACTC 804
QY 61 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLysLeuArg 80
DB 805 CTGATATACCTGGCACATATCAGAGACACATTCATGCCATGCTGCTGAAGCTGGCG 864
QY 81 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 100
DB 865 CAGAGGGTCTTTTCCCTTCTTGATGGCTACATGATTAATCAAGCCCAAGTCCAGAA 924
QY 101 IleguAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValIleThrThr 120
DB 925 ATCGAAGCCCTGATTAAGAAACACCGCTTCAAGAACATGATGTCATGTCACCACTAC 984
QY 121 ThrGluCysLeuArgHisIleArgGlnPheGlyValaLeuThrAlaGluValAspMet 140
DB 985 ACTGATGCTCTGAGGACATATGAGGAGATTGTGGCTCGACTGCTGAGAGTGGGGATATG 1044
QY 141 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 160
DB 1045 ACAGAAGACAGCGCCAGGCTCTCATCGAAGATGCTGATCAAGAGACTTGTCAAGGC 1104
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Qy      161 LeuDeuLeu 163
Db      1105 TTGTGGCTC 1113

RESULT 4
AK095467
LOCUS   AK095467
DEFINITION Homo sapiens cDNA FLJ38148 f1s, clone D90ST2003791, highly similar to Homo sapiens ICE-protease activating factor mRNA.
ACCESSION AK095467
VERSION   AK095467.1 GI:21754727
KEYWORDS  oligo capping; f1s (full insert sequence).
SOURCE    Homo sapiens CD34+ Cells cDNA to mRNA, clone_11b:D90ST2 clone:D90ST2003791.
ORGANISM  Homo sapiens
Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS  Minomlya,K., Magatsuma,M., Kanda,K., Kondo,H., Yokoi,T., Kodaira,H., Furuya,T., Takahashi,M., Kikkawa,E., Omura,Y., Abe,K., Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Murakawa,K., Kanehori,K., Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K., Masubo,Y., Nagai,K. and Isogai,T.
TITLE     NEDO human cDNA sequencing project
JOURNAL   Unpublished
REFERENCE 2 (bases 1 to 3355)
AUTHORS   Isogai,T. and Yamamoto,J.
TITLE     Direct Submission
JOURNAL   Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (E-mail:genomeseihri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
FEATURES
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           /cell_type="CD34+ Cells"
           /clone_11b="D90ST2"
           /note="Cloning vector: PME18SFL3-mRNA from CD34+ cells after 9-days ODF induction.-primary culture, CD34+ Cells"

BASE COUNT 986 a 726 c 774 g 869 t

ORIGIN
Alignment Scores:
Pred. No.:      9.81e-92      Length:      3355
Score:          829.00      Matches:      163
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             9          Gaps:      0

US-09-697-089-2_COPY_161_323 (1-163) x AK095467 (1-3355)
Qy      1 LeuGlnSerProCysIleIleGluGluGlnSerGlyLysGlyLysSerThrLeuLeuGln 20
Db      742 CTTGAGGCCCTGCATCATTTGAAGGGGAATCTGGCAAGGCAAGTCCACCTCTGAG 801
Qy      21 ArgTleAlaMetLeuTTPGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40
Db      802 CGAATTCCATGCTCTGGGGCTCCGGAAGTGCAAGGCTGTGACCAAGTCAAAATTCGTC 861

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Qy      41 PhePheLeuArgLeuSerArgAlaGlnGlyLysLeuPheGlnThrLeuCysAspGlnLeu 60
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Qy      61 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 80
Db      922 CTGATATACCTGGCACATCATCAGAGACAGACATTCATGGCCATGCTGGAACCTCGG 981
Qy      81 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGlnLysProGlnAsnGlyProGlu 100
Db      982 CAGAGGCTTCTTCTCTTCTTGATGGCTACATATTAATTCAGCCCAAGACTGCCAGAA 1041
Qy      101 ILeGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThrThr 120
Db      1042 ATCGAAGCCCTGATTAAGAAAGAAACACCCCTTCAGAAACATGCTATCCTCACCAC 1101
Qy      121 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 140
Db      1102 ACTGAGTGCCTGAGGACATACGCGCATTTGGTCCCTGACTGCTGAGGTGGGGATATG 1161
Qy      141 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 160
Db      1162 ACAGAAGCACGGCCAGGCTCTATCCGAGAACTGTGATCAAGAGCTTGTGAAGGC 1221
Qy      161 LeuDeuLeu 163
Db      1222 TTGTGGCTC 1230

RESULT 5
BC031555
LOCUS    BC031555
DEFINITION Homo sapiens, caspase recruitment domain protein 12, clone MGC:35330 IMAGE:5179909, mRNA, complete cds.
ACCESSION BC031555
VERSION   BC031555.1 GI:21594975
KEYWORDS  MGC.
SOURCE    human.
ORGANISM  Homo sapiens
Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 3360)
AUTHORS   Strausberg,R.
TITLE     Direct Submission
JOURNAL   Submitted (06-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK
COMMENT   NIH-MGC Project URL: http://mgc.ncl.nih.gov
Contact: MGC help desk
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunnarite, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M., Yoon, V.S., Kovis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M., Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLN at: http://image.lln.gov
Series: IRAK plate: 50 Row: a Column: 10
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.
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/note="Vector: pCMV-SPORT6"  
232. .3306  
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/db\_xref="GI:21594976"

BASE COUNT 1011 a 718 c 768 g 863 t

ORIGIN

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Score: 829.00 Matches: 163  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-697-089-2\_COPY\_161\_323 (1-163) x BC031555 (1-3360)

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Db 772 CGAATTGCCATGCTCTGGGCGCTCCGGAAGTGCAAGCTCTGACCAAGTCAAAATTCGTC 831  
QY 41 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuCysAspGlnLeu 60  
Db 832 TTCTTCCTCCGCTCAGCAGGAGCCAGGGTGACTTTTGAAGCCCTGTGATCAACTC 891  
QY 61 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 80  
Db 892 CTGGATATACCTGGACACATCAGAGACATTCATGCCCATCTCTGAAGCTGGCG 951  
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QY 121 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValAlaGlyAspMet 140  
Db 1072 ACTGAGTCCCTGAGGACATAGCGAGTTTGTCCTGCTGACTGCTGAGAGTGGGGATATG 1131  
QY 141 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGlnLeuAlaGluGly 160  
Db 1132 ACAGAAAGACAGCCCGCAGGCTCTATCCGAGAAAGTGTGATCAAGAGACTTGTCAAGAGC 1191

QY 161 LeuLeuLeu 163  
Db 1192 TTGTTGCTC 1200

RESULT 6  
LOCUS AX318091 3396 bp DNA linear PAT 14-DEC-2001  
DEFINITION Sequence 96 from Patent WO0190156.  
ACCESSION AX318091  
VERSION AX318091.1 GI:17900820  
KEYWORDS  
SOURCE  
ORGANISM human.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
1 Reed,J.C., Plo,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H.,  
Oliveira,V.A., Hayashi,H. and Pawlowski,K.  
CARD domain containing polypeptides, encoding nucleic acids, and  
methods of use  
Patent: WO 0190156-A 96-29-NOV-2001;  
The Burnham Institute (US)  
LOCATION/Qualifiers  
1. .3396  
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ENYLEKDGNEALHELIDRMNVLEQITLALPMGCDVGSLSILKHLIEVPOLVKGL  
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BASE COUNT 992 a 737 c 793 g 874 t

ORIGIN

Alignment Scores:  
Pred. No.: 9.96e-92 Length: 3396  
Score: 829.00 Matches: 163  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-09-697-089-2\_COPY\_161\_323 (1-163) x AX318091 (1-3396)

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Db 817 CGCATTCGATGCTTGGGGCTCCGGAAGTGCAAGCTCTGACCAAGTCAAAATTCGTC 876  
QY 41 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuCysAspGlnLeu 60  
Db 877 TTCTTCCTCCGCTCAGCAGGAGCCAGGGTGACTTTTGAAGCCCTGTGATCAACTC 936



BASE COUNT	992 a	737 c	793 g	874 t
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Alignment Scores:	Pred. No.: 9.96e-92 Length: 3396 Score: 829.00 Matches: 163 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatch: 0 Query Match: 100.00% Indels: 0 DB: Gaps: 9			
US-09-697-089-2_COPY_161_323 (1-163) x AY027787 (1-3396)				
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DB 757	CTTCGAGACCCCTGCATCTATTCAGAGGGAATCTGGCAAGGCAAGTCACCTGCTGTGAG 816			
QY 21	ArgIleIaMetLeuTirPglySerGIlyScylYsAlaLeuThrLysPheLysPheVal 40			
DB 817	CGCATTTGCCATGCTCTGGGGGCTCCGGAAAGTGCAGAGCTCTGACCACCAAGTTCAAAATTCGTC 876			
QY 41	PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuCysAspGlnLeu 60			
DB 877	TTCTCTCTCCGCTCAGAGGGCCAGGGGTGACTTTTGGAAACCTCTGTGATCACTTC 936			
QY 61	LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 80			
DB 937	CTGGATATACCTCGGCACATCAGAGACAGACATTCATGGCATCTCTGAGAGTCGCG 996			
QY 81	GlnArgValLeuPheLeuLeuAspGIlyTrpAsnGluPheLysProGlnAsnCysProGlu 100			
DB 997	CAGAGGGTCTTTCTCTCTTGATGGCTACATGAAATTCAGGCCCCACAGACTGCCACAGA 1056			
QY 101	IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThrThr 120			
DB 1057	ATCCGAGGCCCTGATTAAGAAACCAACCGCTTCAAGAACATGATGTCATGTCACACATACC 1116			
QY 121	ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 140			
DB 1117	ACTGATGCTCCTGAGCACAATACGACAGTTGTGTGCTTCATGCTGAGAGTGGGGGATATG 1176			
QY 141	ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 160			
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QY 161	LeuLeuLeu 163			
DB 1237	TTGTGTCTC 1245			
RESULT 8				
AF376061				
LOCUS	AF376061 3581 bp mRNA linear PRI 15-MAY-2001			
DEFINITION	Homo sapiens caspase recruitment domain protein 12 mRNA, complete cds.			
ACCESSION	AF376061			
VERSION	AF376061.1 GI:14040074			
KEYWORDS				
SOURCE	Homo sapiens.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 3581) Gingits,M.-C., Qiu,J. and Margolin,J.F. Differential expression of the caspase recruitment domain protein			
AUTHORS				
TITLE				

12 (CARD12) during monocytic differentiation  
Unpublished  
2 (bases 1 to 3581)  
Gingras, M.-C., Oiu, J. and Margolin, J. F.  
Direct Submission  
Submitted (03-MAY-2001) Pediatric/Texas Children's Cancer Center,  
Baylor College of Medicine, 6621 Fannin St. MC3-3320, Houston, TX  
77030, USA

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LOSPCIEGSGKSKSTLLORIAMLMGSKKATLTKFVPELISRAQSGLEFELCD  
QLDIPETIRKQTMAMILKLRQRYVELDQYNEFRPNCPETALIKENREKMYI  
VTTTECLRHIRQFGALAEYDMDTDSQAQLIEVILKEALBELLQIQSKRLRL  
MKTPLFVITCAIQMGSEFHSHTQTLFHFYDLILQKNHKGKGAASDFISLH  
CGDLALBGFVSHKEDFLODYVNEDELITGGLCKTARFKPKKFEKTSQET  
AGRLSSILTSHEPEVTKGNGYLOKMAVSTIDISTYSLRQYSGVPEKTRAVM  
LAAYHOCCLIGLSIAKRLPMROSLSQVKTQEOELIKANINSPVCGIHLQEST  
SKSLASQFEAFQFGKSLIYNSGIPDLDFEHLPMCSALDFIKLDFEGMAAM  
EKAEDVGGHMEAPETVLPRAVSLFFNMKQEFRLVTLRDFSKINKQDITLTK  
IFSSATSLRLQIKRCAGAVGSLSLVSTCKNIYSIWEASPLTEDEHRTSVTNLT  
LSIHDLNORLPGLTDSIGLNKMLTKIMNININEDAKIKLEGLKMLKMLFHL  
THSIDGEGMDYIVKSLSEPCDEBIQVSCCLSAUNAVKILAEONLNLVLTSLDIS  
ENYLEKNGENALHELIDRMVNLBOLITALIMPDCDYGCSLSLKHLFVQYKICL  
KNMLRLETRILICAFEGKPNKLFQOLNAGNVSSDGLAFEGVENLKQLYFFDR  
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502..741

BASE COUNT 1033 a 781 c 843 g 924 t  
ORIGIN

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Score: 829.00 Matches: 163  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-697-089-2\_COPY\_161\_323 (1-163) x AF376061 (1-3581)

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Oy 21 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40  
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Db 1030 CGCAATGGCCATGCTCTGGGGCTCCGGAAGTGCAAGGCTGACCAAGTCAAAATTCGTC 1089  
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Oy 41 PhePheLeuAlaGlyLeuSerArgAlaGlnGlyLeuPheGluThrLeuCysAspGlnLeu 60  
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Db 1090 TTCTTCCCTCCGCTCAGAGGCCCCAGGCTGACTTTTGAAGCCCTCTGATCACTTC 1149  
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Oy 61 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysArg 80  
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Oy 81 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGlnPheLysProGlnAsnCysProGlu 100  
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1210 CAGAGGCTCTTCTTCCTTCATGCTACAAATGAATTCAGAGCCCAAGTCCAGAGA 1269  
Oy 101 IlegIuaIleuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThr 120  
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Oy 141 ThrGluAspSerArgAlaGlnAlaLeuIleuArgGluValLeuIleLysGluLeuAlaGluGly 160  
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Oy 161 LeuLeuLeu 163  
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RESULT 9  
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LOCUS  
DEFINITION BAC sequence from the SPG4 candidate region at 2p21-2p22 BAC 164M19  
of 1library CITB\_978\_skb from chromosome 2 of Homo sapiens (Human).  
ACCESSION AL121653  
VERSION AL121653.2 GI:7159616  
KEYWORDS SPG4 genomic DNA interval.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 138909)  
Hazan, J., Fonknechten, N., Mavel, D., Paternotte, C., Samson, D.,  
Artiguenave, F., Davoine, C. S., Crisau, C., Durr, A., Wincker, P.,  
Brothier, P., Cactolico, L., Barbe, V., Burgunder, J. M.,  
Prud'Homme, J. F., Brice, A., Fontaine, B., Hellig, R. and  
Weissenbach, J.  
Spastin, a novel AAA protein, is altered in the most frequent form  
of autosomal dominant spastic paraplegia  
Nat. Genet. (1999) in press  
2 (bases 1 to 138909)  
Genoscope.  
Direct Submission  
Submitted (18-APR-2002) Genoscope - Centre National de Sequencage :  
BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
On Mar 6, 2000 this sequence version replaced gi:6002386.

COMMENT  
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Pred. No.: 1.03e-89 Length: 138909  
Score: 829.00 Matches: 163  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-697-089-2\_COPY\_161\_323 (1-163) x CNS01DS3 (1-138909)

Oy 1 LeuGInSerProCysIleIleGluGlyIuSerGlyLysGlySerThrLeuEngIn 20  
|||||  
Db 75091 CTTGAGAGCCCTGCATATTTGAAGGGAATCTGGCAAGGCAATCTGCTGCAG 75032  
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Oy 21 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40  
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Db 75031 CGAATTCACATGCTCTGGGGCTCCGGAAGTGCAAGGCTGACCAAGTCAAAATTCGTC 74972  
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QY 41 PhaePheLeuArgIleuSerArgAlaGlnGlyLeuPheGlnThrIleuCysAspGlnLeu 60  
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 QY 61 LeuAspIleuProGlyThrIleuArgGlnThrPheMetAlaMetLeuLeuLysLeuArg 80  
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 Db 74911 CTGATATACCTGGCAATCAGAACACAGATTCATGGCCATGCTGTAACCTGCGG 74852  
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 QY 81 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGlnPheLysProGlnAsnGlyProGln 100  
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 Db 74851 CAGAGGTTCTTTCTCTTCTTGATGCTACATATTCAGCCCGAGAACTGCCAGAA 74792  
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 QY 101 IleGlnAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValThrThr 120  
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 Db 74791 ATGCAACCCCTGATAAAGAAACACACCGCTCAAGAAACATGATGTCACACATAC 74732  
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 QY 121 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 140  
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 Db 74731 ACTGAGTGCCTGAGGACATACAGCGCACTTGTGCTCCTGACTGCTGAGTGGGATATG 74672  
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 QY 141 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGlnLeuAlaGlnGly 160  
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 Db 74671 ACAGAAACAGCCGCCAGGCTCTCATCCGAGAACTGCTGATCAAGAGCTTCTGAAGGC 74612  
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 LOCUS  
 DEFINITION Homo sapiens chromosome 2 clone RP11-9302, WORKING DRAFT SEQUENCE,  
 11 unordered pieces.  
 AC010968  
 AC010968.5 GI:9845170  
 VERSION HTG: HTGS\_PHASE1; HTGS\_DRAFT.  
 KEYWORDS Homo sapiens.  
 SOURCE Homo sapiens  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 160583)  
 Waterston,R.H.  
 TITLE The sequence of Homo sapiens clone  
 Unpublished  
 2 (bases 1 to 160583)  
 Waterston,R.H.  
 REFERENCE Direct Submission  
 JOURNAL Submitted (28-SEP-1999) Genome Sequencing Center, Washington  
 AUTHORS University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
 MO 63108, USA  
 COMMENT On Aug 18, 2000 this sequence version replaced g1:8439959.

----- Genome Center -----  
 Center: Washington University Genome Sequencing Center  
 Center code: WUGSC  
 Web site: http://genome.wustl.edu/gsc/index.shtml  
 ----- Project Information -----  
 Center project name: H\_NH0093002  
 ----- Summary Statistics -----  
 Sequencing vector: M13; 59%  
 Sequencing vector: plasmid; 41%  
 Chemistry: Dye-terminator Big Dye; 53% of reads  
 Assembly program: Phrap; version 0.990319  
 Consensus quality: bases at least Q40  
 Consensus quality: bases at least Q30  
 Consensus quality: bases at least Q20  
 Insert size: 147000; agarose-ef  
 Insert size: 159583; sum-of-contigs  
 Quality coverage: 6.64 in Q20 bases; agarose-ef  
 Quality coverage: 6.38 in Q20 bases; sum-of-contigs

\* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 11 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

1 1080: contig of 1080 bp in length  
 \* 1081 1180: gap of unknown length  
 \* 1181 2476: contig of 1296 bp in length  
 \* 2477 2576: gap of unknown length  
 \* 2577 5035: contig of 2455 bp in length  
 \* 5036 5135: gap of unknown length  
 \* 5136 9606: contig of 4471 bp in length  
 \* 9607 9706: gap of unknown length  
 \* 9707 17078: contig of 7372 bp in length  
 \* 17079 17178: gap of unknown length  
 \* 17179 27159: contig of 9980 bp in length  
 \* 27159 27258: gap of unknown length  
 \* 27259 45137: contig of 17879 bp in length  
 \* 45138 45237: gap of unknown length  
 \* 45238 65522: contig of 20285 bp in length  
 \* 65523 65622: gap of unknown length  
 \* 65623 91496: contig of 25876 bp in length  
 \* 91499 91598: gap of unknown length  
 \* 91599 116835: contig of 25237 bp in length  
 \* 116836 116935: gap of unknown length  
 \* 116936 160583: contig of 43648 bp in length.

## FEATURES

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Pred. No.: 1.24e-89 length: 160583  
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 Percent Similarity: 100.00% Conserves: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 2 Gaps: 0

US-09-697-089-2\_COPY\_161\_323 (1-163) x AC010968 (1-160583)

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OY      1  LeuGlnSerProCysIleIleGluGlyGlySerGlyGlySerThrLeuGln 20
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OY      41  PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuGlyAspGlnLeu 60
DB      49526  TTCTTCTCCCGCTCAGCAGGCGCCAGGGGTGACATTTTGAACCCCTGTGATCAGTAC 49585
OY      61  LeuAspIleProGlyThrIleArgGlyGlnThrPheMetAlaMetLeuLeuGlyLeuArg 80
DB      49586  CTTGGATATACCTGGSCACATTCGGAAGACACATTCATGCGCATGCTGTGAAGCTGCGG 49645
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DB      49646  CAGAGGGTCTTTCTTCTTCTTATGCTACATGATGATCAAGCCCAAGACTGCCAGAA 49705
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DB      49886  TTGTTGCTC 49894

RESULT 11
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DEFINITION Mus musculus clone RP24-178L2, WORKING DRAFT SEQUENCE, 43 unordered
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ACCESSION AC101793.2 GI:22381529
VERSION   AC101793.2
KEYWORDS  HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE    house mouse.
ORGANISM  Mus musculus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 185469)
AUTHORS  Birren, B., Nusbaum, C. and Lander, E.
JOURNAL  Unpublished
TITLES   2 (bases 1 to 185469)
AUTHORS  Anderson, S., Barna, N., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
          Birren, B., Linton, L., Bastien, V., Boguslavsky, L., Boukhalter, B.,
          Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,
          Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,
          Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Fato, S.,
          Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,
          Glende, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
          Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,
          Jones, C., Kamat, A., Karatas, A., Kells, C., Labrecque, K.,
          Lamazares, R., Landers, T., Lehoczy, D., Levine, R., Liu, G.,
          Maclean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,
          McCarthy, M., McKernan, P., McKernan, K., McPheters, R., Meldrim, J.,
          Menes, L., Mihova, T., Mlenga, Y., Murphy, T., Naylor, J., Nguyen, C.,
          Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D.,
          Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
          Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
          Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupack, R.,
          Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
          Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,

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TITLES   Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
          Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
          Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
JOURNAL  Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome
          Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE 3 (bases 1 to 185469)
AUTHORS  Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
          Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhalter, B.,
          Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,
          Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
          Fato, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J.,
          Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B.,
          Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,
          Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K.,
          Liu, G., Maclean, C., Macdonald, P., Major, J., Matthews, C.,
          McCarthy, M., Meldrim, J., Menes, L., Mihova, T., Mlenga, Y.,
          Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H.,
          O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,
          Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P.,
          Roman, J., Roy, A., Schauer, S., Schupack, R., Seaman, S., Severy, P.,
          Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J.,
          Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,
          Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,
          Zembek, L., Zimmer, A. and Zody, M.

TITLES   Direct Submission
JOURNAL  Submitted (21-AUG-2002) Whitehead Institute/MIT Center for Genome
          Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT  On Aug 21, 2002 this sequence version replaced gi:17060568.
          All repeats were identified using RepeatMasker:
          Smit, A.F.A. & Green, P. (1996-1997)
          http://ftp.genome.washington.edu/RM/RepeatMasker.html

TITLES   Genome Center
JOURNAL  Center: Whitehead Institute/ MIT Center for Genome Research
          Center code: WIBR
          Web site: http://www-seq.wi.mit.edu
          Contact: sequence.submissions@genome.wi.mit.edu

TITLES   Project Information
JOURNAL  Center project name: L17408
          Center clone name: 178_L_2
          ----- Summary Statistics -----
          Sequencing vector: Plasmid; n/a; 100% of reads
          Chemistry: Dye-terminator Big Dye; 100% of reads
          Assembly program: Phrap; version 0.960731
          Consensus quality: 173992 bases at least Q40
          Consensus quality: 177954 bases at least Q30
          Consensus quality: 180012 bases at least Q20
          Insert size: 168000; agarose-fp
          Insert size: 181269; sum-of-coverage
          Quality coverage: 7.1 in Q20 bases; agarose-fp
          Quality coverage: 6.6 in Q20 bases; sum-of-coverage
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          * NOTE: This is a 'working draft' sequence. It currently
          * consists of 43 contigs. The true order of the pieces
          * is not known and their order in this sequence record is
          * arbitrary. Gaps between the contigs are represented as
          * runs of N, but the exact sizes of the gaps are unknown.
          * This record will be updated with the finished sequence
          * as soon as it is available and the accession number will
          * be preserved.
          *
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          * 61 160: gap of 100 bp in length
          * 161 824: contig of 664 bp in length
          * 825 924: gap of 100 bp
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          * 1844 1943: gap of 100 bp
          * 1944 2615: contig of 672 bp in length
          * 2616 2715: gap of 100 bp
          * 2716 3318: contig of 603 bp in length
          * 3319 3418: gap of 100 bp
          * 3419 4524: contig of 1106 bp in length
          * 4525 4624: gap of 100 bp
          * 4625 5485: contig of 861 bp in length

```



[illegible]

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
LOCUS E23944	Excessive ovulatory animal and excessive ovulation method.	E23944	E23944.1	GI:13024605	JP 1999113444-A/2.	Homo sapiens.	Shigenryo, I., Kazuya, M., Harumi, S. and Hitoshi, O.	Excessive ovulatory animal and excessive ovulation method	Patent: JP 1999113444-A 2-27-APR-1999;	SCIENCE & TECH AGENCY, HARUMI SAKAI	OS Homo sapiens (human) PN JP 1999113444-A/2 PD 27-APR-1999 PF 14-OCT-1997 JP 1997280830 PR
Db 1782	ATTGCTGCGCGTACAAACAGGCGCCAGGACATCCGCCGATAC	1823									
Db 1781	ValThrThrThrThrGluCysLeuArgHisIleArgGlnPhe	130									
Db 1730	TTAAAGAAATCAGAGCTCTTATCTCTTTAGATGATCAAAAGAAATATGTTCATATCCCTCAA	1730									
Db 1671	LeuArgGlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPhe	96									
Db 1610	TTCTACCTTCTCCCTTAGTTCCACACGACGACGAGGGGCTGCCAGTATCATCTGTGAC	1610									
Db 1551	PhePheLeuArgLeuSer	58									
Db 1491	AAAAAGAGTTTCTTCTGGGACATCTGAGAGCTGTCCTCCCTGTTAAACAGGTTCCAGCTGGTT	1550									
Db 1431	TTGACCTCTGTATCTGTGTGGAGGGGTGAAGCTGGAAGTGGAAACAGGCTCTCTGAG	1490									
Db 1301	ArgIleAlaMetLeuTyrPheGlySerGlyCysLysAlaLeuThrLysPheLysPheVal	40									
Db 1201	CAGCTCCTAGAGAAAGAGATCTGTTACTGAAATGTGATGAGGACATATATTCACAGCAG	1670									
Db 1101	GlnLeuLeuAspPheProGlyThrIleLeuArgLysGlnThrPheMetAlaMetLeuLeuLys	78									
Db 1001	ValThrThrThrThrGluCysLeuArgHisIleArgGlnPhe	130									
Db 901	TTAAAGAAATCAGAGCTCTTATCTCTTTAGATGATCAAAAGAAATATGTTCATATCCCTCAA	1730									
Db 801	LeuArgGlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPhe	96									
Db 701	TTCTACCTTCTCCCTTAGTTCCACACGACGACGAGGGGCTGCCAGTATCATCTGTGAC	1610									
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Qy 59 GlnleuleuAspIleproglythrilearglysglnthrpheMetAlmetleuleuLys 78  
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LOCUS Apoptosis-inhibiting protein, gene encoding the same and cDNA  
DEFINITION E24990  
E24990  
VERSION E24990.1 GI:13024688  
KEYWORDS JP 1999116599-A/2.  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 5366)  
AUTHORS Shigeniro, I. and Kenji, Y.  
TITLE Apoptosis-inhibiting protein, gene encoding the same and cDNA  
JOURNAL Patent: JP 1999116599-A 2 27-APR-1999;  
SCIENCE & TECH AGENCY  
OS Homo sapiens (human)  
PN JP 1999116599-A/2  
PD 27-APR-1999  
PF 14-OCT-1997 JP 1997280831  
PR  
PI SHIGENIRO IKEDA, KENJI YAMAMOTO  
PC C07K14/52, C07K16/28, C12N15/09, C12Q1/68, //C12P21/02, (C12P21/02,  
PC C12R1:19),  
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FT Location/Qualifiers  
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Db 1735 AAAATAGCTTCTGTGTGGCATGTGATGCTGCCCTGTTAAACAGGTTCCAGCTGGTT 1794  
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Qy 79 LeuArgIleArgValleupheleuleuAspIlyTyraSngluPhe-----LysProgin 96  
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Qy 97 AsnCysProgluIleGluAlaleuileLysGluAnHlsArgPheLysAsnMetValIle 116  
Db 1975 -----GTCATAGGAAACTGATTCAAAAAACCATTATCCCGACCTGCTATTG 2025  
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RESULT 15  
A64509 5502 bp DNA linear PAT 29-MAR-1999  
LOCUS A64509  
DEFINITION Sequence 1 from Patent WO9726331.  
ACCESSION A64509  
VERSION A64509.1 GI:3717908  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 5502)  
AUTHORS Korneluz, R.G., Mackenzie, A.E., Roy, N., Robertson, G. and Tamai, K.  
TITLE USE OF NEURONAL APOPTOSIS INHIBITOR PROTEIN (NAIP)  
JOURNAL Patent: WO 9726331-A 1 24-JUL-1997;  
UNIV OTTAWA (CA)  
COMMENT Other publication AU 1614997 19970811.  
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Qy 21 ArgilealmetleutrglyserglyslysalaLeuthrlyspheVal 40  
Db 1839 AAAATAGCTTCTGTGTGGCATGTGATGCTGCCCTGTTAAACAGGTTCCAGCTGGTT 1898  
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Db 1899 TTCTACCTCTCCCTTAGTTCACACAGACAGAGGGGCTGCCAGTATCATCTGTGAC 1958

[illegible]

Search completed: January 31, 2003, 15:15:32  
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GenCore version 5.1.3  
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OM protein - nucleic search, using frame\_plus.p2n model

Run on: January 31, 2003, 10:49:01 ; Search time 193.092 Seconds

(without alignments)  
1901.038 Million cell updates/sec

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Fgapop 6.0 , Fgapext 7.0  
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Searched: 2185239 seqs, 1125999159 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	829	100.0	891	24	ABK22766	Human CDNA encoding
2	829	100.0	2215	22	AAH78218	Nucleotide sequenc
3	829	100.0	3133	22	AA503945	Human caspase recr
4	829	100.0	3213	22	AAH78219	Nucleotide sequenc
5	829	100.0	3396	24	ABK22731	Human CDNA encodin
6	829	100.0	3545	22	AAH98254	Murine EST-derived
7	829	100.0	3615	22	AA503945	Human caspase recr
8	276	33.3	522	22	AA526575	Human CDNA encodin
9	236.5	28.5	5366	20	AA538001	Gonadotropin hormo
10	236.5	28.5	5366	20	AA538001	Gonadotropin hormo
11	236.5	28.5	5502	17	AA730092	Human apoptosis in
12	236.5	28.5	5502	18	AA771263	Neuronal apoptosis
13	236.5	28.5	5984	20	AA558000	Neuronal apoptosis
14	236.5	28.5	5984	20	AA558000	Conodontropic hormo
15	236.5	28.5	5984	21	AA558000	Human apoptosis in
16	236.5	28.5	6124	18	AA771265	Human NALP CDNA.
17	236.5	28.5	6124	24	ABL67992	Neuronal apoptosis
18	236.5	28.5	6133	18	AA771264	Ovary cancer relat
19	236.5	28.5	6228	18	AA771265	Neuronal apoptosis
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21	120.5	14.5	3030	24	ABK22727	Human CDNA #1 enc
22	120.5	14.5	3063	24	ABK22771	Human CDNA #2 enc
23	120.5	14.5	4322	22	AA165591	Nucleotide sequenc
24	120.5	14.5	37443	22	AA165592	Nucleotide sequenc
25	111	13.4	4141	20	AA209251	Murine CARD-4L CDN
26	111	13.4	4141	22	AA230006	Mouse CARD-4L (lon
27	111	13.4	4141	24	AA140764	DNA of murine CAR
28	107	12.9	1470	24	AA140757	DNA of human CARD-
29	107	12.9	2859	24	AA140755	Human CARD-4S (pho
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31	107	12.9	3080	22	AA230003	CDNA of human CARD
32	107	12.9	3080	24	AA140756	Human CARD-4L (lon
33	107	12.9	3382	22	AA230002	Human CARD-4L (lon
34	107	12.9	3382	24	AA140754	CDNA of human CARD
35	107	12.9	4415	21	AA95791	Apoptosis related
36	107	12.9	4570	22	AA51622	Human poly nucleoti
37	107	12.9	4610	22	AAH18313	Human CDNA sequenc
38	107	12.9	5250	22	AA52606	Human poly nucleoti
39	107	12.9	32042	20	AA209252	Human CARD-4 DNA.
40	107	12.9	32042	22	AA230011	Human CARD-4 gene.
41	107	12.9	32042	24	AA140765	Genomic DNA of hum
42	104.5	12.6	3300	24	AA147129	Pylin domain conta
43	102.5	12.4	1557	24	AA147143	Human NALP exon 13
44	100.5	12.1	250	20	AA502906	Human APRC polypep
45	100.5	12.1	2460	24	ABA94363	Human APRC polypep

## ALIGNMENTS

RESULT 1

ABK22766

ID ABK22766 standard; CDNA: 891 BP.

ABK22766; 26-MAR-2002 (first entry)

Human CDNA encoding CLAN NACHT.

Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;  
abnormal cell proliferation; cancer; abnormal cell death; apoptosis;  
autoimmune disease; inflammation; keratinocyte hyperplasia;  
inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;  
balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;  
leukaemia; allergy; arthritis; lupus; Schriegen's syndrome;  
Crohn's disease; graft-versus-host disease; stroke;  
myocardial infarction; heart failure; neurodegenerative disease;

Parkinson's disease; Alzheimer's disease; HIV,  
human immunodeficiency virus infection.

Homo sapiens.

WO200190156-A2.

29-NOV-2001.

24-MAY-2001; 2001WO-US171158.

24-MAY-2000; 2000US-0579240.  
10-OCT-2000; 2000US-0686347.  
14-MAR-2001; 2001US-275980P.  
23-MAY-2001; 2001US-0864921.

(BURN-) BURNHAM INST.

Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;  
Olliveira VAM, Hayashi H, Pawlowski K;  
WPI; 2002-083086/71.  
P-PSDB; AAU80872.

New caspase recruitment domain (CARD)-containing polypeptides and  
encoding nucleic acids, useful for treating abnormal cell proliferation  
or cell death, autoimmune diseases or inflammation, e.g. carcinomas,  
arthritis or stroke

Claim 1; Page 200-201; 216pp; English.

The invention relates to an isolated caspase recruitment domain (CARD)  
-containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain  
from it, and the polynucleotides encoding them. Also included are a  
recombinant vector comprising the polynucleotide, recombinant cells  
containing the vector (e.g. bacteria, yeast, plant, animal, mammalian  
and insect cells) and an anti-CARD antibody. The CARD-containing  
polypeptide and CARD-encoding nucleic acid are useful for treating a  
pathology characterised by abnormal cell proliferation (e.g. cancer),  
abnormal cell death (apoptosis), autoimmune diseases or inflammation. It  
particular, the polypeptide and nucleic acid are useful for treating  
keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth  
muscle cell proliferation in arteries following balloon angioplasty  
(restenosis), gliomas, carcinomas, sarcomas, melanomas, leukemias,  
allergies, arthritits, lupus, Schogen's syndrome, Crohn's disease,  
graft-versus-host disease, stroke, myocardial infarction, heart failure,  
neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's  
disease) or immunodeficiency associated disease (e.g. human  
immunodeficiency virus (HIV) infection). The nucleic acids are useful  
in a variety of diagnostic applications. The present sequence is a  
cDNA encoding a CARD domain containing protein.

Sequence 891 BP; 237 A; 228 C; 217 G; 209 T; 0 other:

Alignment Scores:  
Pred. No.: 1.07e-99 Length: 891  
Score: 829.00 Matches: 163  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 24 Gaps: 0

US-09-089-089-2\_COPY\_161\_323 (1-163) x ABK223766 (1-891)

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|||||  
1 CTTCGACCCCTCGATCATTTGAAGGGAAACTGTGGCAAGGCACCTCGCTCAG 60  
|||||  
21 ArgIleAlawetLeuTrpGLYserGLYscSYSLAalaEurThrLYSPhelYSPhVal 40  
|||||  
61 CGCATTCGCATGCTCGCGCTCGCGAAAGTGCAGCAAGGCTCTGCACCAATTTCCTC 120  
|||||  
41 PhePheLeuArgLeuSerArgAlaGLNcLYLeuPheGlnurThrLeuCYASpGINLeu 60

Db	121	TTCTTCCTCCGCTCTAGCAGGGGCCAGGGCTGGACTTTTGGAAACCCCTCTGGATCACTC	180
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Db	361	ACTGATGCTCCTGAGCACATACGACAGTTTGCTGCTCCCTGACTGCTGAGTGGGATATG	420
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Db	421	ACAGAAGACAGCGCCAGCAGCTCTCATCCGAGAAGGCTGATCAAGAGAGCTTGTAAGGC	480
Qy	161	LeuLeuLeu 163	
Db	481	TTGTGTGCTC 489	
RESULT 2			
ID	AAH78218	standard; DNA; 2215 BP.	
AC	AAH78218;		
DE	26-NOV-2001	(first entry)	
Nucleotide sequence of a human secreted polypeptide.			
XX	Human; secreted polypeptide; nervous disease; muscular disease; tumour;		
KW	gastrointestinal ulceration; spinal cord disease; trachea disease;		
KW	thyroid gland disease; ovary disease; prostate disease; heart disease;		
KW	renal gland disease; small intestine disease; thymus disease;		
KW	lymph node disease; muscular system disease; colon disease;		
KW	lipase deficiency; cystic fibrosis; pancreatitis; clot formation;		
KW	myocardial infarction; angiodysplasia; liver disease; coagulation disorder		
KW	microbial disease; immune disorder; inflammation; transplant rejection;		
KW	bone thickness; bone density; ferroxidase loss; apoptosis;		
KW	vascular smooth cell proliferation; vaccine; ss.		
OS	Homo sapiens.		
XX			
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FT		/note= "no termination codon given"	
XX	WO200166690-A2.		
XX			
XX	13-SEP-2001.		
XX			
XX	05-MAR-2001; 2001WO-US07143.		
XX			
PR	06-MAR-2000; 2000US-0187107.		
PR	13-MAR-2000; 2000US-0188916.		
PR	03-OCT-2000; 2000US-0236874.		
PR	03-OCT-2000; 2000US-0237846.		
XX			
PA	(SMIK ) SMITHKLINE BEECHAM CORP.		
XX	(SMIK ) SMITHKLINE BEECHAM PLC.		
PI	Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;		
DR	WPI; 2001-570768/64.		

DR P-PSDB; AAG67526.  
XX Novel isolated secreted polypeptide useful for treating nervous and  
PT muscular diseases, gastrointestinal ulceration, coagulation and immune  
PT disorders, microbial diseases, inflammation and transplant rejection -  
XX  
XX  
PS Claim 2; Page 52-53; 102pp; English.  
XX  
XX The present sequence encodes a human secreted polypeptide. The  
CC secreted polypeptides and polynucleotides are useful for treating  
CC nervous and muscular diseases, for inhibiting tumor formation and  
CC metastasis, for treating gastrointestinal ulceration, for preventing  
CC and treating diseases in spinal cord, thyroid gland, ovary, prostate,  
CC renal gland, small intestine, heart, trachea, thymus, lymph node,  
CC muscular system and colon, for treating lipase deficiency in cystic  
CC fibrosis and pancreatitis, for treating undesirable clot formation  
CC such as myocardial infarction, during angioplasty and all surgical  
CC procedures that require decreased blood clot formation, for treating  
CC liver diseases, coagulation disorders and microbial diseases, for  
CC treating immune disorders, for treating inflammation and transplant  
CC rejection, for enhancing bone thickness and increasing bone density,  
CC for reducing the loss of essential ferrooxides, for suppressing  
CC apoptosis, and for regulating vascular smooth cell proliferation. They  
CC may also be used as vaccines.  
XX  
XX

Sequence 2215 BP; 621 A; 522 C; 519 G; 553 T; 0 other;

#### Alignment Scores:

Pred. No.: 3,94e-99 Length: 2215  
Score: 829.00 Matches: 163  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 22 Gaps: 0

US-09-697-089-2\_COPY\_161\_323 (1-163) x AAH78218 (1-2215)

OY 1 LeuGlnSerProCySIIleIleGlnGluSerGlyGlySerThrLeuGln 20  
DB 439 CTTGATACGCCCCGTCATTTGAAGGGAATCTGGCAAGCAATCTCTGTCGAG 498  
OY 21 ArgIIlealmetLeuTrpGlySerGlyScylsAlaLeuThrLysPheLysPheVal 40  
DB 499 CGAATGGCATGCTCTGGGGCTCCGGAAAGTGCAGGCTCTGACCAATTCATTCGTC 558  
OY 41 PhePheLeuAArgLeuSerAArgAlaGlnGlyLeuPheGluThrLeuCysAspGlnLeu 60  
DB 559 TTCTTCCCTCCGTCACAGGAGGCCAGGCTGATTTTGAACCCCTGTCATCACTC 618  
OY 61 LeuAspIleProGlyThrIleArgGlyGlnThrPheMetAlaMetLeuLeuLysLeuArg 80  
DB 619 CTGGATATACCTGGGCACATACAGGAAGCAACATTCATGCGCATCTCTGAAGCTGCGG 678  
OY 81 GlnAArgValLeuPheLeuLeuAspGlyTyrAsnGlnPheLysProGlnAsnCysProGlu 100  
DB 679 CAGAGGATTTCTTCTCTTCTGATGGCTACATGAAATTCAGGCCACAGACAGCCACAGA 738  
OY 101 IleGlnAlaLeuIleLysGlnAsnHisAArgPheLysAsnMetValIleValIleThrThr 120  
DB 739 ATCGAAGCCCTGATMAAGAAACACCCGCTTCAGAACATGTCATGTCACCTACCC 798  
OY 121 ThrGlnCysLeuArgHisIleAArgGlnPheGlyAlaLeuThrAlaGluValAGlySmet 140  
DB 799 ACTGATGCTCCGAGGACATACGAGGAGTTTGGTGGCTCTGACTGCTGAGAGTGGGGATATG 858  
OY 141 ThrGlnAspSerAlaGlnAlaLeuIleAArgGlnValLeuIleLysGlnLeuAlaGlnLcyl 160  
DB 859 ACAGAAAGACAGGCGCCAGGCTCTATCGAGAAAGTGTATCAAGAGACTTGTCTAAAGC 918  
OY 161 LeuLeuLeu 163  
DB 919 TTGTTGCTC 927

#### RESULT 3

AAS03945

ID AAS03945 standard; CDNA: 3133 BP.

AC AAS03945;

DT 12-SEP-2001 (first entry)

DE Human caspase recruitment domain 12 (CARD-12) CDNA.

XX Caspase recruitment domain; CARD-12; apoptosis; stress-related pathway;  
XX cancer; viral infection; poxvirus; adenovirus; autoimmune disorder;  
KW systemic lupus erythematosus; arthritis; neurological disorder; stroke;  
KW Alzheimer's disease; amyotrophic lateral sclerosis; haematologic disease;  
KW aplastic anaemia; myocardial infarction; inflammatory disorder;  
KW Crohn's disease; insulin-dependent diabetes; contact dermatitis;  
KW psoriasis; graft rejection; bacterial infection; lepromatous leprosy;  
KW tuberculosis; ischaemic brain injury; hypoxic brain injury; ss;  
KW kidney ischaemia; reperfusion injury; acute bacterial meningitis;  
KW excitotoxic brain damage; liver disease.  
XX  
XX

OS Homo sapiens.

FT Key Location/Qualifiers

FT CDS 36..3110

FT /tag= a

FT /product= "Human CARD-12"

FN WO200130971-A2.

XX 03-MAY-2001.

XX 26-OCT-2000; 2000WO-US29643.

XX 27-OCT-1999; 99US-0161822.

XX (MILL-) MILENNIUM PHARM INC.

XX Bertin J, Robison KE;

XX WPI; 2001-308628/32.

XX P-PSDB; AAU02880.

PT Isolated caspase recruitment domain-12 polypeptide and nucleic acids

PT encoding them, useful for treating and diagnosing disorders associated

PT with abnormal apoptosis such as cancer, arthritis and Alzheimer's

PT disease -

PS Claim 2; Fig 1; 93pp; English.

XX The sequence represents a cDNA which encodes the human caspase  
CC recruitment domain 12 (CARD-12) polypeptide. CARD domains are found in a  
CC number of proteins that transmit signals that activate apoptosis and  
CC inflammatory pathways in response to stress and other stimuli. Therefore,  
CC CARD-12 and its corresponding nucleic acid may be used in treatment and  
CC diagnosis of patients suffering from disorders associated with an  
CC abnormal level (an increase or a decrease) of apoptotic cell death or  
CC abnormal activity of stress-related pathways. The disorders include  
CC cancer, viral infections (e.g. caused by poxviruses, adenoviruses),  
CC autoimmune disorders (e.g. systemic lupus erythematosus, arthritis),  
CC neurological disorders (e.g. Alzheimer's disease, amyotrophic lateral  
CC sclerosis), haematologic diseases (e.g. aplastic anaemia, myocardial  
CC infarction, stroke), inflammatory and immune system disorders (e.g.  
CC Crohn's disease, insulin-dependent diabetes, contact dermatitis,  
CC psoriasis, graft rejection), bacterial infections (e.g. tuberculosis),  
CC lepromatous leprosy), ischaemic and hypoxic brain injury, kidney  
CC ischaemia/reperfusion injury, excitotoxic brain damage, acute bacterial  
CC meningitis and liver disease.  
XX

SO Sequence 3133 BP; 903 A; 691 C; 729 G; 810 T; 0 other;

#### Alignment Scores:

Pred. No.: 6.48e-99 Length: 3133

Score: 829.00 Matches: 163  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 22 Gaps: 0

US-09-697-089-2\_COPY\_161\_323 (1-163) x AAS03945 (1-3133)

QY 1 LeuGlnSerProCysIleIleGlnGlyLeuSerGlyLysGlySerThrLeuGln 20  
 Db 516 CTTAGAGCCCTCATCATTTGAAGGGGAATCTGGCAAGCAAGTCACCTGCTGAG 575  
 QY 21 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuTrpLysPheLysPheVal 40  
 Db 576 CGCATGGCATGCTCTGGGGCTCCGGAAGTGAAGGCTGTGACCAAGTTCAAAATTGCTC 635  
 QY 41 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGlnThrLeuCysAspGlnLeu 60  
 Db 636 TTCTTCTCCGCTCAGAGGGCCAGGGTGGACTTTTGAACCCCTGTGATCAACTC 695  
 QY 61 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLysLeuArg 80  
 Db 696 CTGATATACCTGGCAATCAAGAGCAAGCATTCATGCCATGCTGCTGAAGCTGGG 755  
 QY 81 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGlnPheLysProGlnAsnCysProGln 100  
 Db 756 CAGAGGGTTCTTCTTCTGATGGCTACAAATGAAATCAAGCCCAAGTCCAGAA 815  
 QY 101 IleGlnAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValThrThr 120  
 Db 816 ATCAAAACCCCGATAAAGAAACCCCGCTTCAAGAAACATGGTCATGTCACCACTACC 875  
 QY 121 ThrGlnLysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGlnValGlyAspMet 140  
 Db 876 ACTAGAGCGCTGAGCAATCAAGAGCAAGTGGTCCCTGCACTGCTGAGCTGGGGATATG 935  
 QY 141 ThrGlnAspSerAlaGlnAlaLeuIleArgGlnValLeuIleLysGlnLeuAlaGlnGly 160  
 Db 936 ACAGAAACAGAGCCGAGGCTCTCATCGAGAGTGTGATCAAGAGAGCTTGTGAAGGC 995  
 QY 161 LeuLeuLeu 163  
 Db 996 TTGTTGCTC 1004

# RESULT 4

AAH78219 standard; DNA: 3213 BP.

AAH78219;

26-NOV-2001 (first entry)

Nucleotide sequence of a human secreted polypeptide.

Human: secreted polypeptide; nervous disease; muscular disease; tumour;  
 gastrointestinal ulceration; spinal cord disease; trachea disease;  
 thyroid gland disease; ovary disease; prostate disease; heart disease;  
 renal gland disease; small intestine disease; thymus disease;  
 lymph node disease; muscular system disease; colon disease;  
 lipase deficiency; cystic fibrosis; pancreatitis; clot formation;  
 myocardial infarction; angioplasty; liver disease; coagulation disorder;  
 microbial disease; immune disorder; inflammation; transplant rejection;  
 bone thickness; bone density; ferroxidase loss; apoptosis;  
 vascular smooth cell proliferation; vaccine; ss.

Homo sapiens.

Location/Qualifiers

1..3213

/\*tag= a /product= "secreted polypeptide"

MO200166690-A2.

XX 13-SEP-2001.  
 PD 05-MAR-2001; 2001WO-US07143.  
 XX 06-MAR-2000; 2000US-0187107.  
 PR 13-MAR-2000; 2000US-0188916.  
 PR 03-OCT-2000; 2000US-0236874.  
 PR 03-OCT-2000; 2000US-0237846.  
 XX (SMK) SMITHKLINE BEECHAM CORP.  
 PA (SMK) SMITHKLINE BEECHAM PLC.  
 DR Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;  
 DR WPI: 2001-570768/64.  
 DR P-PSDB: AAG67527.  
 PT Novel isolated secreted polypeptide useful for treating nervous and  
 PT muscular diseases, gastrointestinal ulceration, coagulation and immune  
 PS disorders, microbial diseases, inflammation and transplant rejection -  
 PS Claim 2; Page 53-54; 102pp; English.

The present sequence encodes a human secreted polypeptide. The  
 secreted polypeptides and polynucleotides are useful for treating  
 nervous and muscular diseases, for inhibiting tumour formation and  
 metastasis, for treating gastrointestinal ulceration, for preventing  
 and treating diseases in spinal cord, thyroid gland, ovary, prostate,  
 renal gland, small intestine, heart, trachea, thymus, lymph node,  
 CC muscular system and colon, for treating lipase deficiency in cystic  
 CC fibrosis and pancreatitis, for treating undesirable clot formation  
 CC such as myocardial infarction, during angioplasty and all surgical  
 CC procedures that require decreased blood clot formation, for treating  
 CC liver diseases, coagulation disorders and microbial diseases, for  
 CC treating immune disorders, for treating inflammation and transplant  
 CC rejection, for enhancing bone thickness and increasing bone density,  
 CC for reducing the loss of essential ferroxidases, for suppressing  
 CC apoptosis, and for regulating vascular smooth cell proliferation. They  
 CC may also be used as vaccines.

Sequence 3213 BP: 916 A; 704 C; 756 G; 837 T; 0 other;

## Alignment Scores:

Alignment Scores: 6,72e-99 Length: 3213  
 Pred. No.: 829.00 Matches: 163  
 Score: 829.00  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 22 Gaps: 0

US-09-697-089-2\_COPY\_161\_323 (1-163) x AAH78219 (1-3213)

QY 1 LeuGlnSerProCysIleIleGlnGlyLeuSerGlyLysGlySerThrLeuGln 20  
 Db 619 CTTAGAGCCCTCATCATTTGAAGGGGAATCTGGCAAGCAAGTCACCTGCTGAG 678  
 QY 21 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuTrpLysPheLysPheVal 40  
 Db 679 CGATTCGCATGCTCTGGGGCTCCGGAAGTGAAGGCTGTGACCAAGTTCAAAATTGCTC 738  
 QY 41 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGlnThrLeuCysAspGlnLeu 60  
 Db 739 TTCTTCTCCGCTCAGAGGGCCAGGGTGGACTTTTGAACCCCTGTGATCAACTC 798  
 QY 61 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLysLeuArg 80  
 Db 799 CTGATATACCTGGCAATCAAGAGCAAGCATTCATGCCATGCTGAAAGCTGGG 858  
 QY 81 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGlnPheLysProGlnAsnCysProGln 100  
 Db 859 CAGAGGGTTCTTCTTCTGATGGCTACATGAATTCAGAGCCCAAGTCCAGAA 918

QY 101 ILEGJUALaleuIleuIleuSGluASnHISArghelYsASmetValIleValThrThrThr 120  
DB 919 ATCGAAGCCCTGATTAAGAAACACACCCCTTCAAGACATGTGTCATCCACTACC 978  
QY 121 ThrGluCysLeuArghISleArghInPheglYAlaLeuThrAlaGluValGlyAspMet 140  
DB 979 ACTGAGTCCCTGAGCAGATACGAGCGAGTTTGGTCCCTGACTGCTGAGGTGGGGATATNG 1038  
QY 141 ThrGluAspSerAlaGlnAlaLeuIleArghGluValIleuIleuSGluLeuAlaGluGly 160  
DB 1039 ACAGAAGACAGCCGACGCTCTCATCCGAGAAAGTGATCAAGAGCCTTGCTGAAGGC 1098  
QY 161 LeuLeuLeu 163  
DB 1099 TTGTGCTC 1107  
RESULT 5  
ABK22731  
ID ABK22731 standard; cDNA: 3396 BP.  
XX  
AC ABK22731;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Human cDNA encoding CLAN A.  
XX  
KW Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;  
KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;  
KW autoimmune disease; inflammation; keratinocyte hyperplasia;  
KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;  
KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;  
KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;  
KW Crohn's disease; graft-versus-host disease; stroke;  
KW myocardial infarction; heart failure; neurodegenerative disease;  
KW Parkinson's disease; Alzheimer's disease; HIV;  
KW human immunodeficiency virus infection.  
XX  
OS Homo sapiens.  
XX  
PN WO200190156-A2.  
XX  
PD 29-NOV-2001.  
XX  
PE 24-MAY-2001; 2001WO-US17158.  
XX  
PR 24-MAY-2000; 2000US-0579240.  
PR 10-OCT-2000; 2000US-0686347.  
PR 14-MAR-2001; 2001US-275980P.  
PR 23-MAY-2001; 2001US-0864921.  
XX  
PA (BURN-) BURHAM INST.  
PI Reed JC, Plo FF, Godzik A, Stehlik C, Damiano JS, Lee SH;  
PI Oliveira VAM, Hayashi H, Pawlowski K;  
XX  
XX WPI: 2002-083086/11.  
DR P-PSDB: AA080861.  
XX  
XX New caspase recruitment domain (CARD)-containing polypeptides and  
PT encoding nucleic acids, useful for treating abnormal cell proliferation  
PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,  
PT arthritis or stroke  
XX  
XX Claim 1; Page 166-171; 216pp; English.  
XX  
XX The invention relates to an isolated caspase recruitment domain (CARD)  
CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain  
CC from it, and the polynucleotides encoding them. Also included are a  
CC recombinant vector comprising the polynucleotide, recombinant cells  
CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian  
CC and insect cells) and an anti-CARD antibody. The CARD-containing  
CC polypeptide and CARD-encoding nucleic acid are useful for treating a  
CC pathology characterised by abnormal cell proliferation (e.g. cancer),

CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In  
CC particular, the polypeptide and nucleic acid are useful for treating  
CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth  
CC muscle cell proliferation in arteries following balloon angioplasty  
CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,  
CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,  
CC graft-versus-host disease, stroke, myocardial infarction, heart failure,  
CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's  
CC disease) or immunodeficiency associated disease (e.g. human  
CC immunodeficiency virus (HIV) infection). The nucleic acids are useful  
CC in a variety of diagnostic applications. The present sequence is a  
CC cDNA encoding a CARD domain containing protein.  
XX  
SQ Sequence 3396 BP; 992 A; 737 C; 793 G; 874 T; 0 other.  
  
Alignment Scores:  
Pred. No.: 7,27e-99 Length: 3396  
Score: 829.00 Matches: 163  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 24 Gaps: 0  
  
US-09-697-089-2\_COPY\_161\_323 (1-163) x ABK22731 (1-3396)  
QY 1 LeuGlnSerProCysAlleIleGluGluSerGlyLySGlyLysSerThrLeuLeuGln 20  
DB 757 CTTTCAGAGCCCTTGATCATTTGAAGGGAAATGTGGCAAGGACCTTGCTGTCGAG 816  
QY 21 ArgIleAlaMetLeuTrpLysSerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40  
DB 817 CCGATTGGCATCTCTGGGGGCTCCGGAAGTGCAGAGCCTTACCAAGTTCAAATTGCG 876  
QY 41 PhePheLeuArghLeuSerArghAlaGlnGlyLeuPheGluThrLeuCysAspGlnLeu 60  
DB 877 TTCTTCCTCCGTCGTCAGCAGGCGCCAGGGGTGGACTTTTGAACCCCTCTGATCAACTC 936  
QY 61 LeuAspIleProGlyThrIleArghLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 80  
DB 937 CTGGATATACCTGGGCACATTCAGGAAGCAGACATTATGCGCATGCTGTAAGCTGCGG 996  
QY 81 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 100  
DB 997 CAGAGGGTTCTTTCCTCTTGTATGCTACATTAATTAACCCCAAGACTGCCAGAA 1056  
QY 101 ILEGJUALaleuIleuSGluASnHISArghelYsASmetValIleValThrThrThr 120  
DB 1057 ATCGAAGCCCTGATTAAGAAACACACCCCTTCAAGAACATGTGTCATCCACTACC 1116  
QY 121 ThrGluCysLeuArghISleArghInPheglYAlaLeuThrAlaGluValGlyAspMet 140  
DB 1117 ACTGAGTCCCTGAGCAGATACGAGCGAGTTTGGTCCCTGACTGCTGAGGTGGGGATATNG 1176  
QY 141 ThrGluAspSerAlaGlnAlaLeuIleArghGluValIleuIleuSGluLeuAlaGluGly 160  
DB 1177 ACAGAAGACAGCCGACGCTCTCATCCGAGAAAGTGATCAAGAGCCTTGCTGAAGGC 1236  
QY 161 LeuLeuLeu 163  
DB 1237 TTGTGCTC 1245  
RESULT 6  
AAH98254  
ID AAH98254 standard; cDNA: 3545 BP.  
XX  
XX AAH98254;  
AC  
DT 12-OCT-2001 (first entry)  
XX  
XX Murine EST-derived coding sequence SEQ ID NO: 111.  
DE Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;  
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;

KW	diagnostics; forensic test; gene mapping; genetic disorder;
KW	biodeficiency; gene therapy; nutrition; ss.
XX	
OS	Mus musculus.
XX	
PN	WO200154477-A2.
XX	
PD	02-AUG-2001.
XX	
PE	25-JAN-2001; 2001WO-US02687.
XX	
PR	25-JAN-2000; 2000US-0491404.
PR	17-JUL-2000; 2000US-0617746.
PR	03-AUG-2000; 2000US-0631451.
PR	15-SEP-2000; 2000US-0663870.
XX	
PA	(HYSE-) HYSEQ INC.
XX	
PI	Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI	Cao Y, Drmanac RA, Zhang J, Wehrman T;
XX	
DR	WPI: 2001-476164/51.
DR	P-PSDB; AAM23595.
XX	
PT	Isolated polypeptide for treatment of diseases, diagnostics, raising
XX	antibodies and research use -
XX	
PS	Claim 1; Page 250-251; 1275pp; English.
XX	
CC	The present invention provides the protein and coding sequences of novel
CC	proteins from a variety of organisms, including human, dog, cat, horse,
CC	cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC	urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC	from the organism of interest. They can be used in diagnostics,
CC	forensics, gene mapping, identification of mutations, to assess
CC	biodiversity and for nutritional purposes. The present sequence is a cDNA
CC	of the invention.

Alignment Scores:	
Pred. No.:	7.73e-99
Score:	829.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	22
Length:	3545
Matches:	163
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

QY	1	LeuGlnSerProCysIleIleGlnGlyGlnSerGlyLysGlyLysSerThrLeuLeuGln	20
Db	712	CTTAGAGACCCTTCATCATTTGAAGGGGAATCTGGCAAGGCAAGTCCACTCGCTGGCAG	771
QY	21	ArgIleAlaMetLeuThrPglYserGlyLysCysLysAlaLeuThrLysPheLysPheVal	40
Db	772	CGCAATTGGCAGTCTCGGGGGCTCGGGAATGCAAGGCTGTGACCAAGTTCAAATTCTGTC	831
QY	41	PhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGlnThrLeuCysAspGlnLeu	60
Db	832	TTCTTCCTCCGCTGCACACAGGGCCCAAGGGTGAGCTTTTGAAACCCCTGTGTATCAATC	891
QY	61	LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg	80
Db	892	CTGATTTACTCTGGCACAAATCAGGAAGCAACATTCATGCGCATCTGCTGAAGCTGCGG	951
QY	81	GlnArgValLeuPheLeuLeuAspGlyTyrAsnGlnPheLysProGlnAsnGlyProGlu	100
Db	952	CAGAGGGTCTTTTTCCTTTGTGATGGGTACAATGAATTCAGGCCCCAGCAACTGCCAGAA	1011
QY	101	IleGlnAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValThrThrThr	120
Db	1012	ATTCAGAGCCCTGATTAAGGAAGAACACCGCTTTAAGAACATGGTCATGTCCACCATAC	1077

Oy	121	ThrlgucysleuAaGHISiIIEaRGiInPhaGLyAlaLeuThrAlaIaGLyAspMet	140		
Db	1072	ACTGaGtCCtCGAGGGCAcATaGGcAcTTtGGtCCCTGaCTGAGtGGGGGATATG	1131		
Oy	141	ThrlgIuSpSerAlaGLaIAlaLeuIIEaRGiIuValLeuIIElySGiLdeuAaIaGLuGly	160		
Db	1132	ACAGAGAcAGAcGCCcCAGGCTcATCCAGAGAGTcGTGATCAAGAGcCTTGCTGAAGcC	1191		
Oy	161	leuIeuIeu	163		
Db	1192	TTtGTtGCTC	1200		
RESULT 7					
AA503946	AA503946 standard; DNA; 3615 BP.				
XX	AA503946;				
AC					
XX					
DT	12-SEP-2001	(first entry)			
XX					
DE	Human caspase recruitment domain 12 (CARD-12) genomic DNA.				
XX					
KW	Caspase recruitment domain; CARD-12; apoptosis; stress-related pathway;				
KW	cancer; viral infection; poxvirus; adenovirus; autoimmune disorder;				
KW	systemic lupus erythematosus; arthritis; neurological disorder; stroke;				
KW	Alzheimer's disease; amyotrophic lateral sclerosis; hematologic disease;				
KW	aplastic anemia; myocardial infarction; inflammatory disorder;				
KW	Crohn's disease; insulin-dependent diabetes; contact dermatitis;				
KW	psoriasis; graft rejection; bacterial infection; lepromatous leprosy;				
KW	tuberculosis; ischemic brain injury; hypoxic brain injury; ds;				
KW	kidney ischemia; reperfusion injury; acute bacterial meningitis;				
KW	excitotoxic brain damage; liver disease.				
XX					
OS	Homo sapiens.				
XX					
FH	Key	Location/Qualifiers			
FT	CDS	1..3615			
FT		/*tag= a			
FT		/product= "Human CARD-12"			
XX					
PN	W0200130971-A2.				
XX					
PD	03-MAY-2001.				
XX					
PF	26-OCT-2000; 2000MO-US92643.				
XX					
PR	27-OCT-1999; 99US-0161822.				
XX					
PA	(MILL-) MILLENNIUM PHARM INC.				
XX					
PI	Bertin J, Robison KE;				
XX					
DR	WPI: 2001-308628/32.				
XX					
XX	P-PSDB; AA002881.				
PT	Isolated caspase recruitment domain-12 polypeptide and nucleic acids				
PT	encoding them, useful for treating and diagnosing disorders associated				
PT	with abnormal apoptosis such as cancer, arthritis and Alzheimer's				
XX	disease -				
XX					
PS	Disclosure; Fig 2; 93bp; English.				
XX					
CC	The sequence represents a genomic DNA which encodes the human caspase				
CC	recruitment domain 12 (CARD-12) polypeptide. CARD domains are found in a				
CC	number of proteins that transmit signals that activate apoptosis and				
CC	inflammatory pathways in response to stress and other stimuli. Therefore				
CC	CARD-12 and its corresponding nucleic acid may be used in treatment and				
CC	diagnosis of patients suffering from disorders associated with an				
CC	abnormal level (an increase or a decrease) of apoptotic cell death or				
CC	abnormal activity of stress-related pathways. The disorders include				
CC	cancer, viral infections (e.g. caused by poxviruses, adenoviruses),				
CC	autoimmune disorders (e.g. systemic lupus erythematosus, arthritis),				

Disclosure; Fig 2; 93pp; English.

The sequence represents a genomic DNA which encodes the human caspase recruitment domain 12 (CARD-12). polypeptide CARD domains are found in a number of proteins that transmit signals that activate apoptosis and inflammatory pathways in response to stress and other stimuli. Therefore CARD-12 and its corresponding nucleic acid may be used in treatment and diagnosis of patients suffering from disorders associated with an abnormal level (an increase or a decrease) of apoptotic cell death or abnormal activity of stress-related pathways. The disorders include cancer, viral infections (e.g. caused by poxviruses, adenoviruses), autoimmune disorders (e.g. systemic lupus erythematosus, arthritis),

CC neurological disorders (e.g. Alzheimer's disease, amyotrophic lateral sclerosis), haematologic diseases (e.g. aplastic anaemia, myocardial infarction, stroke), inflammatory and immune system disorders (e.g. Crohn's disease, insulin-dependent diabetes, contact dermatitis, psoriasis, graft rejection), bacterial infections (e.g. tuberculosis, lepromatous leprosy), ischaemic and hypoxic brain injury, kidney ischaemia/reperfusion injury, excitotoxic brain damage, acute bacterial meningitis and liver disease.

XX Sequence 3615 BP; 1041 A; 811 C; 845 G; 918 T; 0 other;

Alignment Scores:

Pred. No.:	7.95e-99	Length:	3615
Score:	829.00	Matches:	163
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	22	Gaps:	0

US-09-697-089-2\_copy\_161\_323 (1-163) x AAS03946 (1-3615)

QY 1 LeuGlnSerProCysIleIleGluGlyIleuSerGlyLysGlyLysSerThrLeuGln 20  
|||  
Db 952 CTTCAAGCCCTGCATCATTCGAAGGGAATCTGGCAAGGCAAGTCCACTCTGCTGAG 1011  
QY 21 ArgIleAlaMetLeuTrpGlySerGlyLysCysIleAlaLeuThrLysPheVal 40  
|||  
Db 1012 CGAATTGCCATGCTCTGGGGCTCCGGAAAGTGCAGAGCTGTACCAAGCTCAAAATTCGTC 1071  
QY 41 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuCysAspLeu 60  
|||  
Db 1072 TTCTTCCTCCGCTCAGAGGCGCCAGGCTTGATTTGAACCCCTGTGATCAACTC 1131  
QY 61 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 80  
|||  
Db 1132 CTGGATATACCTGGACATATGAGAACGACATCATGCCATGCTGCTGAAGCTGCGG 1191  
QY 81 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAspProGlu 100  
|||  
Db 1192 CAGAGGGTCTTTCTCTTGGATGGCTACAAATGAATTCAGGCCCAAGCTGCCAGAA 1251  
QY 101 IleGluAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValThrThrThr 120  
|||  
Db 1252 ATCGAAGCCCTGATTAAGAAACACCGCTTCAAGAACATGGTCATGCCACTACC 1311  
QY 121 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 140  
|||  
Db 1312 ACTGAGTCCCTGAGGACATACGACAGTGTGCTGCTGACTGCTGAGAGTGGGATATAG 1371  
QY 141 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGlnLeuAlaGluLys 160  
|||  
Db 1372 ACAGAGACAGCCGCCAGGCTCTATCCGAGAGTGTGATCAGAGAGCTTGTGTAAGG 1431  
QY 161 LeuLeuLeu 163  
|||  
Db 1432 TTGTTGCTC 1440

RESULT 8  
AAS26575  
ID AAS26575 standard; cDNA: 522 BP.  
XX  
AC AAS26575;  
XX  
DT 07-NOV-2001 (first entry)  
XX  
XX Human cDNA encoding a novel secreted protein, Seq ID 754.  
KW Human; immunosuppressive; antiarthritic; ss; antirheumatic;  
KW cytosolic; cardiant; vasotropic; cerebroprotective; nootropic;  
KW neuroprotective; antibacterial; vitucide; fungicide; ophthalmological;  
KW vulnerary; secreted protein; rheumatoid arthritis;  
KW hyperproliferative disorder; cardiovascular disorder; cardiac arrest;  
KW cerebrovascular disorder; cerebral ischaemia; angiogenesis;

KW nervous system disorder; Alzheimer's disease; infection; ocular disorder;  
KW corneal infection; wound healing; epithelial cell proliferation;  
KW skin ageing; food additive; preservative; antiproliferative.

OS Homo sapiens.

PN W0200155322-A2.

XX 02-AUG-2001.

PD 17-JAN-2001; 2001WO-US01341.

XX 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
PR 24-FEB-2000; 2000US-0184664.  
PR 02-MAR-2000; 2000US-0186350.  
PR 16-MAR-2000; 2000US-0189874.  
PR 17-MAR-2000; 2000US-0190076.  
PR 18-APR-2000; 2000US-0198123.  
PR 19-MAY-2000; 2000US-0205515.  
PR 07-JUN-2000; 2000US-0209467.  
PR 28-JUN-2000; 2000US-0214886.  
PR 30-JUN-2000; 2000US-0215135.  
PR 07-JUL-2000; 2000US-0216647.  
PR 07-JUL-2000; 2000US-0216880.  
PR 11-JUL-2000; 2000US-0217487.  
PR 11-JUL-2000; 2000US-0217496.  
PR 14-JUL-2000; 2000US-0218290.  
PR 26-JUL-2000; 2000US-0220963.  
PR 26-JUL-2000; 2000US-0220964.  
PR 14-AUG-2000; 2000US-0224518.  
PR 14-AUG-2000; 2000US-0224519.  
PR 14-AUG-2000; 2000US-0225213.  
PR 14-AUG-2000; 2000US-0225214.  
PR 14-AUG-2000; 2000US-0225266.  
PR 14-AUG-2000; 2000US-0225267.  
PR 14-AUG-2000; 2000US-0225268.  
PR 14-AUG-2000; 2000US-0225270.  
PR 14-AUG-2000; 2000US-0225447.  
PR 14-AUG-2000; 2000US-0225757.  
PR 14-AUG-2000; 2000US-0225758.  
PR 14-AUG-2000; 2000US-0225759.  
PR 18-AUG-2000; 2000US-0226279.  
PR 22-AUG-2000; 2000US-0226681.  
PR 22-AUG-2000; 2000US-0226868.  
PR 22-AUG-2000; 2000US-0227182.  
PR 22-AUG-2000; 2000US-0227182.  
PR 23-AUG-2000; 2000US-0228924.  
PR 30-AUG-2000; 2000US-0229287.  
PR 01-SEP-2000; 2000US-0229343.  
PR 01-SEP-2000; 2000US-0229344.  
PR 01-SEP-2000; 2000US-0229345.  
PR 05-SEP-2000; 2000US-0229509.  
PR 05-SEP-2000; 2000US-0229513.  
PR 06-SEP-2000; 2000US-0230437.  
PR 06-SEP-2000; 2000US-0230438.  
PR 06-SEP-2000; 2000US-0230438.  
PR 08-SEP-2000; 2000US-0231242.  
PR 08-SEP-2000; 2000US-0231243.  
PR 08-SEP-2000; 2000US-0231244.  
PR 08-SEP-2000; 2000US-0231413.  
PR 08-SEP-2000; 2000US-0231414.  
PR 08-SEP-2000; 2000US-0232080.  
PR 08-SEP-2000; 2000US-0232081.  
PR 12-SEP-2000; 2000US-0231968.  
PR 14-SEP-2000; 2000US-0232397.  
PR 14-SEP-2000; 2000US-0232398.  
PR 14-SEP-2000; 2000US-0232399.  
PR 14-SEP-2000; 2000US-0232400.  
PR 14-SEP-2000; 2000US-0232401.  
PR 14-SEP-2000; 2000US-0233063.  
PR 14-SEP-2000; 2000US-0233064.  
PR 14-SEP-2000; 2000US-0233065.  
PR 21-SEP-2000; 2000US-0234223.



PR 21-SEP-2000; 2000US-0234274.  
PR 25-SEP-2000; 2000US-0234997.  
PR 25-SEP-2000; 2000US-0234998.  
PR 26-SEP-2000; 2000US-0235484.  
PR 27-SEP-2000; 2000US-0235834.  
PR 27-SEP-2000; 2000US-0235836.  
PR 29-SEP-2000; 2000US-0236327.  
PR 29-SEP-2000; 2000US-0236367.  
PR 29-SEP-2000; 2000US-0236368.  
PR 29-SEP-2000; 2000US-0236369.  
PR 29-SEP-2000; 2000US-0236370.  
PR 02-OCT-2000; 2000US-0236802.  
PR 02-OCT-2000; 2000US-0237037.  
PR 02-OCT-2000; 2000US-0237038.  
PR 02-OCT-2000; 2000US-0237039.  
PR 13-OCT-2000; 2000US-0239393.  
PR 13-OCT-2000; 2000US-0239397.  
PR 20-OCT-2000; 2000US-0240960.  
PR 20-OCT-2000; 2000US-0241221.  
PR 20-OCT-2000; 2000US-0241785.  
PR 20-OCT-2000; 2000US-0241786.  
PR 20-OCT-2000; 2000US-0241787.  
PR 20-OCT-2000; 2000US-0241808.  
PR 20-OCT-2000; 2000US-0241809.  
PR 20-OCT-2000; 2000US-0241809.  
PR 01-NOV-2000; 2000US-0244617.  
PR 08-NOV-2000; 2000US-0246474.  
PR 08-NOV-2000; 2000US-0246475.  
PR 08-NOV-2000; 2000US-0246476.  
PR 08-NOV-2000; 2000US-0246477.  
PR 08-NOV-2000; 2000US-0246478.  
PR 08-NOV-2000; 2000US-0246523.  
PR 08-NOV-2000; 2000US-0246524.  
PR 08-NOV-2000; 2000US-0246525.  
PR 08-NOV-2000; 2000US-0246526.  
PR 08-NOV-2000; 2000US-0246527.  
PR 08-NOV-2000; 2000US-0246532.  
PR 08-NOV-2000; 2000US-0246532.  
PR 08-NOV-2000; 2000US-0246609.  
PR 08-NOV-2000; 2000US-0246610.  
PR 08-NOV-2000; 2000US-0246611.  
PR 08-NOV-2000; 2000US-0246613.  
PR 17-NOV-2000; 2000US-0249207.  
PR 17-NOV-2000; 2000US-0249208.  
PR 17-NOV-2000; 2000US-0249209.  
PR 17-NOV-2000; 2000US-0249210.  
PR 17-NOV-2000; 2000US-0249211.  
PR 17-NOV-2000; 2000US-0249212.  
PR 17-NOV-2000; 2000US-0249212.  
PR 17-NOV-2000; 2000US-0249213.  
PR 17-NOV-2000; 2000US-0249214.  
PR 17-NOV-2000; 2000US-0249215.  
PR 17-NOV-2000; 2000US-0249216.  
PR 17-NOV-2000; 2000US-0249217.  
PR 17-NOV-2000; 2000US-0249218.  
PR 17-NOV-2000; 2000US-0249244.  
PR 17-NOV-2000; 2000US-0249245.  
PR 17-NOV-2000; 2000US-0249264.  
PR 17-NOV-2000; 2000US-0249265.  
PR 17-NOV-2000; 2000US-0249287.  
PR 17-NOV-2000; 2000US-0249297.  
PR 17-NOV-2000; 2000US-0249299.  
PR 17-NOV-2000; 2000US-0249300.  
PR 01-DEC-2000; 2000US-0250160.  
PR 01-DEC-2000; 2000US-0250391.  
PR 05-DEC-2000; 2000US-0251030.  
PR 05-DEC-2000; 2000US-0251968.  
PR 05-DEC-2000; 2000US-0251968.  
PR 06-DEC-2000; 2000US-0251479.  
PR 08-DEC-2000; 2000US-0251856.  
PR 08-DEC-2000; 2000US-0251856.  
PR 08-DEC-2000; 2000US-0251868.  
PR 08-DEC-2000; 2000US-0251869.  
PR 08-DEC-2000; 2000US-0251989.  
PR 08-DEC-2000; 2000US-0251990.

PR 11-DEC-2000; 2000US-0254097.  
PR 05-JAN-2001; 2001US-0259678.  
XX  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX PI Rosen CA, Barash SC, Ruben SM;  
XX  
XX DR WPI; 2001-488783/53.  
DR P-PSDB; AAU16588.  
XX  
PT New nucleic acid molecules encoding 461 human secreted proteins for  
PT diagnosing, preventing, treating or ameliorating medical conditions and  
PT used as food additives or preservatives -  
XX  
XX  
PS Claim 1; SEQ ID NO 754; 980pp; English.

CC The invention relates to isolated nucleic acid molecules and their  
CC encoded secreted proteins. The nucleic acids and proteins are used to  
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,  
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They  
CC are also used in diagnosing a pathological condition or susceptibility  
CC to a pathological condition. Antibodies to the proteins can also  
CC be used in alleviating symptoms associated with the disorders and in  
CC diagnostic immunoassays e.g. radioimmunoassays or enzyme linked  
CC immunosorbant assays (ELISA). Disorders which are diagnosed or treated  
CC include autoimmune diseases e.g. rheumatoid arthritis,  
CC hyperproliferative disorders e.g. neoplasms of the breast or liver,  
CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders  
CC e.g. cerebral ischemia, angiogenesis, nervous system disorders e.g.  
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi  
CC and ocular disorders e.g. corneal infection, and many other  
CC disorders listed in the specification. The polypeptides can also  
CC be used to aid wound healing and epithelial cell proliferation, to  
CC prevent skin aging due to sunburn, to maintain organs before  
CC transplantation, for supporting cell culture of primary tissues, to  
CC regenerate tissues and in chemotaxis. The polypeptides can also be used  
CC as a food additive or preservative to increase or decrease storage  
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,  
CC minerals, cofactors and other nutritional components. The present  
CC sequence encodes a novel secreted protein of the invention.

## Alignment Scores:

Pred. No.: 6.88e-27 Length: 522  
Score: 276.00 Matches: 69  
Percent Similarity: 81.11% Conservative: 4  
Best Local Similarity: 76.67% Mismatches: 13  
Query Match: 33.29% Indels: 6  
DB: 22 Gaps: 1

US-09-697-089-2\_COPY\_161\_323 (1-163) x AAS26575 (1-522)

QY 1 LeuGlnSerProCysIleIleGluGluSerGlyLysGlyLysSerThrLeuGln 20  
DB 246 CTTGAGACCCCTTCATCATTTGAAGGGGAATCTGGCAAGGCAAGTCATTCTGCTCAG 305  
QY 21 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheVa 40  
DB 306 CGCATTCGCATGCTCTGGGGCTCCGGAAGTGAAGGCTGTGACCAAGTTTCANTTGGT 365  
QY 40 Lphe-PheLeuArgLeuSerArgAlaGlnGly-GlyLeuPheGluThrLeuCysASPgl 59  
DB 366 CTTCTTCCTCCTGTTGACGAGGCCGAGGCTGAGCACTTTTAAACCTCTGTGATCAAA 425  
QY 60 LeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLysLeu 79  
DB 426 TTCCG-GGTATACGGGACA-TTCAGAGAGGAGACATTCAAGCCNGGT---GCTGAGGTG 480  
QY 80 ArgGlnArgValLeuPheLeuLeu 87  
DB 481 CGGCAAGAGGGTTCTTTCNTCTTG 504  
RESULT 9  
AAS58001

ID AAX58001 standard; cDNA to mRNA; 5366 BP.  
XX AAX58001;  
AC  
DT 20-JUL-1999 (first entry)  
XX  
DE Gonadotropic hormone coding sequence.  
XX  
KW Gonadotropic hormone; excessive ovulation animal; transgenic animal;  
KM totipotent cell; somatic cell chromosome; ds.  
XX  
OS Homo sapiens.  
XX JP1113444-A.  
XX  
PD 27-APR-1999.  
XX  
PF 14-OCT-1997; 97JP-0280830.  
XX  
PR 14-OCT-1997; 97JP-0280830.  
XX  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
XX (SAKA/) SAKAI H.  
DR WPI; 1999-320709/27.  
XX P-PSDB; AAY14080.  
XX  
XX An excessive ovulation animal - useful for improving the  
PT productivity of animals  
XX  
XX Claim 1; Page 9-11; 18pp; Japanese.  
XX  
CC This sequence encodes a gonadotropic hormone.  
CC The invention relates to an excessive ovulation animal, which is a  
CC transgenic animal with a totipotent cell containing a DNA fragment  
CC containing a promoter sequence and a gonadotropic hormone coding  
CC sequence. The DNA fragment is in the somatic cell chromosome. The  
CC excessive ovulation animal is useful for improving the productivity of  
CC animals. The method can improve the productivity of a useful animal.  
XX  
SQ Sequence 5366 BP; 1483 A; 1173 C; 1222 G; 1488 T; 0 other;  
  
Alignment Scores:  
Pred. No.: 3,266-20 Length: 5366  
Score: 236.50 Matches: 53  
Percent Similarity: 58.96% Conservative: 26  
Best Local Similarity: 39.55% Mismatches: 48  
Query Match: 28.53% Indels: 7  
DB: Gaps: 3  
US-09-697-089-2\_COPY\_161\_323 (1-163) x AAX58001 (1-5366)  
QY 1 LeuGlnSerProCysIleIleGlnGlyIleuSerGlyLysGlyLysSerThrLeuGln 20  
Db 1675 TTGAACCTCTGCATGCTGTGGAGCTGAGCTGGAAGTGAAGACGCTCCTGGAAG 1734  
QY 21 ArgIleAlaMetLeuTrpGlySerGlyLysGlyLysAlaLeuThrLysPheIleVal 40  
Db 1735 AAAATAGCTTTTCTGTGGGCACTGTGATGCTGCCCTGTTAAACAGGTTCCAGCTGTT 1794  
QY 41 PhePheLeuArgLeuSer-----ArgAlaGlnGlyLeuPheGluThrLeuGlyasp 58  
Db 1795 TTTCACCTCTCCCTTAGTCCACGACGACGAGGAGGCTGGCCAGATATCTGTAC 1854  
QY 59 GlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLys 78  
Db 1855 CAGCTCCTCAGAGAAAGAGATCTGTACTGAATGTGCATGAGAACATATATCCAGCAG 1914  
QY 79 LeuArgGlnArgValIleuPheLeuLeuAspGlyIleArgLysGlnPhe-----LysProGln 96  
Db 1915 TTTAAGATTCAGGTCTTATCTTCTTATGATGACTACAAAGAAATATGTCTCAATCCCTCAA 1974  
QY 97 AsnGlyProGluIleGluAlaLeuIleLysGlnLysAsnHisArgPheLysAsnMetValIle 116

Db 1975 -----GTCATAGGAAGAACTGATTCACAAAACACATATATCCGAGACCTGCTATTG 2025  
QY 117 ValThrThrThrThrGlnCysLeuArgHisIleArgGlnPhe 130  
Db 2026 ATTGCTGTCCGTAACAACAGGCGCAGGACATCCCGCATAC 2067  
RESULT 10  
AAX56273  
ID AAX56273 standard; cDNA to mRNA; 5366 BP.  
XX AAX56273;  
AC  
XX 20-JUL-1999 (first entry)  
XX  
DE Human apoptosis inhibiting protein encoding cDNA #2.  
XX  
XX Human; apoptosis inhibitory protein; apoptotic disease; diagnosis;  
KW spinal muscular atrophy; ds.  
XX  
OS Homo sapiens.  
XX JP1116599-A.  
XX  
PD 27-APR-1999.  
XX  
PF 14-OCT-1997; 97JP-0280831.  
XX  
PR 14-OCT-1997; 97JP-0280831.  
XX  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
XX WPI; 1999-323531/27.  
XX P-PSDB; AAY09540.  
XX  
XX New apoptosis inhibitory protein - useful for determining mechanism  
PT of various apoptotic diseases e.g. human spinal muscular atrophy  
XX  
XX Claim 8; Page 13-15; 16pp; Japanese.  
XX  
CC The present sequence encodes a human apoptosis inhibitory protein.  
CC The apoptosis inhibitory protein is useful for the elucidation of  
CC the mechanism of various apoptosis diseases such as human spinal  
CC muscular atrophy and the diagnosis, the prevention and the treatment  
CC of such diseases.  
XX  
SQ Sequence 5366 BP; 1483 A; 1173 C; 1222 G; 1488 T; 0 other;  
  
Alignment Scores:  
Pred. No.: 3,266-20 Length: 5366  
Score: 236.50 Matches: 53  
Percent Similarity: 58.96% Conservative: 26  
Best Local Similarity: 39.55% Mismatches: 48  
Query Match: 28.53% Indels: 7  
DB: Gaps: 3  
US-09-697-089-2\_COPY\_161\_323 (1-163) x AAX56273 (1-5366)  
QY 1 LeuGlnSerProCysIleIleGlnGlyIleuSerGlyLysGlyLysSerThrLeuGln 20  
Db 1675 TTGAACCTCTGCATGCTGTGGAGCTGAGCTGGAAGTGAAGACGCTCCTGGAAG 1734  
QY 21 ArgIleAlaMetLeuTrpGlySerGlyLysGlyLysAlaLeuThrLysPheIleVal 40  
Db 1735 AAAATAGCTTTTCTGTGGGCACTGTGATGCTGCCCTGTTAAACAGGTTCCAGCTGTT 1794  
QY 41 PhePheLeuArgLeuSer-----ArgAlaGlnGlyLeuPheGluThrLeuGlyasp 58  
Db 1795 TTTCACCTCTCCCTTAGTCCACGACGACGAGGAGGCTGGCCAGATATCTGTAC 1854  
QY 59 GlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLys 78  
Db 1855 CAGCTCCTCAGAGAAAGAGATCTGTACTGAATGTGCATGAGAACATATATCCAGCAG 1914

Oy		79	leuarglAlarValIleupheleuleAspGlyTyrAsnIuphe-----LysProGln	96
Oy		79	:   :	
Db		1915	TTRAAAGATACGGCTCTATTATTCCTTTAGACTCAAGAATAATATTGCATCCCTCAA	1974
Oy		97	AsnCysProGIuLeGIuAlaleuileLysGluAsnHisArghelYsAsnMetValIle	116
Db		1975	-----GTCAATAGGAATAAAGTAGATTCANAAAAAACACCATTCATCCGAGCACCCTCATTTG	2025
Oy		117	ValThrThrThrTrglucylSleuArghisIleArgIinPhe	130
Db		2026	ATTGCTGTCCGTACAACAGCGGACGAGGACATCCGCCGATAC	2067
RESULT 11				
ID	AAT30092	standard; cDNA; 5502 BP.		
XX				
AC	AAT30092;			
XX				
DT	30-DEC-1996	(first entry)		
DE		Neuronal apoptosis inhibiting protein coding sequence.		
XX				
KM		Neuronal apoptosis inhibiting protein; human; NAIP; chromosome 5q13; YAC;		
KM		yeast artificial chromosome; spinal muscular atrophy; mammalian cell;		
KM		autosomal recessive; neurodegenerative disorder; alpha motor neuron; SMA;		
KM		spinal cord; proximal voluntary muscle; therapy; apoptotic mechanism; ss.		
XX				
OS	Homo sapiens.			
XX				
FH	Key	Location/Qualifiers		
FT	CDS	396..4094		
FT		/tag= a		
FT		/product= neuronal apoptosis inhibiting protein		
XX				
PN		W09612016-A1.		
XX				
PD	25-APR-1996.			
XX				
PE	17-OCT-1995;	95WO-CA00581.		
XX				
PR	19-DEC-1994;	94CA-2138425.		
PR	18-OCT-1994;	94GB-0021019.		
XX				
PA	(SHKJ ) RES DEV CORP JAPAN.			
PA	(UYOT-) UNIV OTTAWA.			
XX				
PI	Ikega J, Korneluk RG, Mackenzie AE, Mahadevan MS;			
PI	McLean M, Roy N;			
DR	WPI: 1996-222003/22.			
XX	P-PsDB; AAR89217.			
PT		Neuronal apoptosis inhibitor protein gene - used to develop prods.		
PT		for use in the diagnosis and therapy of spinal muscular atrophy		
PS	Claim 4; Page 64-67; 113pp; English.			
XX				
CC	This sequence represents the cDNA sequence for the human neuronal			
CC	apoptosis inhibitor protein (NAIP). This sequence was found on a region			
CC	of the human chromosome 5q13. This sequence was isolated from a yeast			
CC	artificial chromosome (YAC) contig containing the DS5435-DS112 interval			
CC	of the chromosome 5q13. Mutations in this gene, are causative of spinal			
CC	muscular atrophy (SMA) types I, II, and III. SMAs are a group of			
CC	autosomal recessive, neurodegenerative disorders. SMAs are classified			
CC	into three types based upon the age of onset (with type I being the			
CC	characterised form with the earliest age of onset). All three types are			
CC	characterised by the degeneration of the alpha motor neurons of the			
CC	spinal cord manifesting as weakness and wasting of the proximal voluntary			
CC	muscles. The most common mutations of this sequence are thought to be			
CC	deletions of exons 5 and 6, and reductions in the copy number of the			
CC	gene. This gene, (and primers and probes based on this gene) can be used			
CC	for the diagnosis of SMA, and for directing the formulation of			

[illegible]

DR WPI: 1997-38535/35.  
XX New neuronal inhibitor of apoptosis - useful for diagnosing and  
PT treating, e.g. cancer, AIDS or amyotrophic lateral sclerosis  
XX  
XX Example 4; Fig 5A-L; 102pp; English.  
XX  
XX A new neuronal apoptosis inhibitor protein (NAIP) cDNA clone  
CC (AA71263) was isolated from a human foetal spinal cord cDNA library  
CC by probing with the genomic insert in cosmid 25086, containing a  
CC CAAT locus. An additional coding sequence (AA71264), including  
CC exon 14a (see also AA71265 and AA71266), was subsequently obtd.  
CC The NAIP DNA sequence including exon 14a appears to be a  
CC predominant gene isoform which is not deleted or mutated in spinal  
CC muscular atrophy (SMA) patients. The NAIP gene was mapped to  
CC 5q13.1. NAIP (see also AA720032 and AA720033) is a negative regulator  
CC of apoptosis, partic. neuronal apoptosis and, when deficient or  
CC absent, contributes to neurodegenerative phenotypes such as SMA and  
CC amyotrophic lateral sclerosis.  
XX  
SQ Sequence 5502 BP; 1560 A; 1226 C; 1206 G; 1510 T; 0 other;  
  
Alignment Scores:  
Pred. No.: 3.38e-20 Length: 5502  
Score: 236.50 Matches: 53  
Percent Similarity: 58.96% Conservative: 26  
Best Local Similarity: 39.55% Mismatches: 48  
Query Match: 28.53% Indels: 7  
DB: 18 Gaps: 3  
  
US-09-697-089-2\_COPY\_161\_323 (1-163) x AA71263 (1-5502)  
OY 1 LeuGlnSerProCysIleIleGlnGlyGlnSerGlyLysSerThrLeuGln 20  
DB 1779 TTGAACCTGTCATGTCGTGTGGAGGTGAAGCTGGAAGACGGCTCTCTGAAG 1838  
OY 21 ArgIleAlaMetLeuTrpGlySerGlyLysAlaLeuThrLysPheLysPheVal 40  
DB 1839 AAAATAGCTTTTCTGTGGCATCTGATGCTCTCCCTGTTAAACAGGTTCCAGCTGGTT 1898  
OY 41 PhePheLeuArgLeuSer-----ArgAlaGlnGlyLysLeuPheGlnThrLeuGln 58  
DB 1899 TTCTACCTCTCCCTTAGTTCACACAGACAGAGGGGCTGGCAGTATCATCTGTGAC 1958  
OY 59 GlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLys 78  
DB 1959 CAGCTCCTAGAGAAAGAGATCTGTACTGAATGTCATGAGAGACATTATCCAGCAG 2018  
OY 79 LeuArgGlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPhe-----LysProGln 96  
DB 2019 TTAAGAAATCAAGCTTATCTTTCCTTTAGATGACTCAAAAGAAATATGTTCAATCCCTCAA 2078  
OY 97 AsnGlyProGluIleGlnAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIle 116  
DB 2079 -----GTCATAGGAAGAACTGATTCAAAAAACCACTATCCCGGACCTGCTATTG 2129  
OY 117 ValThrThrThrThrGlnCysLeuArgHisIleArgGlnPhe 130  
DB 2130 ATTGCTGTCCGTACAAACAGGCCAGGACATCCGCCGATAC 2171  
  
RESULT 13  
AAK58000 ID AAK58000 standard; cDNA to mRNA; 5984 BP.  
XX  
XX AAK58000;  
AC  
XX  
XX 20-JUL-1999 (first entry)  
DE  
XX Gonadotropic hormone coding sequence.  
XX  
XX Gonadotropic hormone; excessive ovulation animal; transgenic animal;  
KW totipotent cell; somatic cell chromosome; ds.  
XX

OS Homo sapiens.  
XX  
XX JP11113444-A.  
XX  
XX 27-APR-1999.  
XX  
XX 14-OCT-1997; 97JP-0280830.  
XX  
XX 14-OCT-1997; 97JP-0280830.  
XX  
XX 14-OCT-1997; 97JP-0280830.  
XX  
XX (KAGA-) KAGAKU GIUTSU SHINKO JIGYODAN.  
XX (SAKA/) SAKAI H.  
XX  
XX WPI: 1999-320709/27.  
XX P-PSDB: AAV14079.  
XX  
XX  
XX Claim 1; Page 7-9; 18pp; Japanese.  
XX  
XX This sequence encodes a gonadotropic hormone.  
XX The invention relates to an excessive ovulation animal, which is a  
XX transgenic animal with a totipotent cell containing a DNA fragment  
XX containing a promoter sequence and a gonadotropic hormone coding  
XX sequence. The DNA fragment is in the somatic cell chromosome. The  
XX excessive ovulation animal is useful for improving the productivity of  
XX animals. The method can improve the productivity of a useful animal.  
XX  
SQ Sequence 5984 BP; 1777 A; 1267 C; 1267 G; 1673 T; 0 other;  
  
Alignment Scores:  
Pred. No.: 3.81e-20 Length: 5984  
Score: 236.50 Matches: 53  
Percent Similarity: 58.96% Conservative: 26  
Best Local Similarity: 39.55% Mismatches: 48  
Query Match: 28.53% Indels: 7  
DB: 20 Gaps: 3  
  
US-09-697-089-2\_COPY\_161\_323 (1-163) x AAK58000 (1-5984)  
OY 1 LeuGlnSerProCysIleIleGlnGlyGlnSerGlyLysSerThrLeuGln 20  
DB 1675 TTGAACCTGTCATGTCGTGTGGAGGTGAAGCTGGAAGACGGCTCTCTGAAG 1734  
OY 21 ArgIleAlaMetLeuTrpGlySerGlyLysAlaLeuThrLysPheLysPheVal 40  
DB 1735 AAAATAGCTTTTCTGTGGCATCTGATGCTCTCCCTGTTAAACAGGTTCCAGCTGGTT 1794  
OY 41 PhePheLeuArgLeuSer-----ArgAlaGlnGlyLysLeuPheGlnThrLeuGln 58  
DB 1795 TTCTACCTCTCCCTTAGTTCACACAGACAGAGGGGCTGGCAGTATCATCTGTGAC 1854  
OY 59 GlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLys 78  
DB 1855 CAGCTCCTAGAGAAAGAGATCTGTACTGAATGTCATGAGAAATATGTTCAATCCCTCAA 1914  
OY 79 LeuArgGlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPhe-----LysProGln 96  
DB 1915 TTAAGAAATCAAGCTTATCTTTCCTTTAGATGACTCAAAAGAAATATGTTCAATCCCTCAA 1974  
OY 97 AsnGlyProGluIleGlnAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIle 116  
DB 1975 -----GTCATAGGAAGAACTGATTCAAAAAACCACTTATCCCGGACCTGCTATTG 2025  
OY 117 ValThrThrThrThrGlnCysLeuArgHisIleArgGlnPhe 130  
DB 2026 ATTGCTGTCCGTACAAACAGGCCAGGACATCCGCCGATAC 2067  
  
RESULT 14  
AAK56272 ID AAK56272 standard; cDNA to mRNA; 5984 BP.  
XX





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GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus.p2n model

Run on: January 31, 2003, 11:50:07 ; Search time 1331.94 Seconds

(without alignments)  
1981.965 Million cell updates/sec

Title: US-09-697-089-2\_COPY\_161\_323

Perfect score: 829

Sequence: 1 LQSPCTIEGSGKSKTLQ.....SAQALIREVLIKEAGILL 163

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+g2n.model -DEV=xlh  
-O=/cgn2\_1/USPTO.spool/US09697089/runat\_29012003\_092754\_19729/app\_query.fasta.1.981  
-DB=ST -QFMT=faaap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOPEXT=0  
-UNITS-bits -START=1 -END=1 -MATRIX=blousum62 -TRANS=humand0.cdi -LIST=45  
-DOCLALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09697089 -GCN 1.1 -1985 -grunat\_29012003\_092754\_19729 -NCPU=6 -ICPU=3  
-NO\_XLPY -NO\_MMAP -LARGEOUTERY -NEG\_SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120  
-WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEX=7

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vit:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rtd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	612	75.0	650	10	BB627584
2	318	38.4	619	17	BH267158
3	274	33.1	518	17	BH348412
4	272	32.8	817	17	BH358172
5	231.5	27.9	1058	13	BM477340
6	226	27.3	697	17	BH293386
7	139.5	16.8	546	17	AZ362463
8	135	16.3	668	17	AZ762115
9	133.5	16.1	515	14	BQ365804
10	123	14.8	728	9	AL652549
11	121.5	14.7	556	17	AZ941653
12	120	14.5	345	13	BG994836
13	116	14.0	586	13	BG994334
14	110	13.3	361	10	AW504276
15	105.5	12.7	939	12	BE887277
16	103	12.4	981	17	AZ138405
17	98.5	11.9	302	9	AA853292
18	96	11.6	740	13	B1685879
19	95.5	11.5	1156	12	BE731237
20	94.5	11.4	959	10	BE468715
21	94	11.3	870	12	BG745278
22	93.5	11.3	782	17	AZ137956
23	93	11.2	409	9	AA997492
24	91	11.0	1039	17	CNS02NVI
25	90.5	10.9	523	17	AZ171618
26	88.5	10.7	3368	11	BC021272
27	88.5	10.7	3369	11	BC012789
28	87	10.5	538	17	AZ192862
29	86.5	10.4	844	17	AZ209193
30	86	10.4	894	9	AL544013
31	85.5	10.3	708	10	BE374417
32	85.5	10.3	891	17	AZ202697
33	85	10.3	464	12	BE932231
34	85	10.3	691	9	AI344276
35	84	10.1	418	13	BJ228034
36	84	10.1	473	9	AI698228
37	84	10.1	670	10	BB633515
38	83	10.0	699	9	AL505087
39	83	10.0	993	12	BE902227
40	83	10.0	1098	13	BM547125
41	82	9.9	420	17	AZ161566
42	81.5	9.8	831	17	BH467737
43	81	9.8	682	13	BJ215942
44	80.5	9.7	639	9	AU239615
45	80.5	9.7	639	12	BF325534

#### ALIGNMENTS

RESULT 1  
LOCUS BB627584  
DEFINITION BB627584 RIKEN full-length enriched, adult male urinary bladder Mus  
MUSCULUS CDNA clone 9530011P19 5', mRNA sequence.  
ACCESSION BB627584  
VERSION BB627584.1 GI:16465218  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus

REFERENCE  
AUTHORS  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
I (bases 1 to 650)  
Araiawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanaagaki,T., Hara,A.,  
Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,T., Konno,H., Kouda





/A., Gedreggeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, R.

TITLE  
JOURNAL  
COMMENT

Jong, P. and Fraser, C.M.  
Rat BAC End Sequences from Library CHORI-230 EcORI segment  
Unpublished (1999)  
Other GSS: CH230-18E7.TVB  
Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230  
(<http://www.chori.org/bacpac/rat230.htm>). For BAC library  
availability, please contact Pieter de Jong ([pdejong@mail.cho.org](mailto:pdejong@mail.cho.org)).  
Clones may be purchased from BACPAC Resources  
([http://www.chori.org/bacpac/orering\\_information.htm](http://www.chori.org/bacpac/orering_information.htm)). BAC end  
page: [http://www.tigr.org/tdb/bac\\_ends/rat/bac\\_end\\_intro.html](http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html)  
Plate: 18 row: E column: 7  
Seq primer: SP6  
Class: BAC ends.

FEATURES  
source  
Location/Qualifiers

1..817  
/organism="Rattus norvegicus"  
/strain="BN/SSNhsd/MCW"  
/db\_xref="taxon:10116"  
/clone\_lib="CH230-18E7"  
/clone\_1ib="CHORI-230 segment 1"  
/sex="Female"  
/cell\_type="Brain"  
/note="Vector: PTARBAC2.1. Site\_1: EcORI; Site\_2: EcORI;  
CHORI-230 Rat (BN/SSNhsd/MCW) BAC library produced by  
Pieter de Jong"

BASE COUNT 211 a 182 c 199 g 225 t  
ORIGIN

Alignment Scores:  
Pred. No.: 8.55e-26 Length: 817  
Score: 272.00 Matches: 61  
Percent Similarity: 84.88% Conservative: 12  
Best Local Similarity: 70.93% Mismatches: 13  
Query Match: 32.81% Indels: 2  
DB: 17 Gaps: 0

US-09-697-089-2\_COPY\_161\_323 (1-163) x BH358172 (1-817)

QY 1 LeuGlnSerProCysIleIleGlnGlyGluSerGlyLysGlyLysSerThrLeuGln 20  
|||||  
Db 256 CTGAAGAGTCCCTGCGCATGTGAAGGGAGTCTGGCAAGGAGTCCACCTCTGCA 197  
QY 21 ArgIleAlaMetLeuThrPglySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40  
:::|||||  
Db 196 AAAATTGCCATGCTCTGGGCTCTGGGATGTCGCCACCTCTGAACCAAGTTCAATTGGTCT 137  
QY 41 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLysCysAspGlnLeu 60  
|||||  
Db 136 TTCTTCATCCGCTGAGCAGTGTGAGGGGTGGCTGTGTAACATTGTA-GATCAGCTC 78  
QY 61 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 80  
:::|||||  
Db 77 GTGAACATACCTGACTGATCAGCAACCAACCTTCAAGGGCTCTGCTGCT-AACTTACAC 19  
QY 81 GlnArgValLeuPheLeu 86  
:::|||||  
Db 18 AAGAAAGTCTCTTCTC 1

RESULT 5  
BM477340/c 1058 bp mRNA linear EST 05-FEB-2002  
LOCUS BM477340  
DEFINITION AGENCOURT\_6485124 NIH\_MGC\_85 Homo sapiens cDNA clone IMAGE:5554120  
5', mRNA sequence.  
ACCESSION BM477340  
VERSION BM477340.1 GI:18526382  
KEYWORDS EST.

SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 1058)  
NIH-MGC <http://mgs.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabs@mail.nih.gov](mailto:cgabs@mail.nih.gov)  
Tissue Procurement: Lou Staudt  
cDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM12272 row: c column: 17  
High quality sequence stop: 604.

FEATURES  
source  
Location/Qualifiers

1..1058  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_image="5554120"  
/clone\_1ib="NIH\_MGC\_85"  
/tissue\_type="lymphoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: lymph. Vector: pCMV-Sport6; Site\_1: NotI;  
Site\_2: SalI. Cloned unidirectionally; oligo-dT primed.  
Average insert size 1.867 kb. Library enriched for  
full-length clones and constructed by Life Technologies.  
Note: this is a NIH-MGC library."

BASE COUNT 297 a 251 c 243 g 264 t 3 others  
ORIGIN

Alignment Scores:  
Pred. No.: 3.38e-20 Length: 1058  
Score: 231.50 Matches: 52  
Percent Similarity: 58.21% Conservative: 26  
Best Local Similarity: 38.81% Mismatches: 49  
Query Match: 27.93% Indels: 7  
DB: 13 Gaps: 3

US-09-697-089-2\_COPY\_161\_323 (1-163) x BM477340 (1-1058)

QY 1 LeuGlnSerProCysIleIleGlnGlyGluSerGlyLysGlyLysSerThrLeuGln 20  
|||||  
Db 723 TTGAACCTGTCATGTCGTGGAGGTGAAGCTGGAAGTGAAGAGCGTCTCTGTAAG 664  
QY 21 ArgIleAlaMetLeuThrPglySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40  
:::|||||  
Db 663 AAAATACCTTTCTGTCGGCATCTGCATGCTGCCCTGTTAAACAGGTCCAGCTGTGTT 604  
QY 41 PhePheLeuArgLeuSer-----ArgAlaGlnGlyLysGluPheGluThrLysCysAsp 58  
|||||  
Db 603 TTCTACCTCTCCCTTACTTCCACCAAGACAGAGAGGGCTGGCCAGTATCATCTGTGAC 544  
QY 59 GlnLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLys 78  
|||||  
Db 543 CAGCTCTCAGAGAAGAGATCTGTTACTGAATGATGCAATGAGAACATTATCCAGAC 484  
QY 79 LeuArgGlnArgValLeuPheLeuAspLysPheLysPheLysPheLysPheLysPhe 96  
|||||  
Db 483 TTAAAGATCAGCTTATCTTTTGAAGACACAAAGAAATATGTTCAATCCCTCA 424  
QY 97 AsnGlyProGluIleGlnAlaLeuIleLysGlnLysHisArgPheLysAsnMetValIle 116  
|||||  
Db 423 -----GTCAATGAGAAATGATTCATAAAACCACTTATCCCGGACCTGCTATTG 373  
QY 117 ValThrThrThrThrGluCysLeuArgHisIleArgGlnPhe 130  
:::|||||  
Db 372 ATTGCTGTCGTACAAACAGGCGCAGGACATCCGCCGATAC 331

RESULT 6  
BH293386  
LOCUS  
DEFINITION BH293386 697 bp DNA linear GSS 30-NOV-2001  
CH230-44G15.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone  
ACCESSION BH293386  
VERSION BH293386.1 GI:17205794  
KEYWORDS GSS.  
SOURCE Norway rat.  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
REFERENCE 1 (bases 1 to 697)  
Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shwartsbeyn  
, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de  
Jong, P. and Fraser, C.M.  
Rat BAC End Sequences from Library CHORI-230 EcoRI segment  
Unpublished (1999)  
OTHER\_GSS: CH230-44G15.TJ  
COMMENT  
TITLE Department of Eukaryotic Genomics  
JOURNAL The Institute for Genomic Research  
COMMENT 9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhao@tigr.org  
Clones are derived from the rat BAC library CHORI-230  
(http://www.chori.org/bacpac/rat230.htm). For BAC library  
availability, please contact Pieter de Jong (pdejong@mail.cho.org).  
Clones may be purchased from BACPAC Resources  
(http://www.chori.org/bacpac/ordering/information.htm). BAC end  
page: http://www.tigr.org/tdb/bac\_ends/rat/bac\_end\_intro.html  
Plate: 44 Row: 6 Column: 15  
Seq primer: T7  
Class: BAC ends.  
Location/Qualifiers  
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/organism="Rattus norvegicus"  
/strain="BN/SSNhsd/MCW"  
/db\_xref="taxon:10116"  
/clone="CH230-44G15"  
/clone\_lib="CHORI-230 Segment 1"  
/sex="Female"  
/cell\_type="Brain"  
/note="Vector: pVBARAC2.1; Site\_1: EcoRI; Site\_2: EcoRI;  
CHORI-230 Rat (BN/SSNhsd/MCW) BAC library produced by  
Pieter de Jong"

BASE COUNT 182 a 165 c 190 g 160 t  
ORIGIN

Alignment Scores:  
Pred. No.: 1,05e-19 Length: 697  
Score: 226.00 Matches: 50  
Percent Similarity: 89.47% Conservative: 1  
Best Local Similarity: 87.72% Mismatches: 6  
Query Match: 27.26% Indels: 1  
DB: 17 Gaps: 0

US-09-697-089-2\_COPY\_161\_323 (1-163) x BH293386 (1-697)

QY 106 LysGluSnhHsArGpHeLysAsmEtValLLeValThrThrThrThrThrGluCysLeuArg 125  
|||||  
DB 11 AAGGAAACCAATGCG-TTTAAGAACATGGTCATTGTCCACACACCGAGTGCCTGAGG 69  
|||||

QY 126 HisLeaRgGlnPheGlyAlaLeuThraLagLuValGlyAspMetThrGluAspSerAla 145  
|||||  
DB 70 CACATTCAGACACGCTTGGCGCCCTGACTGTGAGGTGGAGATATGACCGAAGACAGCCGCC 129  
|||||

QY 146 GlnAlaLeuLeaRgGlnValLeuLeuLeuLysGluLeuAlaGluGlyLeuLeu 162  
::: |||||||  
DB 130 CGAGTTCATCCGCGAAGTGTGATAATGAACTGAGCTGAAGGCTTGTG 180  
|||||

RESULT 7  
AZ362463/c  
LOCUS  
DEFINITION AZ362463 546 bp DNA linear GSS 02-OCT-2000  
1M0107N03R Mouse 10kb plasmid U06C1M library Mus musculus genomic  
clone U06C1M0107N03 R, DNA sequence.  
ACCESSION AZ362463  
VERSION AZ362463  
KEYWORDS AZ362463.1 GI:10476163  
GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 546)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.  
and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
COMMENT  
TITLE Contact: Robert B. Weiss  
JOURNAL University of Utah  
COMMENT Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0107 row: N column: 03  
Seq primer: CACACAGCAACACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 546.  
Location/Qualifiers  
1..546  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="U06C1M0107N03"  
/clone\_lib="Mouse 10kb plasmid U06C1M library"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnars/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMDA2 (g11473211419b1AFL29072.1) a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT 151 a 111 c 139 g 144 t 1 others  
ORIGIN

Alignment Scores:  
Pred. No.: 3.17e-08 Length: 546  
Score: 139.50 Matches: 37  
Percent Similarity: 51.75% Conservative: 22  
Best Local Similarity: 32.46% Mismatches: 48  
Query Match: 16.83% Indels: 7  
DB: 17 Gaps: 3

US-09-697-089-2\_COPY\_161\_323 (1-163) x AZ362463 (1-546)



Project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?l1=MR2&l2=MR2-GN0030-210900-021-b10&l3=2000-09-21&l4=1>)



Oy 21 ArgIIeAlaMetLeuTrpGlySerGlyScylsAlaLeuThrIysPheIysPheVal 40  
Db 113 AAAATAGCTTTCTGTGGCATGTGATGCTGTCCCTGTAAACAGGTTCCAGCTGGTT 54  
Oy 41 PhePheIysArgIysSerArgAlaGlnGly 51  
Db 53 TTCTACACCTCCCTTGACTCCACGAGACAGGT 21

RESULT 13  
Bg994334/c 586 bp mRNA linear EST 13-JUN-2001  
LOCUS PM0-HT1166-130201-003-cl1 HT1166 Homo sapiens cDNA, mRNA sequence.  
Bg994334  
Bg994334.1 GI:14398404  
VERSION EST.  
KEYWORDS  
ORGANISM human.  
SOURCE Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 586)  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Britones, M.R.,  
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,  
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare  
, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
Simpson, A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
2020263  
COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/ICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM0&cl2=PM0-HT1166-  
130201-003-cl1&cl3=2001-02-13&cl4=1)  
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High quality sequence start: 3  
High quality sequence stop: 586.  
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/db\_xref="taxon:9606"  
/clone\_lib="HT1166"  
/dev\_stage="Adult"  
/note="Organ: head,neck; Vector: puc18; Site\_1: SmaI;  
Site\_2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. letters patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."  
BASE COUNT 156 a 145 c 137 g 147 t 1 others  
ORIGIN

Alignment Scores:  
Pred. No.: 5.03e-05 Length: 586  
Score: 116.00 Matches: 21  
Percent Similarity: 69.05% Conservative: 8  
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Query Match: 13.99% Indels: 0  
DB: 13 Gaps: 0

US-09-697-089-2\_COPY\_161\_323 (1-163) x Bg994334 (1-586)  
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Db 158 TTGACTCTGTGATGTGTGTGAGGTGAGTGAAGTGAAGGAAACGGTCTCTGTAAG 99  
Oy 21 ArgIIeAlaMetLeuTrpGlySerGlyScylsAlaLeuThrIysPheIysPheVal 40  
Db 98 AAAATAGCTTTCTGTGGCATGTGATGCTGTCCCTGTAAACAGGTTCCAGCTGGTT 39  
Oy 41 PhePhe 42  
Db 38 TTCTAC 33

RESULT 14  
AM504276 361 bp mRNA linear EST 02-MAR-2000  
LOCUS AM504276  
DEFINITION UT-HF-BNO-21P-g-07-0-UT.r1 NIH\_MGC\_50 Homo sapiens cDNA clone  
IMAGE:3080628 5', mRNA sequence.  
AM504276  
AM504276.1 GI:7141931  
VERSION EST.  
KEYWORDS  
ORGANISM human.  
SOURCE Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 361)  
NIH-MGC http://mgi.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: cga@bs-remail.nih.gov  
Eco RI site shown at the beginning of the sequence.  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
cDNA Library Preparation: M.B. Soares Lab  
cDNA Library Arrayed by: M.B. Soares Lab  
DNA Sequencing by: M.C. Soares Lab  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/ILNI at:  
www-bio.lnl.gov/bhrp/image/image.html  
Seq primer: M13 Forward  
Location/Qualifiers  
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/tissue\_type="lymph"  
/cell\_type="germinal center B cells"  
/cell\_line="MGC85"  
/lab\_host="DH10B (IRT)"  
/note="Vector: pUT3-Pac; Site\_1: NotI; Site\_2: Eco RI;  
Constructed from size fractionated cytoplasmic mRNA  
(3.5-4.4kb). Directionally cloned. Cells provided by  
Louis M. Staudt, Ph.D. Library preparation by Maria de  
Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D. "  
BASE COUNT 56 a 119 c 104 g 80 t 2 others  
ORIGIN

Alignment Scores:  
Pred. No.: 0.000167 Length: 361  
Score: 110.00 Matches: 36  
Percent Similarity: 42.34% Conservative: 11  
Best Local Similarity: 32.43% Mismatches: 40  
Query Match: 13.27% Indels: 24  
DB: 10 Gaps: 4

US-09-697-089-2\_COPY\_161\_323 (1-163) x AM504276 (1-361)  
Oy 7 IleGlnGlyIleuSerGlyIysSerThrLeuGlnArgIIeAlaMetLeuTrp 26  
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Oy 27 GlySerGlyIysCylsAlaLeuThrIysPheIysPheValPhePheLeuArgIysSer 46  
Db 77 GCCACGGCGCGGTGACGACGAGGGGTCAAAATTCCTTCCACTTTCGCTGCCGATGTC 136



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QY 47 Argala-----gInglyLeuPheGlnThrLeuCys 57
Db 137 AGCTGCTCAAGAAAGTACAGGCTGTGTCTGCAGACGCTCTCTTCAAGACTACTGTC 196
QY 58 AsplnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeu 77
Db 197 -----TACCCAGAGCGGAGACCCCAAGAGAGGTGTTT---GCCCTTCCTGCTG 238
QY 78 LysLeuArgGlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPhe----- 93
Db 239 GCCTTCCCGCCACGNTGGCTCTTACCTTCGATGAGCTGAGAGCTGCACCTCGACTG 298
QY 94 -----LysProGlnAsnCysPro 99
Db 299 GACCTGAGCGCGGTGCTGACAGCTCCTGCCCC 331

RESULT 15
BE887277 939 bp mRNA linear EST 20-OCT-2000
LOCUS 601508592F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909958 5',
DEFINITION MRNA sequence.
ACCESSION BE887277
VERSION BE887277
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 939)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: LLM9724 row: h column: 23
High quality sequence stop: 613.
Location/Qualifiers
1. 939
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/db_xref="taxon:9606"
/clone="IMAGE:3909958"
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/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb."
BASE COUNT 185 a 295 c 276 g 183 t
ORIGIN

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## Alignment Scores:

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Pred. No.: 0.00247 Length: 939
Score: 105.50 Matches: 38
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DB: 12 Gaps: 3

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US-09-697-089-2\_COPY\_161\_323 (1-163) x BE887277 (1-939)

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QY 7 ILeGlnGlyLysSerGlyLysSerThrLeuGlnArgIleAlaMetLeuTrp 26
Db 129 ATCCTGGGTGATGCGGGGTGGCAAGTCATGCTGCTACACGCGCTGCAGAGCTCTGG 188
QY 27 GlySerGlyLysCysLysAlaLeuThrLysPheLysPheValPhePheLeuArgLeu-Se 46

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Db 189 GCCACGGGCGCGCTAGACGACGAGGGGTCAAATCTTCTTCACCTTTCGCTGCGCATGTC 248
QY 46 rArgIaGln-----GlyGlyLeuPheGlnThrLeuCysAsp-GlnLeuLeuAspI 63
Db 249 AGCTGCTCAAGAAAGTACAGGCTGTGTCTGCAGAGCTGCTCTTCAAGACTACTGTC 308
QY 63 IeProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArgGlnArg 83
Db 309 TACCCAGAGCGGAGACCAAGAGAGGTGTTT---GCCCTTCCTGCTGCGCTTCCCCACG 365
QY 83 alLeuPheLeuLeuAspIleTyrAsnGluPhe-----L 94
Db 366 CCTCTTCACCTTGCATGAGCTGAGAGCTGCACTCGACTGAGACTGAGCGCGTGC 425
QY 94 ySProGlnAsnCysPro 99
Db 426 CTGACAGCTCCTGCCCC 442

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Search completed: January 31, 2003, 16:18:52  
Job time : 1335.94 secs

GenCore version 5.1.3  
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## OM protein - nucleic search, using frame\_plus.p2n model

Run on: January 31, 2003, 11:43:51 : Search time 36.8989 Seconds

(without alignments)  
1354.737 Million cell updates/sec

Title: US-09-697-089-2\_COPY\_161\_323

Perfect score: 829

Sequence: 1 LQSPCIEGSGKGRSLQ.....SAQALREVLIKELEBLL 163

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BIOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Fgapop 10.0 , Fgapext 0.5	
Delop 6.0 , Delext 7.0	

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Command line parameters:

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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsun62 -TRANS=human40.cdi  
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-WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7  
-YGAOP=10 -YGAEXT=0.5 -DELop=6 -DELEXT=7

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5: /cgn2\_6/ptodata/2/1na/PCUTUS.COMB.seq.\*  
6: /cgn2\_6/ptodata/2/1na/Backfile1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	236.5	28.5	5502	3	US-08-836-134-1
2	236.5	28.5	5502	4	US-09-493-784-1
3	111	13.4	4141	4	US-09-245-281-42
4	111	13.4	4141	4	US-09-207-359B-42
5	107	12.9	1470	4	US-09-099-041A-27
6	107	12.9	1470	4	US-09-245-281-27
7	107	12.9	1470	4	US-09-207-359B-27
8	107	12.9	2859	4	US-09-099-041A-9
9	107	12.9	2859	4	US-09-245-281-9
10	107	12.9	2859	4	US-09-207-359B-9
11	107	12.9	3080	4	US-09-099-041A-25
12	107	12.9	3080	4	US-09-245-281-25

13	107	12.9	3080	4	US-09-207-359B-25	Sequence 25, Appl
14	107	12.9	3382	4	US-09-099-041A-7	Sequence 7, Appl
15	107	12.9	3382	4	US-09-245-281-7	Sequence 7, Appl
16	107	12.9	3382	4	US-09-207-359B-7	Sequence 7, Appl
17	107	12.9	32042	4	US-09-245-281-44	Sequence 44, Appl
18	100.5	12.1	250	2	US-08-824-701A-8	Sequence 8, Appl
19	82	9.9	626	3	US-09-019-942-4	Sequence 4, Appl
20	82	9.9	626	4	US-09-470-271-4	Sequence 4, Appl
21	78	9.4	3393	1	US-08-295-502-1	Sequence 1, Appl
22	78	9.4	3393	5	PCT-US95-10691-1	Sequence 1, Appl
23	78	9.4	4441	4	US-09-641-999-2	Sequence 2, Appl
24	78	9.4	4543	2	US-08-519-547A-5	Sequence 5, Appl
25	76.5	9.2	7881	2	US-08-751-189-1	Sequence 1, Appl
26	76.5	9.2	7881	2	US-09-060-836-1	Sequence 1, Appl
27	76.5	9.2	7881	4	US-09-184-445-1	Sequence 1, Appl
28	75.5	9.1	732	4	US-08-918-573-3	Sequence 3, Appl
29	75.5	9.1	735	4	US-08-919-573-1	Sequence 1, Appl
30	71.5	8.6	4014	4	US-09-541-782-1	Sequence 1, Appl
31	71.5	8.6	4014	4	US-09-723-820-1	Sequence 1, Appl
32	71.5	8.6	5278	4	US-08-961-527-227	Sequence 227, App
33	71	8.6	834	4	US-09-134-001C-2775	Sequence 2775, Ap
34	70.5	8.5	1761	4	US-09-504-358-19	Sequence 19, Appl
35	70.5	8.5	1761	4	US-09-954-314-19	Sequence 19, Appl
36	70.5	8.5	11471	4	US-09-504-358-16	Sequence 16, Appl
37	70.5	8.5	11471	4	US-09-954-314-16	Sequence 16, Appl
38	69.5	8.4	2634	2	US-08-907-166-7	Sequence 7, Appl
39	69.5	8.4	6464	4	US-09-221-017B-168	Sequence 168, App
40	69.5	8.4	13440	4	US-08-961-527-128	Sequence 128, App
41	69.5	8.4	4411529	4	US-09-103-840A-1	Sequence 1, Appl
42	69	8.3	1776	4	US-09-149-476-59	Sequence 59, Appl
43	69	8.3	4371	1	US-08-803-972-1	Sequence 1, Appl
44	69	8.3	4371	1	US-08-803-972-1	Sequence 1, Appl
45	68.5	8.3	1620	4	US-09-360-197-3	Sequence 3, Appl

## ALIGNMENTS

RESULT 1  
US-08-836-134-1  
: Sequence 1, Application US/08836134A  
: Patent No. 6020127  
: GENERAL INFORMATION:  
: APPLICANT: Mackenzie, Alex E.  
: APPLICANT: Korneluk, Robert G.  
: APPLICANT: Mahadevan, Mani S.  
: APPLICANT: McLean, Michael  
: APPLICANT: Roy, Natalie  
: APPLICANT: Ikeda, John-e  
: TITLE OF INVENTION: Neuronal Apoptosis Inhibitor Protein, Gene Sequence and  
: Patent No. 6020127  
: TITLE OF INVENTION: Mutations Causative of Spinal Muscular Atrophy  
: FILE REFERENCE: 3477-112, 033477/139914  
: CURRENT APPLICATION NUMBER: US/08/836,134A  
: CURRENT FILING DATE: 1997-06-20  
: NUMBER OF SEQ ID NOS: 23  
: SOFTWARE: PatentIn Ver. 2.0  
: SEQ ID NO 1  
: LENGTH: 5502  
: TYPE: DNA  
: ORGANISM: Homo sapiens  
US-08-836-134-1

Alignment Scores:  
Pred. No.: 2.63e-22  
Score: 236.50  
Percent Similarity: 58.96%  
Best Local Similarity: 39.55%  
Query Match: 28.53%  
DB: 3  
Gaps: 3

US-09-697-089-2\_COPY\_161\_323 (1-163) x US-08-836-134-1 (1-5502)  
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Db 1779 TTGAACCTGTGATGTGTGGAGGTGAAGCTGGAAGAGGAGGCTCTCTGAG 1838
OY 21 ArgilleaLeuLeuThrpGlySerGlyLysCysLysAlaLeuThrpLysPheVal 40
Db 1839 AAAATACCTTTTCTGTGGCATCTGAGTCTGCTCCCTGTTAAACAGATTCACCTGTT 1898
OY 41 PheLeuLeuArgLeuSer-----ArgAlaGlnGlyLeuPheGlnThrpLeuCysAsp 58
Db 1899 TTCTACCTTCCTTACTTATTCACACAGACAGAGGGCTGGCCAGTATCATCTGTGAC 1958
OY 59 GlnLeuLeuAspLeuProGlyThrIleArgLysGlnThrpMetAlaMetLeuLeuLys 78
Db 1959 CAGCTCTAAGAGAAAGAGAGATCTGTACTGAAATGTGCATGAGGAACATTATTCACAG 2018
OY 79 LeuArgGlnArgValLeuPheLeuLeuAspGlyTyraSnglnPhe-----LysProGln 96
Db 2019 TTAAAGATCATGAGTCTATTCTTTAGATGACTACAAAGAAATATGTCAATCCCTCAA 2078
OY 97 AsnCysProGlnIleGlnAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIle 116
Db 2079 -----GTCAATAGGAAACAGGAGGCGGACATCCGCGATAC 2129
OY 117 ValThrThrThrThrGlyCysLeuArgHisIleArgGlnPhe 130
Db 2130 ATTGCTGTCCGTACAAACAGGCGGACATCCGCGATAC 2171

RESULT 2
US-09-493-784-1
; Sequence 1, Application US/09493784
; Patent No. 6429011
; GENERAL INFORMATION:
; APPLICANT: Mackenzie, Alex E.
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mahadevan, Mani S.
; APPLICANT: McLean, Michael
; APPLICANT: Roy, Natalie
; APPLICANT: Ikeda, John
; TITLE OF INVENTION: Neuronal Apoptosis Inhibitor Protein, Gene Sequence and
; Patent No. 6429011
; FILE REFERENCE: 3477-112, 033477/139914
; CURRENT APPLICATION NUMBER: US/09/493,784
; PRIOR FILING DATE: 2000-01-28
; PRIOR FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 5502
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-493-784-1

Alignment Scores:
Pred. No.: 2,63e-22 Length: 5502
Score: 236.50 Matches: 53
Percent Similarity: 58.96% Conservative: 26
Best Local Similarity: 39.55% Mismatches: 48
Query Match: 28.53% Indels: 7
Gaps: 3

US-09-697-089-2_COPY_161_323 (1-163) x US-09-493-784-1 (1-5502)
OY 1 LeuGlnSerProCysIleIleGlnGlyLysSerGlyLysSerThrLeuLeuGln 20
Db 1779 TTGAACCTGTGATGTGTGGAGGTGAAGCTGGAAGAGGAGGCTCTCTGAG 1838
OY 21 ArgilleaLeuLeuThrpGlySerGlyLysCysLysAlaLeuThrpLysPheVal 40
Db 1839 AAAATACCTTTTCTGTGGCATCTGAGTCTGCTCCCTGTTAAACAGATTCACCTGTT 1898
OY 41 PheLeuLeuArgLeuSer-----ArgAlaGlnGlyLeuPheGlnThrpLeuCysAsp 58
Db 1899 TTCTACCTTCCTTACTTATTCACACAGACAGAGGGCTGGCCAGTATCATCTGTGAC 1958
OY 59 GlnLeuLeuAspLeuProGlyThrIleArgLysGlnThrpMetAlaMetLeuLeuLys 78
Db 1959 CAGCTCTAAGAGAAAGAGAGATCTGTACTGAAATGTGCATGAGGAACATTATTCACAG 2018
OY 79 LeuArgGlnArgValLeuPheLeuLeuAspGlyTyraSnglnPhe-----LysProGln 96
Db 2019 TTAAAGATCATGAGTCTATTCTTTAGATGACTACAAAGAAATATGTCAATCCCTCAA 2078
OY 97 AsnCysProGlnIleGlnAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIle 116
Db 2079 -----GTCAATAGGAAACAGGAGGCGGACATCCGCGATAC 2129
OY 117 ValThrThrThrThrGlyCysLeuArgHisIleArgGlnPhe 130
Db 2130 ATTGCTGTCCGTACAAACAGGCGGACATCCGCGATAC 2171

RESULT 3
US-09-245-281-42
; Sequence 42, Application US/09245281
; Patent No. 6369196
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/09/245,281
; EARLIER FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: US 09/207,359
; EARLIER FILING DATE: 1998-12-08
; EARLIER APPLICATION NUMBER: US 09/099,041
; EARLIER FILING DATE: 1998-06-17
; EARLIER APPLICATION NUMBER: US 09/019,942
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 4141
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (261)...(3119)
US-09-245-281-42

Alignment Scores:
Pred. No.: 5.2e-05 Length: 4141
Score: 111.00 Matches: 45
Percent Similarity: 41.21% Conservative: 23
Best Local Similarity: 27.27% Mismatches: 63
Query Match: 13.39% Indels: 34
Gaps: 7

US-09-697-089-2_COPY_161_323 (1-163) x US-09-245-281-42 (1-4141)
OY 9 GlyLysSerGlyLysGlyLysSerThrLeuLeuGlnArgIleAlaMetLeuThrpGlySer 28
Db 864 GGGAGCGGGAGTGGCGAAGTCTCATGCTGTGCGAGGTGCGAGACCTCTGGGGCTCA 923
OY 29 GlyLysCysLysAlaLeuThrpLysPheLysPheValPheLeuLeuArgLeuSerArgAla 48
Db 924 GCGAGGTGACCTTCACAGCAAAATTTCTTCTCCACTTCGCGCTCCGCAATGTTACGTGC 983
OY 49 -----GlnGlyLeuPheGlnThrpLeuCysAspGln 59
Db 984 TTCAAGAGAGACGACATGATGTCTGACAGACCTGCTTCAAGCAATTTCTGTC----- 1037
OY 60 LeuLeuAspLeuProGlyThrIleArgLysGlnThrpMetAlaMetLeuLeuLysLeu 79
Db 1038 -----TACCGGAGACAGACCCGAGAGAGGTTC--TCTCTTGTGTGCGCTTT 1085
```

```

Db 1899 TTCTACCTTCCTTACTTATTCACACAGACAGAGGGCTGGCCAGTATCATCTGTGAC 1958
OY 59 GlnLeuLeuAspLeuProGlyThrIleArgLysGlnThrpMetAlaMetLeuLeuLys 78
Db 1959 CAGCTCTAAGAGAAAGAGAGATCTGTACTGAAATGTGCATGAGGAACATTATTCACAG 2018
OY 79 LeuArgGlnArgValLeuPheLeuLeuAspGlyTyraSnglnPhe-----LysProGln 96
Db 2019 TTAAAGATCATGAGTCTATTCTTTAGATGACTACAAAGAAATATGTCAATCCCTCAA 2078
OY 97 AsnCysProGlnIleGlnAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIle 116
Db 2079 -----GTCAATAGGAAACAGTATTCAAAACACATTCACCGAGCTGCTATTG 2129
OY 117 ValThrThrThrThrGlyCysLeuArgHisIleArgGlnPhe 130
Db 2130 ATTGCTGTCCGTACAAACAGGCGGACATCCGCGATAC 2171

RESULT 3
US-09-245-281-42
; Sequence 42, Application US/09245281
; Patent No. 6369196
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/09/245,281
; EARLIER FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: US 09/207,359
; EARLIER FILING DATE: 1998-12-08
; EARLIER APPLICATION NUMBER: US 09/099,041
; EARLIER FILING DATE: 1998-06-17
; EARLIER APPLICATION NUMBER: US 09/019,942
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 4141
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (261)...(3119)
US-09-245-281-42

Alignment Scores:
Pred. No.: 5.2e-05 Length: 4141
Score: 111.00 Matches: 45
Percent Similarity: 41.21% Conservative: 23
Best Local Similarity: 27.27% Mismatches: 63
Query Match: 13.39% Indels: 34
Gaps: 7

US-09-697-089-2_COPY_161_323 (1-163) x US-09-245-281-42 (1-4141)
OY 9 GlyLysSerGlyLysGlyLysSerThrLeuLeuGlnArgIleAlaMetLeuThrpGlySer 28
Db 864 GGGAGCGGGAGTGGCGAAGTCTCATGCTGTGCGAGGTGCGAGACCTCTGGGGCTCA 923
OY 29 GlyLysCysLysAlaLeuThrpLysPheLysPheValPheLeuLeuArgLeuSerArgAla 48
Db 924 GCGAGGTGACCTTCACAGCAAAATTTCTTCTCCACTTCGCGCTCCGCAATGTTACGTGC 983
OY 49 -----GlnGlyLeuPheGlnThrpLeuCysAspGln 59
Db 984 TTCAAGAGAGACGACATGATGTCTGACAGACCTGCTTCAAGCAATTTCTGTC----- 1037
OY 60 LeuLeuAspLeuProGlyThrIleArgLysGlnThrpMetAlaMetLeuLeuLysLeu 79
Db 1038 -----TACCGGAGACAGACCCGAGAGAGGTTC--TCTCTTGTGTGCGCTTT 1085
```

```

OY 80 ArgGlnIrryValIleuPheLeuLeuAspGlyuTyraAsnGlnPheLys----- 94
Db 1086 CCCACACAGAGCGCTTCTACTTTTGAACGGCTGAGAGAGCTCCACTAGACTCTGACACTG 1145
OY 95 -----ProGlnAsnCysProGluIleGluAlaLeuLeuIleLysGluAsnHisArgPhe 111
Db 1146 AGCGCGCTGGCGGATAGACTCTGCGCCCTGGAGCGG----- 1181
OY 112 LysAsmEtyAlIleValIThrIThrIThrGluCysLeuArgHisIleArgGlnPheGly 131
Db 1182 GCTACACCTGTGGCTGCTGCGCTAACTCCTAACTGAGAGAGGCTCTCAAGAGGTGCGCG 1241
OY 132 ---AlaLeuThrAlaGluValGlyAspMetIThrGluAspSerAlaGluAlaLeuIleArg 150
Db 1242 AAATGTGCTACTGCTGCGACAGCG-----GTGAGAGTCCCGCCGACAGCTCTGCGCAA 1295
OY 151 GluValLeuIleLys 155
Db 1296 AAGGTGCTGCTCCGG 1310

```

```

RESULT 4
US-09-207-359B-42
; Sequence 42, Application US/09207359B
; Patent No. 6469140
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-112001
; CURRENT APPLICATION NUMBER: US/09/207,359B
; CURRENT FILING DATE: 1998-11-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 4141
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (261)...(3119)
US-09-207-359B-42

```

Alignment Scores:	
Pred. No.:	5.2e-05
Score:	111.00
Percent Similarity:	41.21%
Best Local Similarity:	27.27%
Query Match:	13.39%
DB:	4
	7
	4141
Length:	4141
Matches:	45
Conservative:	23
Mismatches:	63
Indels:	34
Gaps:	7

US-09-697-089-2\_COPY\_161\_323 (1-163) x US-09-207-359B-42 (1-4141)

[illegible]

```

Db 1086 CCCACACAGAGCGCTTTCACCTTTTGTAGAGCGCTGGATGAGACTGTGCACTACAGACTTTCGACCTG 1145
      ||||| ||||| :|||
QY 95 -----ProGlnAsnCysProGluIleGluAlaLeuIleLysGluAsnHisArgPhe 111
      ||| :||| |||
Db 1146 AGCGCGCGTGGCGGATACCTGCTGCCCCGTGGACCGC----- 1181
      ||| :||| |||
QY 112 LysAsnMetValIleValIleThrThrThrThrGluCysLeuArgHisIleArgGlnPheGly 131
      :||| :||| |||
Db 1182 GCTCACCGCTCGGTCGTCGCGGGCTAACGTCGCTAAAGTGGGAGGCTGCTCAAGGCTCCGCGC 1241
      :||| :||| |||
QY 132 ---AlaLeuThrAlaGluValIleLysAspMetThrGluAspSerAlaGlnAlaLeuIleArg 150
      ||||| ||||| ||| ||| :|||
Db 1242 AAATGTCGCTACGTGCTGCCACAGGC-----GTGAGAGTCCCGCCGACGCTCTGTGGCANA 1295
      :||| :|||
QY 151 GluValLeuIleLys 155
      :||| :|||
Db 1296 AAGGTGCTGCTCCGG 1310
      :||| :|||

```

```

RESULT 5
US-09-099-041A-27
; Sequence 27, Application US/09099041A
; Patent No. 6340576
; GENERAL INFORMATION:
; APPLICANT: Berlin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-076001
; CURRENT APPLICATION NUMBER: US/09/099,041A
; CURRENT FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: fastSeq for Windows Version 4.0
; SEQ ID NO 27
;
; LENGTH: 1470
;
; TYPE: DNA
;
; ORGANISM: Homo sapiens
US-09-099-041A-27

```

Alignment Scores:	
Pred. No.:	3.98e-05
Score:	107.00
Percent Similarity:	42.34%
Best Local Similarity:	31.55%
Query Match:	12.91%
DB:	4
Gaps:	4
Length:	1470
Matches:	35
Conservative:	12
Mismatches:	40
Indels:	24

US-09-697-089-2\_COPY\_161\_323 (1-163) X US-09-099-041A-27 (1-1470)

OY	7	IIeGIuGIuSerGIyLyGIyLysSerThrIeuLeuGInArgIleAlaMetLeuTrp	26
Db	481	ATTCGGGTGAAGCTGGGGGGGGAAGGCACATGCTGACAGCGGGCTGCAGAGCTTTGG	540
OY	27	GIySerGIyLysCysLysAlaLeuThrLysPheLysPheValPhePheLeuArgLysSer	46
Db	541	GCCAGGCGCCGGCTAGACGACGAGGGGTCAAAATTTCTTCCACTTTCCTGCGCGCATGTC	600
OY	47	ArgAla	
		-----GIuGIyLeuPheGIuThrLeuCys	57
Db	601	AGCTGCTTCAGGAAGTGCAGCGCTGTCTGCAGGACCTGCTTCACAGACACTACTGC	660
OY	58	AspGIuLeuAspIleProGIyThrIleArgLysGInThrPheMetAlaMetLeu	77
Db	661	-----TACCACAGACGGGACCCCGAGGAGGGT-----GCCCTTCGCTG	702
OY	78	LysLeuArgGIuArgValLeuPheLeuLeuAspLysIyIraGInPhe	93
Db	703	CGCTTCCCCCAGCGGCCCTTCTTACCTTCGATGGCTGGGACGAGCTGCACCTGGACTTG	762
OY	94	-----LysProGIuAsnCysPro	99
Db	763	GACCTGAGCCGCTGCTGACAGCTCCGCGCCC	795

```
RESULT 6
US-09-245-281-27
; Sequence 27, Application US/09245281
; Patent No. 6369196
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/09/245,281
; EARLIER FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: US 09/207,359
; EARLIER FILING DATE: 1998-12-08
; EARLIER APPLICATION NUMBER: US 09/099,041
; EARLIER FILING DATE: 1998-06-17
; EARLIER APPLICATION NUMBER: US 09/019,942
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 1470
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-245-281-27

Alignment Scores:
Pred. No.: 3.98e-05 Length: 1470
Score: 107.00 Matches: 35
Percent Similarity: 42.34% Conservative: 12
Best Local Similarity: 31.53% Mismatches: 40
Query Match: 12.91% Indels: 24
Gaps: 4

US-09-697-089-2_COPY_161_323 (1-163) x US-09-245-281-27 (1-1470)
QY 7 lileglugluserglylysglylysserthrlleuenglarginaleuamleutrip 26
Db 481 ATCTGGGTGATGCTGGGGTGGGCAAGTCATGCTGTACAGCGGCTCAGAGCCTCTGG 540
QY 27 glyserglylyscyslysalaleuthrllyspheleuasphevalpheuargleuser 46
Db 541 GCCACGGGCGCGGTAGACGACGAGGGGCAATTCCTCCACTTCCGCTGCCGATGTC 600
QY 47 Argala-----glnglylyleuphegluThrlleucys 57
Db 601 AGCTGCTCAAGAAAGTACAGCGCTGTCTGTGACGAGCCTCTTCAAGCAGCTACTGC 660
QY 58 AspglnleuaspheleuproglyThrllearglysglnthrpheleuamleu 77
Db 661 -----TACCCAGAGCGGAGCCCGAGAGGAGGTGTTT---GCTTCTCTGCTG 702
QY 78 Lysleuarglnargvalleupheleuaspheleuaspheleuaspheleuaspheleu 93
Db 703 CGCTTCCCGCCACGTCGGCCCTTTCACCTTCGATGCGCTGAGCAGCTGCACTCGACTTG 762
QY 94 -----Lysproglinasncyspro 99
Db 763 GACCTGAGCGCGTGCCTGACAGCTCCTGCCCC 795

RESULT 7
US-09-207-359B-27
; Sequence 27, Application US/09207359B
; Patent No. 6469140
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-112001
; CURRENT APPLICATION NUMBER: US/09/207,359B
; CURRENT FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
```

```
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 1470
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-207-359B-27

Alignment Scores:
Pred. No.: 3.98e-05 Length: 1470
Score: 107.00 Matches: 35
Percent Similarity: 42.34% Conservative: 12
Best Local Similarity: 31.53% Mismatches: 40
Query Match: 12.91% Indels: 24
Gaps: 4

US-09-697-089-2_COPY_161_323 (1-163) x US-09-207-359B-27 (1-1470)
QY 7 lileglugluserglylysglylysserthrlleuenglarginaleuamleutrip 26
Db 481 ATCTGGGTGATGCTGGGGTGGGCAAGTCATGCTGTACAGCGGCTCAGAGCCTCTGG 540
QY 27 glyserglylyscyslysalaleuthrllyspheleuasphevalpheuargleuser 46
Db 541 GCCACGGGCGCGGTAGACGACGAGGGGCAATTCCTCCACTTCCGCTGCCGATGTC 600
QY 47 Argala-----glnglylyleuphegluThrlleucys 57
Db 601 AGCTGCTCAAGAAAGTACAGCGCTGTCTGTGACGAGCCTCTTCAAGCAGCTACTGC 660
QY 58 AspglnleuaspheleuproglyThrllearglysglnthrpheleuamleu 77
Db 661 -----TACCCAGAGCGGAGCCCGAGAGGAGGTGTTT---GCTTCTCTGCTG 702
QY 78 Lysleuarglnargvalleupheleuaspheleuaspheleuaspheleuaspheleu 93
Db 703 CGCTTCCCGCCACGTCGGCCCTTTCACCTTCGATGCGCTGAGCAGCTGCACTCGACTTG 762
QY 94 -----Lysproglinasncyspro 99
Db 763 GACCTGAGCGCGTGCCTGACAGCTCCTGCCCC 795

RESULT 8
US-09-099-041A-9
; Sequence 9, Application US/09099041A
; Patent No. 6340576
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-076001
; CURRENT APPLICATION NUMBER: US/09/099,041A
; CURRENT FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2859
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-099-041A-9

Alignment Scores:
Pred. No.: 0.000108 Length: 2859
Score: 107.00 Matches: 35
Percent Similarity: 42.34% Conservative: 12
Best Local Similarity: 31.53% Mismatches: 40
Query Match: 12.91% Indels: 24
Gaps: 4
```

US-09-697-089-2\_COPY\_161\_323 (1-163) x US-09-099-041A-9 (1-2859)

Oy	7	IIlegluIgluIysuIysCylsYlglYlvsSerThrIleuenuInrArgIeAlaIleuIleuTrp	26
Db	598	ATTCCTGGGTATGCTGGGGGCGGCAATCTCATGCTGTGTACAGGGCTGCAGACCTCTGG	657
Oy	27	GIysErGIyIysCylsYlalaLeuThrLysPheIysPheValPhePheIleuArgIeuSer	46
Db	658	GCCACGGGCGGCTAGACGACGAGGGGTCAAATTCCTCTCCATCTTCGCTCCGCGCATGTC	717
Oy	47	ArgIaIe	57
Db	718	AGCTGCTTCAAGAAAGTGCAGGCTGTCTGTGCAGGACCTGCTTTCACAGCACTACTGC	777
Oy	58	AspGIuIleuIeuAspIleProGIyThrIleArgIysGIInthrPheMetAlaIleuIeu	77
Db	778	-----TACCAGACGCGGAGCCCGGAGAGAGGTGT-----GCCTTCGTGCTG	819
Oy	78	LysIeuArGIuArGIaValIlePheIleuIeuAspGIyTyrsnGIuPhe	93
Db	820	CGCTTCCCCCAGCGGGCCCTTTCACCTTGATGAGCGCTGACACGACTGCACCTGGGACTTG	879
Oy	94	-----LysProGIuAsnGysPro	99
Db	880	GACCTGAGCCGCGTCCCTGCAGCTGCCTGCGCCG	912

RESULT 9

Alignment Scores:	
Pred. No.:	0.000108
Score:	107.00
Percent Similarity:	42.34%
Best Local Similarity:	3.55%
Query Match:	12.91%
DB:	4
	4
Length:	2859
Matches:	35
Conservative:	12
Mismatches:	40
Indels:	24
Gaps:	4

[illegible]

OY	58	AspGlnLeuLeuAspIleProGlyTyrLileArgylsgcInthrPheMetAlaMetLeuLeu	77
Db	778	-----TACCAGACGGGAGCCCGAGGAGGTGT--GCCTTCCTGCTG	819
OY	78	LysLeuArgGlnArgValLeuPheLeuLeuAspGlyTyrasnGluPhe-----	93
		:::	
Db	820	GCGTTCCCCCAGCGTGCCCTTCACCTTCATCGACTGGCCGTGACGAGCTGCACTCGACTTG	879
OY	94	-----LysProGlnAsnCysPro	99
		:::	
Db	880	GACCTGACCCGCGTCCCTGACAGCTCCTGCGCCC	912

```

RESULT 10
; US-09-207-359B-9
; Sequence 9, Application US/09207359B
; Patent No. 6469140
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARP-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-112001
; CURRENT APPLICATION NUMBER: US/09/207,359B
; CURRENT FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2855
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-207-359B-9

```

Alignment Scores:	
Pred. No.:	0.000108
Score:	107.00
Percent Similarity:	42.74%
Local Similarity:	31.53%
Query Match:	12.91%
DB:	4
	Matches:
	Mismatches:
	Indels:
	Gaps:

```

QY      7  ILeGluGlyGluSerGlyLysGlyLysSerThrLeuLeuGlnArgIleAlaMetLeuTrp 26
           |||  |||:::|||||  ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      598  ATCCGGGTGTATGCTGGGGGTGGGCAAGTCCATGCTGTACAGCGCGCTGAGAGCTCTGG 657
QY      27  GlySerGlyLysCysLysAlaLeuThrLysPheLysPheValPhePheLeuArgLeuSer 46
           ::|||::|::|::|  |||  ||| ||| ||| ||| ||| ||| ||| |||
Db      658  GCCACGAGCGCCGCGTACAGACGAGGGGTCAAAATCTTCTTCCACTTGCCTGCCGCAATTC 717
QY      47  ArgAla-----GlnGlyGlyLeuPheGluThrLeuCys 57
           |||  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      718  AGCTGCTTCAAAGAAAGTGCAGAGCGTGTGTCGACGAGCACTGCTTTCAAAGCACTACTGC 777
QY      58  AspGlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeu 77
           |||  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      778  -----TACCCAGACGGGAGACCCCGAGGAGGGT---GCCTTCTCTGCTG 81.9
QY      78  LysLeuArgGlnArgValLeuPheLeuLeuAspIleTyrAsnGluPhe----- 93
           ::|  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      820  CGGCTTCCCCACAGGGGCCCTCTTCACTTCGATGGCTCGACGAGCTGCACACTCGGACTTG 87.9
QY      94  -----LysProGlnAsnCysPro 99
           ::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      880  GACCTGACCGCGTGCCTGCAGACAGCTCTGCGCCC 912

RESULT 11
US-09-099-041A-25
: Sequence 25, Application US/09099041A
: Patent No. 6340576

```

```
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-076001
; CURRENT APPLICATION NUMBER: US/09/099,041A
; PRIOR FILING DATE: 1998-06-17
; PRIOR FILING DATE: 09/019,942
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 3080
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1470)
US-09-099-041A-25

Alignment Scores:
Pred. No.: 0.000121 Length: 3080
Score: 107.00 Matches: 35
Percent Similarity: 42.34% Conservative: 12
Best Local Similarity: 31.53% Mismatches: 40
Query Match: 12.91% Indels: 24
Gaps: 4

US-09-697-089-2_COPY_161_323 (1-163) x US-09-099-041A-25 (1-3080)
QY 7 lIeGlUgIuSeRgLySgLySgSerThrLeuGlnArgIleAlaMetLeuTrp 26
    ||| |||:::||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 481 ATCTGGGTATGCTGGGGGGGCGACAGCCATGCTGTACAGCGGCGACAGCTCTGG 540
QY 27 gLySeRgLyScYsLySAlaLeuThrLySPhelYsPheValPhePheLeuArgLeuSer 46
    ::|||:::||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 541 GCCACGGGGCGGCTAGACGAGGGGCAAAATTCCTTCCTCCGCTCGCATGTC 600
QY 47 ArgAla-----GlnGlyLeuPheGlnuThrLeuCyS 57
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 601 AGCTGCTTCAAGAACTGACAGGCTGTCTGTGACGAGACCGCTCTTCAAGCACTACTGC 660
QY 58 AspGlnLeuLeuAspIleProGlyThrIleArgLySgInThrPheMetAlaMetLeuLeu 77
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 661 -----TACCCAGACGGGACCCGAGAGAGGTGT---GCCTTCCTGCTG 702
QY 78 LysLeuArgGlnArgValLeuPheLeuLeuAspGlyTyraSngIuPhe----- 93
    ::|||:::||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 703 GCGTTCCTCCACGCGCCCTCTTACCTTGATGCTGCGACGAGCTGCACCTCGGACTTG 762
QY 94 -----LysProGlnAsnCysPro 99
    ::|||:::||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 763 GACCTGAGCGCGCTGCTGACAGCTCCTCGCCCC 795

RESULT 12
US-09-245-281-25
; Sequence 25, Application US/09245281
; Patent No. 6369196
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 07334/118001
; CURRENT APPLICATION NUMBER: US/09/245,281
; CURRENT FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: US 09/207,359
; EARLIER FILING DATE: 1998-12-08
; EARLIER APPLICATION NUMBER: US 09/099,041
; EARLIER FILING DATE: 1998-06-17
; EARLIER APPLICATION NUMBER: US 09/019,942
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
```

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; SEQ ID NO 25
; LENGTH: 3080
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-245-281-25

Alignment Scores:
Pred. No.: 0.000121 Length: 3080
Score: 107.00 Matches: 35
Percent Similarity: 42.34% Conservative: 12
Best Local Similarity: 31.53% Mismatches: 40
Query Match: 12.91% Indels: 24
Gaps: 4

US-09-697-089-2_COPY_161_323 (1-163) x US-09-245-281-25 (1-3080)
QY 7 lIeGlUgIuSeRgLySgLySgSerThrLeuGlnArgIleAlaMetLeuTrp 26
    ||| |||:::||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 481 ATCTGGGTATGCTGGGGGGGCGACAGCCATGCTGTACAGCGGCGACAGCTCTGG 540
QY 27 gLySeRgLyScYsLySAlaLeuThrLySPhelYsPheValPhePheLeuArgLeuSer 46
    ::|||:::||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 541 GCCACGGGGCGGCTAGACGAGGGGCAAAATTCCTTCCTCCGCTCGCATGTC 600
QY 47 ArgAla-----GlnGlyLeuPheGlnuThrLeuCyS 57
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 601 AGCTGCTTCAAGAACTGACAGGCTGTCTGTGACGAGACCGCTCTTCAAGCACTACTGC 660
QY 58 AspGlnLeuLeuAspIleProGlyThrIleArgLySgInThrPheMetAlaMetLeuLeu 77
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 661 -----TACCCAGACGGGACCCGAGAGAGGTGT---GCCTTCCTGCTG 702
QY 78 LysLeuArgGlnArgValLeuPheLeuLeuAspGlyTyraSngIuPhe----- 93
    ::|||:::||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 703 GCGTTCCTCCACGCGCCCTCTTACCTTGATGCTGCGACGAGCTGCACCTCGGACTTG 762
QY 94 -----LysProGlnAsnCysPro 99
    ::|||:::||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 763 GACCTGAGCGCGCTGCTGACAGCTCCTCGCCCC 795

RESULT 13
US-09-207-359B-25
; Sequence 25, Application US/09207359B
; Patent No. 6469140
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-112001
; CURRENT APPLICATION NUMBER: US/09/207,359B
; CURRENT FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 3080
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1470)
US-09-207-359B-25

Alignment Scores:
Pred. No.: 0.000121 Length: 3080
Score: 107.00 Matches: 35
Percent Similarity: 42.34% Conservative: 12
Best Local Similarity: 31.53% Mismatches: 40
Query Match: 12.91% Indels: 24
Gaps: 4
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US-09-697-089-2\_copy\_161\_323 (1-163) x US-09-207-359B-25 (1-3080)

QY 7 lIeGlUGlYgIuSerGlyLySgIyLysSerThrLeuLeuGlnArgIleAlaMetLeuTrp 26  
Db 481 ATCTGGGTGATGCTGGGGGTGGCAAGTCATGCTGACAGCGGCTGCAGAGCCTCTGG 540

QY 27 GlySerGlyLysCysLysAlaLeuThrLysPheLysPheValPhePheLeuArgLeuSer 46  
Db 541 GCCACGGGCGGCTAGACGACGGGCTCAATCTCTTCCACTTCCCTGCTGCGGCAATGTC 600

QY 47 ArgAla-----GlnGlyGlyLeuPheGluThrLeuCys 57  
Db 601 AGCTGCTTCAAGAAAGTACAGGCTGTGTCTGACAGACCTGCTTCTTCAACGACTGTC 660

QY 58 AspGlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeu 77  
Db 661 -----TACCCAGACGGGACCCGAGGAGGTGTTT---GCCCTCTCTGCTG 702

QY 78 LysLeuArgGlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPhe----- 93  
Db 703 CGCTTCCCGCCACGTCGGCCCTTTCACCTTCGATGCGCTGAGACGACTGCACTCGACTTG 762

QY 94 -----LysProGlnAsnCysPro 99  
Db 763 GACCTGAGCCGCGTGCCTGACAGCTCCTGCCCC 795

RESULT 14  
US-09-099-041A-7  
; Sequence 7, Application US/09099041A  
; Patent No. 6340576  
; GENERAL INFORMATION:  
; APPLICANT: Berlin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
; FILE REFERENCE: 07334-076001  
; CURRENT APPLICATION NUMBER: US/09/099,041A  
; CURRENT FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: 09/019,942  
; PRIOR FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 3382  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (245)...(3103)  
US-09-099-041A-7

Alignment Scores:  
Pred. No.: 0.000139 Length: 3382  
Score: 107.00 Matches: 35  
Percent Similarity: 42.34% Conservative: 12  
Best Local Similarity: 31.53% Mismatches: 40  
Query Match: 12.91% Indels: 24  
Gaps: 4

US-09-697-089-2\_copy\_161\_323 (1-163) x US-09-099-041A-7 (1-3382)

QY 7 lIeGlUGlYgIuSerGlyLySgIyLysSerThrLeuLeuGlnArgIleAlaMetLeuTrp 26  
Db 842 ATCTGGGTGATGCTGGGGGTGGCAAGTCATGCTGACAGCGGCTGCAGAGCCTCTGG 901

QY 27 GlySerGlyLysCysLysAlaLeuThrLysPheLysPheValPhePheLeuArgLeuSer 46  
Db 902 GCCACGGGCGGCTAGACGACGGGCTCAATCTCTTCCACTTCCCTGCTGCGGCAATGTC 961

QY 47 ArgAla-----GlnGlyGlyLeuPheGluThrLeuCys 57  
Db 962 AGCTGCTTCAAGAAAGTACAGGCTGTGTCTGACAGACCTGCTTCAACGACTGTC 1021

QY 58 AspGlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeu 77  
Db 1022 -----TACCCAGACGGGACCCGAGGAGGTGTTT---GCCCTCTCTGCTG 1063

QY 78 LysLeuArgGlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPhe----- 93  
Db 1064 CGCTTCCCGCCACGTCGGCCCTTTCACCTTCGATGCGCTGAGACGACTGCACTCGACTTG 1123

QY 94 -----LysProGlnAsnCysPro 99  
Db 1124 GACCTGAGCCGCGTGCCTGACAGCTCCTGCCCC 1156

RESULT 15  
US-09-245-281-7  
; Sequence 7, Application US/09245281  
; Patent No. 6369196  
; GENERAL INFORMATION:  
; APPLICANT: Berlin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY  
; FILE REFERENCE: 07334/118001  
; CURRENT APPLICATION NUMBER: US/09/245,281  
; CURRENT FILING DATE: 1999-02-05  
; EARLIER APPLICATION NUMBER: US 09/207,359  
; EARLIER FILING DATE: 1998-12-08  
; EARLIER APPLICATION NUMBER: US 09/099,041  
; EARLIER FILING DATE: 1998-06-17  
; EARLIER APPLICATION NUMBER: US 09/019,942  
; EARLIER FILING DATE: 1998-02-06  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 3382  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-245-281-7

Alignment Scores:  
Pred. No.: 0.000139 Length: 3382  
Score: 107.00 Matches: 35  
Percent Similarity: 42.34% Conservative: 12  
Best Local Similarity: 31.53% Mismatches: 40  
Query Match: 12.91% Indels: 24  
Gaps: 4

US-09-697-089-2\_copy\_161\_323 (1-163) x US-09-245-281-7 (1-3382)

QY 7 lIeGlUGlYgIuSerGlyLySgIyLysSerThrLeuLeuGlnArgIleAlaMetLeuTrp 26  
Db 842 ATCTGGGTGATGCTGGGGGTGGCAAGTCATGCTGACAGCGGCTGCAGAGCCTCTGG 901

QY 27 GlySerGlyLysCysLysAlaLeuThrLysPheLysPheValPhePheLeuArgLeuSer 46  
Db 902 GCCACGGGCGGCTAGACGACGGGCTCAATCTCTTCCACTTCCCTGCTGCGGCAATGTC 961

QY 47 ArgAla-----GlnGlyGlyLeuPheGluThrLeuCys 57  
Db 962 AGCTGCTTCAAGAAAGTACAGGCTGTGTCTGACAGACCTGCTTCAACGACTGTC 1021

QY 58 AspGlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeu 77  
Db 1022 -----TACCCAGACGGGACCCGAGGAGGTGTTT---GCCCTCTCTGCTG 1063

QY 78 LysLeuArgGlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPhe----- 93  
Db 1064 CGCTTCCCGCCACGTCGGCCCTTTCACCTTCGATGCGCTGAGACGACTGCACTCGACTTG 1123

QY 94 -----LysProGlnAsnCysPro 99  
Db 1124 GACCTGAGCCGCGTGCCTGACAGCTCCTGCCCC 1156



Mon Feb 3 14:11:39 2003

us-09-697-089-2\_copy\_161\_323.p2n.rni

Page 8

Job time : 43.8989 secs



```

: LENGTH: 891
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)...(891)
US-09-864-921-179

Alignment Scores:
Pred. No.:          9.63e-106          Length:          891
Score:             829.00             Matches:          163
Percent Similarity: 100.00%           Conservative:    0
Best Local Similarity: 100.00%         Mismatches:     0
Query Match:       100.00%            Indels:         0
DB:                9                  Gaps:           0

US-09-697-089-2_COPY_161_323 (1-163) x US-09-864-921-179 (1-891)

OY      1 leuGInserProCySIIleGluGlyLUSeRgLySgLySseThLeuLIn 20
         |||||||
Db       1 CTTGAGACCCCTGCATATTGAAGGGGAATCTGGCAAAAGCAATCCACTCTGTGCAG 60
         |||||||

OY      21 ArgIleAMeLLeuTrpGlySerGlyScLySAlaLeuThLysPheLysPheAl 40
         |||||||
Db       61 CGCATTTGCCATGCTGTGGGGCTCCGGAAAGTCCAAAGCTCTGACCAATTCAATTTGTC 120
         |||||||

OY      41 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuCyAspLIneu 60
         |||||||
Db       121 TTCTTCCTCCGCTCAGCAGGGCCAGGGGTGGACTTTTGAACCCTCTGTGATCACTC 180
         |||||||

OY      61 LeuAspLLeProGlyThrIleArgLySglnThrPheMetAlaMeLLeuLysLeuArg 80
         |||||||
Db       181 CTGGATTATACCTGGGCACATCAGGAAGCAGACATTTCATGCGCATGCTCTGTAAGCTGCGG 240
         |||||||

OY      81 GlnArgValIleuPheLeuLeuAspLyTyraSngluPheLysProGlnAsnCysProGlu 100
         |||||||
Db       241 CAGAGGGTCTTTTCTTCTCTGTGATGCTACATGATTCATCAAGCCCACTGCCAGAA 300
         |||||||

OY      101 ILeGuaLaleuLleLySgluAsnHisArgPheLysAsnMetValIleValThrThrThr 120
         |||||||
Db       301 ATCGAAGCCCTGATAAAGAAACCCACCGCTTCAAGAACATGATGTCACCCACTACC 360
         |||||||

OY      121 ThrGlyCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 140
         |||||||
Db       361 ACTGATGCTCCTGAGGACCATACGGCAGATTGGTGGCCCTGACTGCTGAGAGTGGGGATATG 420
         |||||||

OY      141 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGlnLeuAlaGlnGly 160
         |||||||
Db       421 ACAGAAAGACAGCGCCACAGCTCTCATCCGAGAAAGTCTGATCATCAAGAGACTTGTCAAGGC 480
         |||||||

OY      161 LeuLeuLeu 163
         |||||||
Db       481 TTGTTGCTC 489

RESULT 2
US-09-841-739-3
: Sequence 3, Application US/09841739
: Patent No. US20020034784A1
: GENERAL INFORMATION:
: APPLICANT: Bertin, John
: TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
: FILE REFERENCE: 07334-329001
: CURRENT APPLICATION NUMBER: US/09/841,739
: CURRENT FILING DATE: 2001-08-29
: PRIOR APPLICATION NUMBER: US 09/697,089
: PRIOR FILING DATE: 2000-10-26
: PRIOR APPLICATION NUMBER: US 60/161,822
: PRIOR FILING DATE: 1999-10-27
: NUMBER OF SEQ ID NOS: 16
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 3
: LENGTH: 3072
: TYPE: DNA

```

```

: ORGANISM: Homo sapiens
US-09-841-739-3

Alignment Scores:
Pred. No.: 6,11e-105 Length: 3072
Score: 829.00 Matches: 163
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatch: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-697-089-2_COPY_161_323 (1-163) x US-09-841-739-3 (1-3072)

QY 1 LeuGlnSerProCysIleIleGlnGlyIleSerGlyGlySerThrLeuGln 20
DB 481 CTTGAGACCCCTGTCATCATGAAAGGGAACCTGCAAAAGCAAGTCACCTCTCCAG 540
QY 21 ArgIleAlaMetLeuTrpGlySerGlyGlySerGlyAlaLeuThrLysPheLysPheVal 40
DB 541 GCATTTGCCATGCTCTGSGGCTCCGGAAGTCAAGGCTCTGACCACAGTTCAAAATTCGTC 600
QY 41 PhePheLeuArgLeuSerArgAlaGlnGlyIleLeuPheGluThrLeuCysAspGlnLeu 60
DB 601 TTCTTCCTCCCGTCTCAGAGGGCCAGGGTGGACTTTTGAACCTCTGTGATCACTC 660
QY 61 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 80
DB 661 CTGCATATACCTGCGCACATCAGACAGCATTCATCAAGCCATGCTGCAACCTGCGG 720
QY 81 GlnArgValIleuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 100
DB 721 CAGAGGGTCTTCTTCTCTTGATGGCTACAAATGATTCAAGCCCGCAACTGCCAGAA 780
QY 101 IleGlnAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValThrThrThr 120
DB 781 ATCGAAGCCCTGATTAAGAAAGAAACACCGCTTCAAGAACATGTCATGTCACCACTACC 840
QY 121 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 140
DB 841 ACTGATGCTCGTAGCGACATACGGCAGTTGGTCCCTGACTGCTGAGGTGGGGATATG 900
QY 141 ThrGluAspSerAlaGlnAlaLeuIleArgGluValIleuIleLysGlnLeuAlaGlnGly 160
DB 901 ACAGAGACAGCGCCAGGCTCTCATCCGAGAGTGTGATCAAGAGACTGTGAAAGGC 960
QY 161 LeuLeuLeu 163
DB 961 TTGTTGCTC 969

RESULT 3
US-09-841-739-1
: Sequence 1, Application US/09841739
: Patent No. US20020034784A1
: GENERAL INFORMATION:
: APPLICANT: Berlin, John
: TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
: FILE REFERENCE: 07334-329001
: CURRENT APPLICATION NUMBER: US/09/841,739
: CURRENT FILING DATE: 2001-08-29
: PRIOR APPLICATION NUMBER: US 09/697,089
: PRIOR FILING DATE: 2000-10-26
: PRIOR APPLICATION NUMBER: US 60/161,822
: PRIOR FILING DATE: 1999-10-27
: NUMBER OF SEQ ID NOS: 16
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1
: LENGTH: 3133
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (36) ... (3107)
: US-09-841-739-1

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## Alignment Scores:

Pred. No.:	6.3e-105	Length:	3133
Score:	829.00	Matches:	163
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-09-697-089-2\_COPY\_161\_323 (1-163) x US-09-841-739-1 (1-3133)

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QY 1 LeuGlnSerProCysIleIleGlnGlyGluSerGlyLysSerThrLeuLeuGln 20
    |||||||
DB 516 CTCACAGAGCCCTGCATCATGGAAGGGAAATCGCAAGCAAGCTCCTGCTGCAG 575
QY 21 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheVal 40
    |||||||
DB 576 CGCATTCGCATGCTCTGGGCTCCGGAAGCTGCAGCAAGCTCTGACCAATTGCTC 635
QY 41 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGlnThrLeuCysAspGlnLeu 60
    |||||||
DB 636 TTCTTCTCCGCTCTCACAGAGGCCAGGGTGACTTTTGAAACCTCTGATCAACTC 695
QY 61 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLysLeuArg 80
    |||||||
DB 696 CTGGATATACCTGGCAACATCAGGAAGCAGACATTCATGGCCATGCTGGAAGCTCGG 755
QY 81 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGlnPheLysProGlnAsnCysProGlu 100
    |||||||
DB 756 CAGAGGCTTCTTCTCTCTTCTGATGGCTACAAATCAATCAAGCCCAAGCTGCCAGAA 815
QY 101 IleGlnAlaLeuLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValIleThrThr 120
    |||||||
DB 816 ATGAAAGCCCTGTAAGGAAGAAACACCGCTTCAAGAACATGGTCATCGTACCACATAC 875
QY 121 ThrGlnCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGlnValIleGlyAspMet 140
    |||||||
DB 876 ACTGAGTGCTTGAGGACATACAGGAGTTGGTGCCCTGACTGCTGAGGTGGGGGATATG 935
QY 141 ThrGlnAspSerAlaGlnAlaLeuIleArgGlnValLeuIleLysGlnLeuAlaGlnGly 160
    |||||||
DB 936 ACAGAAAGACAGCCGCCAGGCTCTCATCCGAGAAAGTGCTGATCAAGAGGCTTGCGTGAAGCC 995
QY 161 LeuLeuLeu 163
    |||||||
DB 996 TTGTGTGCTC 1004
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## RESULT 4

```
US-09-864-921-96
; Sequence 96, Application US/09864921
; Patent No. US20020176853A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Plo, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sung-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: NO. US20020176853A1el Card Domain Containing
; FILE REFERENCE: P-1J 4752
; CURRENT APPLICATION NUMBER: US/09/864,921
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
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; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 96
; LENGTH: 3396
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (277)...(3348)
US-09-864-921-96
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## Alignment Scores:

Pred. No.:	7.1e-105	Length:	3396
Score:	829.00	Matches:	163
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-697-089-2\_COPY\_161\_323 (1-163) x US-09-864-921-96 (1-3396)

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QY 1 LeuGlnSerProCysIleIleGlnGlyGluSerGlyLysSerThrLeuLeuGln 20
    |||||||
DB 757 CTCACAGAGCCCTGCATCATGGAAGGGAAATCGCAAGCAAGCTCCTGCTGCAG 816
QY 21 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheVal 40
    |||||||
DB 817 CGCATTCGCATGCTCTGGGCTCCGGAAGTGCAAGGCTCTGACCAAGTTCAAATTGCTC 876
QY 41 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGlnThrLeuCysAspGlnLeu 60
    |||||||
DB 877 TTCTTCTCCGCTCTCACAGAGGCCAGGGTGACTTTTGAAACCTCTGATCAACTC 936
QY 61 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLysLeuArg 80
    |||||||
DB 937 CTGGATATACCTGGCAACATCAGGAAGCAGACATTCATGGCCATGCTGGAAGCTCGG 996
QY 81 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGlnPheLysProGlnAsnCysProGlu 100
    |||||||
DB 997 CAGAGGCTTCTTCTCTCTTCTGATGGCTACAAATCAATCAAGCCCAAGCTGCCAGAA 1056
QY 101 IleGlnAlaLeuLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValIleThrThr 120
    |||||||
DB 1057 ATCGAAAGCCCTGTAAGGAAGAAACACCGCTTCAAGAAATGTCATCGTACACACTATAC 1116
QY 121 ThrGlnCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGlnValIleGlyAspMet 140
    |||||||
DB 1117 ACTGAGTGCTTGAGGACATACAGGAGTTGGTGCCCTGACTGCTGAGGTGGGGATATG 1176
QY 141 ThrGlnAspSerAlaGlnAlaLeuIleArgGlnValLeuIleLysGlnLeuAlaGlnGly 160
    |||||||
DB 1177 ACAGAAAGACAGCCGCCAGGCTCTCATCCGAGAAAGTGCTGATCAAGAGGCTTGCGTGAAGCC 1236
QY 161 LeuLeuLeu 163
    |||||||
DB 1237 TTGTGTGCTC 1245
```

## RESULT 5

```
US-09-841-739-6
; Sequence 6, Application US/09841739
; Patent No. US20020034784A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Novell
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES TH
; FILE REFERENCE: 07334-339001
; CURRENT APPLICATION NUMBER: US/09/841,739
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
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LENGTH: 3612  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-841-739-6

Alignment Scores:  
Pred. No.: 7.79e-105 Length: 3612  
Score: 829.00 Matches: 163  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 10 Gaps: 0

US-09-697-089-2\_COPY\_161\_323 (1-163) x US-09-841-739-6 (1-3612)

QY 1 LeuGInserProCysIleIleGluGlyGInserGlyGlySerThrLeuGln 20  
DB 952 CTTCAAGCCCTGCTATCTTGAAGGGATCTGGCAAGGCCACTCTGCTGCAG 1011  
QY 21 ArgIleAlaMetLeuTrpGlySerGlyLysCysAlaLeuThrLysPheVal 40  
DB 1012 CGAATTGCCATGCTCTGGGGCTCCGAAAGTGCAGGCTGTGACCAAGTTCAATTCTGTC 1071  
QY 41 PhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGluThrLeuCysAspGlnLeu 60  
DB 1072 TTCTTCTCTCGTCTCAGCAGGGCCAGGGTGGACTTTTGAACCTCTGTGATCAACTC 1131  
QY 61 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLysLeuArg 80  
DB 1132 CTGGATATACCTGGCAATCAGGAAGACACATTCATGCGCCATGCTGGAAGCTGGCG 1191  
QY 81 GlnArgValLeuPheLeuLysAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 100  
DB 1192 CAGAGGCTCTTTCTCTCTGATGGCTACAAATTCAGGCCACAGAACTGCCAGAA 1251  
QY 101 IleGluAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValThrThr 120  
DB 1252 ATCGAAGCCCTGATTAAGAAACACCCCTTCAGAACATGCTCATCCACTACC 1311  
QY 121 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 140  
DB 1312 ACTGATGCTCTGAGCAGCATACGGCAGTTGGTCCCTGACTGCTAGGGGGGATATG 1371  
QY 141 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGlnLeuAlaGlnGly 160  
DB 1372 ACAGAAGACAGCCGCCAGCTCTCATCCAGAAGTGTGATCAAGAGCTGCTGAAGGC 1431  
QY 161 LeuLeuLeu 163  
DB 1432 TTGTTGCTC 1440

RESULT 6

US-09-841-739-4

Sequence 4, Application US/09841739

Patent No. US20020034784A1

GENERAL INFORMATION:

APPLICANT: Berlin, John

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE

FILE REFERENCE: 07334-329001

CURRENT APPLICATION NUMBER: US/09/841,739

PRIOR FILING DATE: 2001-08-29

PRIOR APPLICATION NUMBER: US 09/697,089

PRIOR FILING DATE: 2000-10-26

PRIOR APPLICATION NUMBER: US 60/161,822

PRIOR FILING DATE: 1999-10-27

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 4

LENGTH: 3615

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (1)...(3612)  
US-09-841-739-4

Alignment Scores:  
Pred. No.: 7.8e-105 Length: 3615  
Score: 829.00 Matches: 163  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 10 Gaps: 0

US-09-697-089-2\_COPY\_161\_323 (1-163) x US-09-841-739-4 (1-3615)

QY 1 LeuGInserProCysIleIleGluGlyGInserGlyGlySerThrLeuGln 20  
DB 952 CTTCAAGCCCTGCTATCTTGAAGGGATCTGGCAAGGCCACTCTGCTGCAG 1011  
QY 21 ArgIleAlaMetLeuTrpGlySerGlyLysCysAlaLeuThrLysPheVal 40  
DB 1012 CGAATTGCCATGCTCTGGGGCTCCGAAAGTGCAGGCTGTGACCAAGTTCAATTCTGTC 1071  
QY 41 PhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGluThrLeuCysAspGlnLeu 60  
DB 1072 TTCTTCTCTCGTCTCAGCAGGGCCAGGGTGGACTTTTGAACCTCTGTGATCAACTC 1131  
QY 61 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLysLeuArg 80  
DB 1132 CTGGATATACCTGGCAATCAGGAAGACACATTCATGCGCCATGCTGGAAGCTGGCG 1191  
QY 81 GlnArgValLeuPheLeuLysAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 100  
DB 1192 CAGAGGCTCTTTCTCTCTGATGGCTACAAATTCAGGCCACAGAACTGCCAGAA 1251  
QY 101 IleGluAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValThrThr 120  
DB 1252 ATCGAAGCCCTGATTAAGAAACACCCCTTCAGAACATGCTCATCCACTACC 1311  
QY 121 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 140  
DB 1312 ACTGATGCTCTGAGCAGCATACGGCAGTTGGTCCCTGACTGCTAGGGGGGATATG 1371  
QY 141 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGlnLeuAlaGlnGly 160  
DB 1372 ACAGAAGACAGCCGCCAGCTCTCATCCAGAAGTGTGATCAAGAGCTGCTGAAGGC 1431  
QY 161 LeuLeuLeu 163  
DB 1432 TTGTTGCTC 1440

RESULT 7

US-09-841-739-12/C

Sequence 12, Application US/09841739

Patent No. US20020034784A1

GENERAL INFORMATION:

APPLICANT: Berlin, John

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES TH

FILE REFERENCE: 07334-329001

CURRENT APPLICATION NUMBER: US/09/841,739

PRIOR FILING DATE: 2001-08-29

PRIOR APPLICATION NUMBER: US 09/697,089

PRIOR FILING DATE: 2000-10-26

PRIOR APPLICATION NUMBER: US 60/161,822

PRIOR FILING DATE: 1999-10-27

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 12

LENGTH: 3615

TYPE: DNA

ORGANISM: Homo sapiens

US-09-841-739-12

Alignment Scores:

Pred. No.: 7.8e-105 Length: 3615

Score: 829.00 Matches: 163  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 10 Gaps: 0

US-09-697-089-2\_COPY\_161\_323 (1-163) x US-09-841-739-12 (1-3615)

```
OY 1 LeuGlnSerProCysIleIleGlnGlyIuSerGlyLysGlySerThrLeuGln 20
DB 2664 CTTGAGAGCCCTGCATCTTAAGAGGATGTGGCAAGGCAAGTCCACTGCTGCGAG 2605
OY 21 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40
DB 2604 CGAATGGCATGCTCTGGGGCTCCGGAAGTCCAGAGGCTGTGACCAAGTCAAAATTCGTC 2545
OY 41 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuCysAspGlnLeu 60
DB 2544 TTCTTCCCTCCGTACAGAGGCGCCAGGGGTGACTTTTGAAGCCCTGTGATCAACTC 2485
OY 61 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 80
DB 2484 CTGGAATACCTGGCAACATCAAGAAAGACATTGATGCGCATGCTGAGAGCTGGCG 2425
OY 81 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnGlyProGlu 100
DB 2424 CAGAGGGTTCTTCTTCTTCTTATGCTGATGATGATTAAGCCCAAGAACTGCCAGAA 2365
OY 101 IleGluAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValThrThrThr 120
DB 2364 ATCGAAGCCCTGATTAAGAAACACACCGCTTCAAGAAACATGCTATCGTCAACACTAC 2305
OY 121 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValLysPmet 140
DB 2304 ACTGATGCTGAGGACATACGCAATGTTGGTCCCTGACTGCTGAGGTGGGATTAAG 2245
OY 141 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGlnLeuAlaGlnGly 160
DB 2244 ACAGAAAGACAGGCGCCAGGCTCTCATCGAAGAAAGCTGATCAAGAGCTTCTGAAGGC 2185
OY 161 LeuLeuLeu 163
DB 2184 TTGTGTCTC 2176
```

## RESULT 8

US-09-764-864-754  
Sequence 754, Application US/09764864  
Patent No. US20020132753A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
FILE REFERENCE: PT723  
CURRENT APPLICATION NUMBER: US/09/764,864  
CURRENT FILING DATE: 2001-01-17  
Prior application data removed - consult PALM or file wrapper  
NUMBER OF SEQ ID NOS: 1792  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 754  
LENGTH: 522  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (360)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: SITE  
LOCATION: (468)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: SITE  
LOCATION: (499)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: SITE  
LOCATION: (505)

OTHER INFORMATION: n equals a,t,g, or c  
US-09-764-864-754

Alignment Scores: 2,82e-29 Length: 522  
Pred. No.: 276.00 Matches: 69  
Score: 81.11% Conservative: 4  
Percent Similarity: 76.67% Mismatches: 13  
Best Local Similarity: 33.29% Indels: 6  
Query Match: 10 Gaps: 1  
DB: 1

US-09-697-089-2\_COPY\_161\_323 (1-163) x US-09-764-864-754 (1-522)

```
OY 1 LeuGlnSerProCysIleIleGlnGlyIuSerGlyLysGlySerThrLeuGln 20
DB 246 CTTGAGAGCCCTGCATCTTAAGAGGATGTGGCAAGGCAAGTCCACTGCTGCGAG 305
OY 21 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLys-PheVal 40
DB 306 CGCATTTGCCATGCTCTGGGGCTCCGGAAGTCCAGAGGCTGTGACCAAGTTCAANTTCGT 365
OY 40 Phe-PheLeuArgLeuSerArgAlaGlnGly-GlyLeuPheGluThrLeuCysAspGln 59
DB 366 CTTCTTCTCCTGTTACAGAGGCGCCAGGGGTGACTTTTGAAGCCCTGTGATCA 425
OY 60 LeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeu 79
DB 426 TTCCG-GGTATACGGGACA-TTCAAGAGGCGACATTCAGCCNGGT---GCTGAGGTG 480
OY 80 ArgGlnArgValLeuPheLeuLeu 87
DB 481 CGGCAAGAGGTTCTTTCTCCTTG 504
```

## RESULT 9

US-08-913-322-1  
Sequence 1, Application US/08913322  
Patent No. US20020137028A1  
GENERAL INFORMATION:  
APPLICANT: Korneluk, Robert G.  
APPLICANT: Mackenzie, Alexander E.  
APPLICANT: Roy, Natalie  
APPLICANT: Robertson, George  
APPLICANT: Tamal, Katsu  
TITLE OF INVENTION: USER OF NEURONAL APOPTOSIS INHIBITOR  
FILE REFERENCE: (NAIP)  
CURRENT APPLICATION NUMBER: US/08/913,322  
CURRENT FILING DATE: 1997-09-12  
EARLIER APPLICATION NUMBER: PCT/JP97/00142  
EARLIER FILING DATE: 1997-01-17  
EARLIER APPLICATION NUMBER: GB 9601108.5  
EARLIER FILING DATE: 1996-01-19  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1  
LENGTH: 5504  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-08-913-322-1

Alignment Scores: 2,91e-22 Length: 5504  
Pred. No.: 236.50 Matches: 53  
Score: 58.96% Conservative: 26  
Percent Similarity: 39.55% Mismatches: 48  
Best Local Similarity: 28.53% Indels: 7  
Query Match: 8 Gaps: 3  
DB: 3

US-09-697-089-2\_COPY\_161\_323 (1-163) x US-08-913-322-1 (1-5504)

```
OY 1 LeuGlnSerProCysIleIleGlnGlyIuSerGlyLysGlySerThrLeuGln 20
DB 1779 TTGAACCTGTCATGTGTGTGAGGGTGAACCTGGAAGTGAAGAAAGCGTCTCTGAAG 1838
```

```
QY 21 Arg11eAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheVal 40
    ::::::::::::::::::::
Db 1839 AAATAGCTTTCTGTGGGCGATCGATGCTGCCCTGTTAAACAGTTCCAGCTGTT 1898
QY 41 PhePheLeuArgLeuSer-----ArgAlaGlnGlyGlyLeuPheGlnThrLysCysASP 58
    ::::::::::::::::::::
Db 1899 TTCTACTCTCCCTTAGTCCACAGCCAGACGAGGGGCTGGCCAGTATCATCTGTGAC 1958
QY 59 GlnLeuLeuAsp1LeProGlyThr1LeArgLysGlnThrPheMetAlaMetLeuLys 78
    ::::::::::::::::::::
Db 1959 CAGCTCTAGAGAAAGAGATCTGTACTGAAATGTCATGAGAGACATTAATCCACAG 2018
QY 79 LeuArgGlnArgValLeuPheLeuLeuAspGlyTyraSngLuphe-----LysProGln 96
    ::::::::::::::::::::
Db 2019 TTAAAGATCAGGCTTATCTCTTTAGATGACTACAAAGAAATATGTCATCCCTCA 2078
QY 97 AsnCysProGlu1LeGlnAlaLeu1LeLysGlnLysHisArgPheLysAsnMetVal1Le 116
    ::::::::::::::::::::
Db 2079 -----GTCAATAGCAAAAGATGATTCAAAACCACTTATCCCGACCTGCTATTG 2129
QY 117 ValThrThrThrThrGlyCysLeuArgHis1LeArgGlnPhe 130
    ::::::::::::::::::::
Db 2130 ATTGCTGTCCGTACAAACAGGCGCCAGGACATCCGCCGATAC 2171

RESULT 10
US-08-913-322-21
; Sequence 21, Application US/08913322
; Patent No. US20020137028A1
; GENERAL INFORMATION:
; APPLICANT: Korneiluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Roy, Natalie
; APPLICANT: Robertson, George
; APPLICANT: Tama, Katsu
; TITLE OF INVENTION: USER OF NEURONAL APOPTOSIS INHIBITOR
; FILE REFERENCE: 07891/013001
; CURRENT APPLICATION NUMBER: US/08/913,322
; CURRENT FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: PCT/IB97/00142
; EARLIER FILING DATE: 1997-01-17
; EARLIER APPLICATION NUMBER: GB 9601108.5
; EARLIER FILING DATE: 1996-01-19
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 6124
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-913-322-21

Alignment Scores:
Pred. No.: 3,42e-22 Length: 6124
Score: 236.50 Matches: 53
Percent Similarity: 58.96% Conservative: 26
Best Local Similarity: 39.53% Mismatches: 48
Query Match: 28.53% Indels: 7
Gaps: 3

US-09-697-089-2_COPY_161_323 (1-163) x US-08-913-322-21 (1-6124)
QY 1 LeuGlnSerProCys1Le1LeGlnGlyGlnSerGlyLysGlyLysSerThrLeuLeuGln 20
    ::::::::::::::::::::
Db 1675 TTGAACCTGTGCATGTGTGGAGGTGAAGCTGGAAGAGAGCGTCTCTCTGAAG 1734
QY 21 Arg11eAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40
    ::::::::::::::::::::
Db 1735 AAATAGCTTTCTGTGGGCGATCTGAGATGCTGCCCTGTTAAACAGGTTCCAGCTGTT 1794
QY 41 PhePheLeuArgLeuSer-----ArgAlaGlnGlyGlyLeuPheGlnThrLysCysASP 58
    ::::::::::::::::::::
Db 1795 TTCTACTCTCCCTTAGTCCACAGCCAGACGAGGGGCTGGCCAGTATCATCTGTGAC 1854
```

```
QY 59 GlnLeuLeuAsp1LeProGlyThr1LeArgLysGlnThrPheMetAlaMetLeuLys 78
    ::::::::::::::::::::
Db 1855 CAGCTCTAGAGAAAGAGATCTGTACTGAAATGTCATGAGAGACATTAATCCACAG 1914
QY 79 LeuArgGlnArgValLeuPheLeuLeuAspGlyTyraSngLuphe-----LysProGln 96
    ::::::::::::::::::::
Db 1915 TTAAAGATCAGGCTTATCTCTTTAGATGACTACAAAGAAATATGTTCAATCCCTCA 1974
QY 97 AsnCysProGlu1LeGlnAlaLeu1LeLysGlnLysHisArgPheLysAsnMetVal1Le 116
    ::::::::::::::::::::
Db 1975 -----GTCAATAGCAAAAGATGATTCAAAACCACTTATCCCGACCTGCTATTG 2025
QY 117 ValThrThrThrThrGlyCysLeuArgHis1LeArgGlnPhe 130
    ::::::::::::::::::::
Db 2026 ATTGCTGTCCGTACAAACAGGCGCCAGGACATCCGCCGATAC 2067

RESULT 11
US-09-967-768A-184
; Sequence 184, Application US/09967768A
; Patent No. US20020150877A1
; GENERAL INFORMATION:
; APPLICANT: Augustus, Meena
; APPLICANT: Cancer Gene Determination and Therapeutic Screening Using Sign
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-72
; CURRENT APPLICATION NUMBER: US/09/967,768A
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/60/236,109
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,034
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,111
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 325
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 184
; LENGTH: 6124
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-967-768A-184

Alignment Scores:
Pred. No.: 3,42e-22 Length: 6124
Score: 236.50 Matches: 53
Percent Similarity: 58.96% Conservative: 26
Best Local Similarity: 39.53% Mismatches: 48
Query Match: 28.53% Indels: 7
Gaps: 3

US-09-697-089-2_COPY_161_323 (1-163) x US-09-967-768A-184 (1-6124)
QY 1 LeuGlnSerProCys1Le1LeGlnGlyGlnSerGlyLysGlyLysSerThrLeuLeuGln 20
    ::::::::::::::::::::
Db 1675 TTGAACCTGTGCATGTGTGGAGGTGAAGCTGGAAGAGAGCGTCTCTCTGAAG 1734
QY 21 Arg11eAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40
    ::::::::::::::::::::
Db 1735 AAATAGCTTTCTGTGGGCGATCTGAGATGCTGCCCTGTTAAACAGGTTCCAGCTGTT 1794
QY 41 PhePheLeuArgLeuSer-----ArgAlaGlnGlyGlyLeuPheGlnThrLysCysASP 58
    ::::::::::::::::::::
Db 1795 TTCTACTCTCCCTTAGTCCACAGCCAGACGAGGGGCTGGCCAGTATCATCTGTGAC 1854
QY 59 GlnLeuLeuAsp1LeProGlyThr1LeArgLysGlnThrPheMetAlaMetLeuLys 78
    ::::::::::::::::::::
Db 1855 CAGCTCTAGAGAAAGAGATCTGTACTGAAATGTCATGAGAGACATTAATCCACAG 1914
QY 79 LeuArgGlnArgValLeuPheLeuLeuAspGlyTyraSngLuphe-----LysProGln 96
    ::::::::::::::::::::
Db 1915 TTAAAGATCAGGCTTATCTCTTTAGATGACTACAAAGAAATATGTTCAATCCCTCA 1974
QY 97 AsnCysProGlu1LeGlnAlaLeu1LeLysGlnLysHisArgPheLysAsnMetVal1Le 116
    ::::::::::::::::::::
Db 1975 -----GTCAATAGCAAAAGATGATTCAAAACCACTTATCCCGACCTGCTATTG 2025
```





```
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing
; FILE REFERENCE: Polypeptides, Encoding Nucleic Acids, and Methods of Use
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 173
; LENGTH: 888
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(888)
US-09-864-921-173

Alignment Scores:
Pred. No.: 2.48e-07 Length: 888
Score: 120.50 Matches: 33
Percent Similarity: 48.98% Conservative: 15
Best Local Similarity: 33.67% Mismatches: 33
Query Match: 14.54% Indels: 17
DB: 9 Gaps: 3

US-09-697-089-2_COPY_161_323 (1-163) x US-09-864-921-173 (1-888)
QY 6 llelleglugluserglylsrlylsySerrhrleuLeuGlnArglleaIleamelleu 25
      ::::: |||||::: ||||| ||||| ||||| ||||| :::::
Db 19 CTGCTGTGGTGGAGCGGCGAGTGCAGACAGCAGCTCTGCAGCGGCTGCAGCTGCTG 78
QY 26 TTPGlySerrglylsCyslsAlaLeuThrlySPheIysPheValPhePheLeuArgleu 45
      ||| ::::: ||| ::::: ||| ::::: ||| ::::: ||| :::::
Db 79 TGGGCTGCAGGg-----CAAGACTTCAGAGATTCTCTTGTCTCCATTCAGCTGC 132
QY 46 SerArgAlaGln-----GlyGlyLeuPheGlnThrleu 56
      ::::: ||| |||||
Db 133 CGGCAAGCTGCAGTGCATGGCCAAACCACTCTCTGTGCGAGCTCTTTCAGCACATGC 192
QY 57 CysAspGlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetaIleamelleu 76
      |||
Db 193 TGTGGCT-----GATGTTGTGTCAGAGACATCTTCAGATTACTC 234
QY 77 LeuLysLeuArgGlnArgValleuPheLeuLeuAspGlyTyrAsnGlnPheLys 94
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 235 CTTGACCACCTGACCGGTCTCTGTTAACTTTGATGGCTTTCAGAGATTCAAG 288

RESULT 15
US-09-833-381-1214
; Sequence 1214, Application us/09833381
; Patent No. US20020132090A1
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: NO. US20020132090A1el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT FILING DATE: 2001-04-11
; CURRENT APPLICATION NUMBER: US/09/833,381
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 09/516,448
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1214
; LENGTH: 2724
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```
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (1)..(2724)
; OTHER INFORMATION: n = A,T,C or G
US-09-833-381-1214

Alignment Scores:
Pred. No.: 1.32e-06 Length: 2724
Score: 120.50 Matches: 33
Percent Similarity: 48.98% Conservative: 15
Best Local Similarity: 33.67% Mismatches: 33
Query Match: 14.54% Indels: 17
DB: 10 Gaps: 3

US-09-697-089-2_COPY_161_323 (1-163) x US-09-833-381-1214 (1-2724)
QY 6 llelleglugluserglylsrlylsySerrhrleuLeuGlnArglleaIleamelleu 25
      ::::: |||||::: ||||| ||||| ||||| ||||| :::::
Db 1108 CTGCTGTGGTGGAGCGGCGAGTGCAGACAGCAGCTCTGCAGCGGCTGCAGCTGCTG 1167
QY 26 TTPGlySerrglylsCyslsAlaLeuThrlySPheIysPheValPhePheLeuArgleu 45
      ||| ::::: ||| ::::: ||| ::::: ||| ::::: ||| :::::
Db 1168 TGGGCTGCAGGg-----CAAGACTTCAGAGATTCTCTTGTCTCCATTCAGCTGC 1221
QY 46 SerArgAlaGln-----GlyGlyLeuPheGlnThrleu 56
      ::::: ||| |||||
Db 1222 CGGCAAGCTGCAGTGCATGGCCAAACCACTCTCTGTGCGAGCTCTTTCAGCACATGC 1281
QY 57 CysAspGlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetaIleamelleu 76
      |||
Db 1282 TGTGGCT-----GATGTTGTGTCAGAGACATCTTCAGATTACTC 1323
QY 77 LeuLysLeuArgGlnArgValleuPheLeuLeuAspGlyTyrAsnGlnPheLys 94
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1324 CTTGACCACCTGACCGGTCTCTGTTAACTTTGATGGCTTTCAGAGATTCAAG 1377
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Search completed: January 31, 2003, 18:05:15  
Job time : 51.1385 secs

GenCore version 5.1.3  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 31, 2003, 13:16:47 : Search time 2073.15 Seconds  
(without alignments)  
1976.816 Million cell updates/sec

Title: US-09-697-089-2\_COPY\_161\_323  
Perfect score: 829  
Sequence: 1 LQSPCIEGSGKGRKSTLQ.....SAQALIREVLKELAEGLL 163

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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFWT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US09697089 -ECN\_L1\_3083 -Runat\_29012003\_092754\_19749  
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-FGAPEXT=7 -YGAPOP=10 -YGAEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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2: /cgn2\_6/ptodata/2/pna/US06\_COMB.seq:\*  
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19: /cgn2\_6/ptodata/2/pna/US095B\_COMB.seq:\*  
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32: /cgn2\_6/ptodata/2/pna/US098B\_COMB.seq:\*  
33: /cgn2\_6/ptodata/2/pna/US098C\_COMB.seq:\*  
34: /cgn2\_6/ptodata/2/pna/US099A\_COMB.seq:\*  
35: /cgn2\_6/ptodata/2/pna/US099B\_COMB.seq:\*  
36: /cgn2\_6/ptodata/2/pna/US099C\_COMB.seq:\*  
37: /cgn2\_6/ptodata/2/pna/US099D\_COMB.seq:\*  
38: /cgn2\_6/ptodata/2/pna/US100A\_COMB.seq:\*  
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50: /cgn2\_6/ptodata/2/pna/US6006\_COMB.seq:\*  
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52: /cgn2\_6/ptodata/2/pna/US6008\_COMB.seq:\*  
53: /cgn2\_6/ptodata/2/pna/US6009\_COMB.seq:\*  
54: /cgn2\_6/ptodata/2/pna/US6010\_COMB.seq:\*  
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68: /cgn2\_6/ptodata/2/pna/US6024\_COMB.seq:\*  
69: /cgn2\_6/ptodata/2/pna/US6025\_COMB.seq:\*  
70: /cgn2\_6/ptodata/2/pna/US6026\_COMB.seq:\*  
71: /cgn2\_6/ptodata/2/pna/US6027\_COMB.seq:\*  
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73: /cgn2\_6/ptodata/2/pna/US6029\_COMB.seq:\*  
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79: /cgn2\_6/ptodata/2/pna/US6035\_COMB.seq:\*  
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82: /cgn2\_6/ptodata/2/pna/US6038\_COMB.seq:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	829	100.0	891	US-09-864-921-179	Sequence 179, App
2	829	100.0	1976	US-10-029-386-22860	Sequence 22860, A
3	829	100.0	2002	US-10-029-386-25135	Sequence 25135, A
4	829	100.0	2215	PCT-0501-07143-22	Sequence 22, Appl
5	829	100.0	2215	US-10-221-097-22	Sequence 22, Appl
6	829	100.0	2343	US-09-578-789-15	Sequence 15, Appl

7	829	100.0	2343	22	US-09-579-240-15	Sequence 15, Appl
8	829	100.0	2415	22	US-09-578-789-17	Sequence 17, Appl
9	829	100.0	2415	22	US-09-579-240-17	Sequence 17, Appl
10	829	100.0	3018	22	US-09-577-808-3077	Sequence 3077, Ap
11	829	100.0	3072	1	PCR-US00-29643-3	Sequence 3, Appl
12	829	100.0	3072	27	US-09-697-089-3	Sequence 3, Appl
13	829	100.0	3072	32	US-09-841-739-3	Sequence 3, Appl
14	829	100.0	3075	41	US-10-156-733-1	Sequence 1, Appl
15	829	100.0	3133	1	PCR-US00-29643-1	Sequence 1, Appl
16	829	100.0	3133	27	US-09-697-089-1	Sequence 1, Appl
17	829	100.0	3133	32	US-09-841-739-1	Sequence 1, Appl
18	829	100.0	3213	1	PCR-US01-07143-23	Sequence 23, Appl
19	829	100.0	3213	42	US-10-221-097-23	Sequence 23, Appl
20	829	100.0	3219	41	US-10-156-733-14	Sequence 14, Appl
21	829	100.0	3260	1	PCR-US01-14226-06	Sequence 66, Appl
22	829	100.0	3260	26	US-09-667-298-66	Sequence 66, Appl
23	829	100.0	3396	27	US-09-667-298-66	Sequence 96, Appl
24	829	100.0	3396	33	US-09-864-921-96	Sequence 96, Appl
25	829	100.0	3345	18	US-09-491-804-1319	Sequence 1319, Ap
26	829	100.0	3345	34	US-09-922-279-1319	Sequence 1319, Ap
27	829	100.0	3545	34	US-09-922-299A-1319	Sequence 1315, Ap
28	829	100.0	3612	27	US-09-697-089-6	Sequence 6, Appl
29	829	100.0	3612	32	US-09-841-739-6	Sequence 6, Appl
30	829	100.0	3615	1	PCR-US00-29643-4	Sequence 4, Appl
31	829	100.0	3615	1	PCR-US00-29643-6	Sequence 6, Appl
32	829	100.0	3615	27	US-09-697-089-4	Sequence 6, Appl
33	829	100.0	3615	27	US-09-697-089-12	Sequence 12, Appl
34	829	100.0	3615	32	US-09-841-739-4	Sequence 4, Appl
35	829	100.0	3615	32	US-09-841-739-12	Sequence 12, Appl
36	829	100.0	4098	22	US-09-557-676-506	Sequence 906, Appl
37	829	100.0	4098	22	US-09-557-676-512	Sequence 912, Appl
38	829	100.0	4098	38	US-10-042-938-906	Sequence 906, Appl
39	829	100.0	4098	38	US-10-042-938-912	Sequence 912, Appl
40	829	100.0	6012	22	US-09-557-676-911	Sequence 911, Appl
41	829	100.0	6012	22	US-09-557-676-917	Sequence 917, Appl
42	829	100.0	6012	38	US-10-042-938-911	Sequence 911, Appl
43	829	100.0	6012	38	US-10-042-938-917	Sequence 917, Appl
44	829	100.0	6800	22	US-09-578-789-73	Sequence 73, Appl
45	829	100.0	6800	22	US-09-579-240-73	Sequence 73, Appl

## ALIGNMENTS

```

RESULT 1
US-09-864-921-179
; Sequence 179, Application US/09864921
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Plo, Frederick F.
; APPLICANT: Godzik, Adam
; APPLICANT: Stehlik, Christian
; APPLICANT: Damiano, Jason S.
; APPLICANT: Lee, Sug-Hyung
; APPLICANT: Oliveira, Vasco A.
; APPLICANT: Hayashi, Hideki
; APPLICANT: Pawlowski, Krzysztof
; TITLE OF INVENTION: Novel Card Domain Containing
; FILE REFERENCE: P-1J 4752
; CURRENT APPLICATION NUMBER: US/09/864,921
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 09/579,240
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/686,347
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/275,980
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 179
; LENGTH: 891
; TYPE: DNA
; ORGANISM: Homo sapiens

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```

FEATURE:
: NAME/KEY: CDS
: LOCATION: (1) ... (891)
US-09-864-921-179

Alignment Scores:
Pred. NO.: 5.98e-95 Length: 891
Score: 829.00 Matches: 163
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatch: 0
Query Match: 100.00% Indels: 0
DB: 33 Gaps: 0

US-09-697-089-2_COPY_161_323 (1-163) x US-09-864-921-179 (1-891)
QY 1 LeuGlnSerProCysIleIleGluGlyLeuSerGlyLysGlyLysSerThrLeuGln 20
Db 1 CTTGAGACCCCTGCATCATTTGAAGGGGAATCTGGCAAGGCAAGTCACCTCTGCGAG 60
QY 21 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40
Db 61 CGCATTTGCCATGCTGTGGGGCTCCGGAAAGTCGAAGGCTTGACCAAGTTCAATTCGTC 120
QY 41 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuCysAspGlnLeu 60
Db 121 TTCTTCCTCCGTCAGCAGGGCCAGGGGTGGACTTTTGAACCCCTGTGATCACTTC 180
QY 61 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 80
Db 181 CTGGATTATACCTGGCAGCATCAGGACGACATTCATCATGCGCATGCTGTAAGCTGCGG 240
QY 81 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnGlyProGlu 100
Db 241 CAGAGGGTCTTTTCTCTTGATGCTACAAATGATTTCAAGCCCAACACTGGCCAGAA 300
QY 101 IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThrThr 120
Db 301 ATCGAAGCCCTGATTAAGAAAGAACCCGCTTCAAGAACATGATGCTCACACATACC 360
QY 121 ThrGlyCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 140
Db 361 ACTGATGCTCTGAGCAGCATACGCGCATTTGGTCCCTGATGCTGAGGTGGGGATATG 420
QY 141 ThrGluAspSerAlaGlnAlaLeuLeuArgGluValLeuIleLysGluLeuAlaGluGly 160
Db 421 ACAGAGACACCGCCAGGCTCTCATCCGAGAAGTGTGATCAAGAGGACGTTGTAAGGC 480
QY 161 LeuLeuLeu 163
Db 481 TTGTTGCTC 489

RESULT 2
US-10-029-386-22860/c
: Sequence 22860, Application US/10029386
: GENERAL INFORMATION:
: APPLICANT: Penn, Sharron G.
: APPLICANT: Hank, David R.
: APPLICANT: Hanzel, David K.
: TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
: TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
: FILE REFERENCE: AEOICA-X-2
: CURRENT APPLICATION NUMBER: US/10/029,386
: CURRENT FILING DATE: 2001-12-20
: NUMBER OF SEQ ID NOS: 34288
: SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
: SEQ ID NO 22860
: LENGTH: 1976
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: MAP TO AL121653.2
: OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1
: OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4

```

OTHER INFORMATION: SWISSPROT HIT: Q9JTB6, EVALU 2.00e-40  
OTHER INFORMATION: NT HIT: g115296399, EVALU 0.00e+00  
OTHER INFORMATION: EST\_HUMAN HIT: AV656315.1, EVALU 0.00e+00  
US-10-029-386-22860

## Alignment Scores:

Pred. No.:	1.77e-94	Length:	1976
Score:	829.00	Matches:	163
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	38	Gaps:	0

US-09-697-089-2\_copy\_161\_323 (1-163) x US-10-029-386-22860 (1-1976)

Qy 1 LeuGlnSerProCysIleIleGlnGlyGlnSerGlyLysGlyLysSerThrLeuLeuGln 20  
Db 1758 CTTGAGAGCCCTCGCATCTTGAAGGGAATCTGGCAAGGCAAGTCCACTCTGCTGCAG 1699  
Qy 21 ArgIleAlaMetLeuThrPheGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40  
Db 1698 CGAATTGCCATCTCTGGGGCTCCGGAAGTCAAGGCTTGACCAAGTTCAAATTCCGTC 1639  
Qy 41 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuCysAspGlnLeu 60  
Db 1638 TTCTTCCTCCGCTCAGCAGAGGCCAGGGTGGACTTTTGAACCCCTCTGTATCACTC 1579  
Qy 61 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 80  
Db 1578 CTGGATATACCTGGGCACATCGAAGCAGACATTCATGGCCATCTGCTGAAGCTGGCG 1519  
Qy 81 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnGlyProGlu 100  
Db 1518 CAGAGGGTCTTTCTCTTCTTGATGGCTACATGTAATTCACCCAGACAGTCCAGAA 1459  
Qy 101 IleGlnAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValIleThrThr 120  
Db 1458 ATCGAAGCCCTGATTAAGAAACACCGCTTCAGAACATGTCATGTCACCACTACC 1399  
Qy 121 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 140  
Db 1398 ACTGAGTCCCTGAGGACATACGCGAGTTGGTCCCTGACACGCTGAGGTGGGGATATG 1339  
Qy 141 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluIleuAlaGluGly 160  
Db 1338 ACAGAAGACAGGCCAGGCTCTCATCCGAGAAGTCTGATCAAGAGACTTCTGAAGGC 1279  
Qy 161 LeuLeuLeu 163  
Db 1278 TTGTGCTC 1270

## RESULT 3

US-10-029-386-25135/c  
Sequence 25135, Application US/10029386  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Hanzel, David R.  
TITLE OF INVENTION: HUMAN GENOME-DRIVEN SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G  
FILE REFERENCE: AEROMICA-X-2  
CURRENT APPLICATION NUMBER: US/10/029.386  
CURRENT FILING DATE: 2001-12-20  
NUMBER OF SEQ ID NOS: 34288  
SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1  
SEQ ID NO 25135  
LENGTH: 2002  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AL121653.1  
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.36  
OTHER INFORMATION: EST\_HUMAN HIT: AV656315.1, EVALU 0.00e+00

OTHER INFORMATION: SWISSPROT HIT: Q9JTB6, EVALU 2.00e-40  
OTHER INFORMATION: NT HIT: g115296399, EVALU 0.00e+00  
US-10-029-386-25135

## Alignment Scores:

Pred. No.:	1.8e-94	Length:	2002
Score:	829.00	Matches:	163
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	38	Gaps:	0

US-09-697-089-2\_copy\_161\_323 (1-163) x US-10-029-386-25135 (1-2002)

Qy 1 LeuGlnSerProCysIleIleGlnGlyGlnSerGlyLysGlyLysSerThrLeuLeuGln 20  
Db 1782 CTTGAGAGCCCTCGCATCTTGAAGGGAATCTGGCAAGGCAAGTCCACTCTGCTGCAG 1723  
Qy 21 ArgIleAlaMetLeuThrPheGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40  
Db 1722 CGAATTGCCATCTCTGGGGCTCCGGAAGTCAAGGCTTGACCAAGTTCAAATTCCGTC 1663  
Qy 41 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuCysAspGlnLeu 60  
Db 1662 TTCTTCCTCCGCTCAGCAGAGGCCAGGGTGGACTTTTGAACCCCTCTGTATCACTC 1603  
Qy 61 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 80  
Db 1602 CTGGATATACCTGGGCACATCGAAGCAGACATTCATGGCCATCTGCTGAAGCTGGCG 1543  
Qy 81 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnGlyProGlu 100  
Db 1542 CAGAGGGTCTTTCTCTTCTTGATGGCTACATGTAATTCACCCAGACAGTCCAGAA 1483  
Qy 101 IleGlnAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValIleThrThr 120  
Db 1482 ATCGAAGCCCTGATTAAGAAACACCGCTTCAGAACATGTCATGTCACCACTACC 1423  
Qy 121 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 140  
Db 1422 ACTGAGTCCCTGAGGACATACGCGAGTTGGTCCCTGACACGCTGAGGTGGGGATATG 1363  
Qy 141 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluIleuAlaGluGly 160  
Db 1362 ACAGAAGACAGGCCAGGCTCTCATCCGAGAAGTCTGATCAAGAGACTTCTGAAGGC 1303  
Qy 161 LeuLeuLeu 163  
Db 1302 TTGTGCTC 1294

## RESULT 4

PCT-US01-07143-22  
Sequence 22, Application PC/TUS0107143  
GENERAL INFORMATION:  
APPLICANT: SMITHKLINE BEECHAM CORPORATION  
APPLICANT: SMITHKLINE BEECHAM P.L.C.  
TITLE OF INVENTION: NOVEL COMPOUNDS  
FILE REFERENCE: GP50016  
CURRENT APPLICATION NUMBER: PCT/US01/07143  
CURRENT FILING DATE: 2001-03-08  
PRIOR APPLICATION NUMBER: 60/187,107  
PRIOR FILING DATE: 2000-03-06  
PRIOR APPLICATION NUMBER: 60/226,874  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/188,916  
PRIOR FILING DATE: 2000-03-13  
PRIOR APPLICATION NUMBER: 60/237,846  
PRIOR FILING DATE: 2000-10-03  
NUMBER OF SEQ ID NOS: 52  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 22  
LENGTH: 2215  
TYPE: DNA

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; ORGANISM: Homo sapiens
PCT-US01-07143-22

Alignment Scores:
Pred. No.: 2,07e-94      Length: 2215
Score: 829.00           Matches: 163
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%    Mismatches: 0
Query Match: 100.00%             Indels: 0
DB: 1                         Gaps: 0

US-09-697-089-2_COPY_161_323 (1-163) x PCT-US01-07143-22 (1-2215)

QY 1 LeuGlnSerProCysIleIleGlnGlyuSerGlyLysGlySserThrLeuLeuGln 20
Db CTTGAGAGCCCTGCATCATTTGAAGGGAAATCTGGCAAGCAAGTCCACCTGCTGCAG 498

QY 21 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40
Db CGAATTGCCATGCTCTGGGGCTCCGGAAGTGCAGAGCTGACCAAGTTCAAATTGCTC 558

QY 41 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGlnThrLeuCysAspGlnLeu 60
Db TTCTTCCCTCCGCTCAGCAGAGGCCAGGGTGGACTTTTGAACCTCTGTGATCAACTC 618

QY 61 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLysLeuArg 80
Db CTGATATACCTGGCACAATCAGAGCAGACATTCATGGCCATGCTGAGAGCTGGCG 678

QY 81 GlnArgValLeuPheLeuLeuAspGlyTyraGlnPheLysProGlnAsnCysProGlu 100
Db CAGAGGGTCTTTCTTCTTCTTGATGGCTACATGATTCAGCCCAAGCTGCCAGAA 738

QY 101 IleGlnAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValThrThrThr 120
Db ATCGAAGCCCTGATTAAGAAACACCGCTTCAGAAACATGATGTCACCACTACC 798

QY 121 ThrGlnCysLeuArgHisIleArgGlnPheGlnAlaLeuThrAlaGlnValGlyAspMet 140
Db ACTGAGTCCCTGAGGACACATACGGCAGTTTGTGCTCCGACGCTGAGAGTGGGATATG 858

QY 141 ThrGlnAspSerAlaGlnAlaLeuIleArgGlnValLeuIleLysGlnLeuAlaGlnGly 160
Db ACAGAAAGACAGCCCGCAGGCTCTCATCCGAGAAAGTGTGATCAAGAGACTGTGTAAGGC 918

QY 161 LeuLeuLeu 163
Db 919 TTGTTGCTC 927

RESULT 5
US-10-221-097-22
; Sequence 22, Application US/10221097
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdoch, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall F.
; APPLICANT: Xiang, Zhaoying
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GB50016
; CURRENT APPLICATION NUMBER: US/10/221,097
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: PCT/US01/07143
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/187,107
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/236,874
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/188,916
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/237,846
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 52
```

```
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 2215
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-221-097-22

Alignment Scores:
Pred. No.: 2,07e-94      Length: 2215
Score: 829.00           Matches: 163
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%    Mismatches: 0
Query Match: 100.00%             Indels: 0
DB: 42                         Gaps: 0

US-09-697-089-2_COPY_161_323 (1-163) x US-10-221-097-22 (1-2215)

QY 1 LeuGlnSerProCysIleIleGlnGlyuSerGlyLysGlySserThrLeuLeuGln 20
Db CTTGAGAGCCCTGCATCATTTGAAGGGAAATCTGGCAAGCAAGTCCACCTGCTGCAG 498

QY 21 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40
Db CGAATTGCCATGCTCTGGGGCTCCGGAAGTGCAGAGCTGACCAAGTTCAAATTGCTC 558

QY 41 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGlnThrLeuCysAspGlnLeu 60
Db TTCTTCCCTCCGCTCAGCAGAGGCCAGGGTGGACTTTTGAACCTCTGTGATCAACTC 618

QY 599 TTCTTCCCTCCGCTCAGCAGAGGCCAGGGTGGACTTTTGAACCTCTGTGATCAACTC 618
Db 559 CTGATATACCTGGCACAATCAGAGCAGACATTCATGGCCATGCTGAGAGCTGGCG 678

QY 61 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLysLeuArg 80
Db 619 CTGATATACCTGGCACAATCAGAGCAGACATTCATGGCCATGCTGAGAGCTGGCG 678

QY 81 GlnArgValLeuPheLeuLeuAspGlyTyraGlnPheLysProGlnAsnCysProGlu 100
Db CAGAGGGTCTTTCTTCTTCTTGATGGCTACATGATTCAGCCCAAGCTGCCAGAA 738

QY 101 IleGlnAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValThrThrThr 120
Db 739 ATCGAAGCCCTGATTAAGAAACACCGCTTCAGAAACATGATGTCACCACTACC 798

QY 121 ThrGlnCysLeuArgHisIleArgGlnPheGlnAlaLeuThrAlaGlnValGlyAspMet 140
Db 799 ACTGAGTCCCTGAGGACACATACGGCAGTTTGTGCTCCGACGCTGAGAGTGGGATATG 858

QY 141 ThrGlnAspSerAlaGlnAlaLeuIleArgGlnValLeuIleLysGlnLeuAlaGlnGly 160
Db 859 ACAGAAAGACAGCCCGCAGGCTCTCATCCGAGAAAGTGTGATCAAGAGACTGTGTAAGGC 918

QY 161 LeuLeuLeu 163
Db 919 TTGTTGCTC 927

RESULT 6
US-09-578-789-15
; Sequence 15, Application US/09578789
; GENERAL INFORMATION:
; APPLICANT: John C. Reed
; APPLICANT: Frederick Pio
; APPLICANT: Adam Godzik
; TITLE OF INVENTION: Novel Card Polypeptides
; FILE REFERENCE: P-LJ 4141
; CURRENT APPLICATION NUMBER: US/09/578,789
; CURRENT FILING DATE: 2000-05-23
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 2343
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2340)
```

## US-09-578-789-15

## Alignment Scores:

Pred. No.: 2,23e-94 Length: 2343  
Score: 829.00 Matches: 163  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 22 Gaps: 0

US-09-697-089-2\_COPY\_161\_323 (1-163) x US-09-578-789-15 (1-2343)

QY 1 LeuGlnSerProCysIleIleGlnGlyGlnSerGlyLysGlyLysSerThrLeuLeuGln 20  
DB 508 CTTGAGAGCCCTGATCATTTGAAGGGAAATCTGGCAAGGCAAGTCCACTGCTGCAG 567  
QY 21 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40  
DB 568 CGCATTTGCCATGCTCTGGGGCTCCGGAAAGTGCAGAGCTTGACCAAGTTCAAAATTCGTC 627  
QY 41 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuCysAspGlnLeu 60  
DB 628 TTCTTCTCTCGTCTCAGAGGGCCAGGTGGACTTTTGAAGCCCTGTGATCAACTC 687  
QY 61 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 80  
DB 688 CTGGAATATACCTGGCACAATCAGAGACAGACATTCATGGCCATGCTGTGAAGCTGCGG 747  
QY 81 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 100  
DB 748 CAGAGGGTCTTTCTCTTCTGATGCTACATGAAATCAACCCCGAGAACTGCCAGAA 807  
QY 101 IleGlnAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValIleThrThrThr 120  
DB 808 ATCGAAGCCCTGATTAAGGAAACACCGCTTCAAGAACATGCTCATCTCACCTAC 867  
QY 121 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 140  
DB 868 ACTGAGTGCCTGAGGACATACGAGATTGGTGCCTGACATGCTGAGGTGGGGATATG 927  
QY 141 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 160  
DB 928 ACAGAAAGACAGGCCAGGCTCTCATCCGAAAGTCGATCAAGAGCTTGTGTGAAGC 987  
QY 161 LeuLeuLeu 163  
DB 988 TTGTTGCTC 996

## RESULT 7

US-09-579-240-15

; Sequence 15, Application US/09579240

## GENERAL INFORMATION:

; APPLICANT: John C. Reed  
; APPLICANT: Frederick Pio  
; APPLICANT: Adam Godzik  
; TITLE OF INVENTION: Novel Card-Domain Containing  
; TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods of Use  
; FILE REFERENCE: P-LJ 4211  
; CURRENT APPLICATION NUMBER: US/09/579, 240  
; NUMBER OF SEQ ID NOS: 79  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15  
; LENGTH: 2343  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(2340)  
US-09-579-240-15

## Alignment Scores:

Pred. No.: 2.23e-94 Length: 2343

Score: 829.00 Matches: 163  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 22 Gaps: 0

US-09-697-089-2\_COPY\_161\_323 (1-163) x US-09-579-240-15 (1-2343)

QY 1 LeuGlnSerProCysIleIleGlnGlyGlnSerGlyLysGlyLysSerThrLeuLeuGln 20  
DB 508 CTTGAGAGCCCTGATCATTTGAAGGGAAATCTGGCAAGGCAAGTCCACTGCTGCAG 567  
QY 21 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40  
DB 568 CGCATTTGCCATGCTCTGGGGCTCCGGAAAGTGCAGAGCTTGACCAAGTTCAAAATTCGTC 627  
QY 41 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuCysAspGlnLeu 60  
DB 628 TTCTTCTCTCGTCTCAGAGGGCCAGGTGGACTTTTGAAGCCCTGTGATCAACTC 687  
QY 61 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 80  
DB 688 CTGGAATATACCTGGCACAATCAGAGACAGACATTCATGGCCATGCTGTGAAGCTGCGG 747  
QY 81 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 100  
DB 748 CAGAGGGTCTTTCTCTTCTGATGCTACATGAAATTAAGCCCAAGACTGCCAGAA 807  
QY 101 IleGlnAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValIleThrThrThr 120  
DB 808 ATCGAAGCCCTGATTAAGGAAACACCGCTTCAAGAACATGCTCATCTCACCTAC 867  
QY 121 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 140  
DB 868 ACTGAGTGCCTGAGGACATACGAGATTGGTGCCTGACATGCTGAGGTGGGGATATG 927  
QY 141 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 160  
DB 928 ACAGAAAGACAGGCCAGGCTCTCATCCGAAAGTCTGATCAAGAGCTTGTGTGAAGC 987  
QY 161 LeuLeuLeu 163  
DB 988 TTGTTGCTC 996

## RESULT 8

US-09-578-789-17

; Sequence 17, Application US/09578789

## GENERAL INFORMATION:

; APPLICANT: John C. Reed  
; APPLICANT: Frederick Pio  
; APPLICANT: Adam Godzik  
; TITLE OF INVENTION: Novel Card Polypeptides  
; FILE REFERENCE: P-LJ 4141  
; CURRENT APPLICATION NUMBER: US/09/578, 789  
; NUMBER OF SEQ ID NOS: 75  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 2415  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(2412)  
US-09-578-789-17

## Alignment Scores:

Pred. No.: 2.33e-94 Length: 2415  
Score: 829.00 Matches: 163  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 22 Gaps: 0

US-09-697-089-2\_COPY\_161\_323 (1-163) x US-09-578-789-17 (1-2415)

```
OY 1 LeuGlnSerProCysIleIleGlnGlyGluSerGlyLysGlyLysSerThrLeuLeuGln 20
    |||
Db 508 CTGAGAGCCCTCGATCATGTAAGGGGAATCTGGCAAGGCAAGTCACCTGCTGCAG 567
OY 21 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40
    |||
Db 568 CGCATTTGCATGCTCTGGGGGCTCCGGAAAGTGCAGAGGCTTGACCAATTAAATTCGTC 627
OY 41 PhePheLeuArgLeuSerArgAlaGlnGlyLysLeuPheGluThrLeuCysAspGlnLeu 60
    |||
Db 628 TTCTTCTCCGCTTCAGAGAGGGCCAGGGTGAGCTTTTGAACCCCTGTGATCACTC 687
OY 61 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 80
    |||
Db 688 CTGATATACCTGGACACATCAGGAAGCAGACATTCATGGCCATGCTGAAAGCTGGGG 747
OY 81 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 100
    |||
Db 748 CAGAGGGTCTTTTCCCTTCTTGATGGCTACATGATTCAGCCCAACTGCCACAGA 807
OY 101 IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThrThr 120
    |||
Db 808 ATCGAAGCCCTGATTAAGAAACACCGCTTCAAGACATGTCATGTCACACCTACC 867
OY 121 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 140
    |||
Db 868 ACTAGTCTCTGAGGACACATAGCGAGTTTGTCCTGAGCTGAGAGTGGGGATATG 927
OY 141 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 160
    |||
Db 928 ACAGAAGACAGCGCCAGAGCTCTCATCCGAGAAGTGTGATCAAGAGACTTGTCAAGGC 987
OY 161 LeuLeuLeu 163
    |||
Db 988 TTGTTGCTC 996
```

## RESULT 9

US-09-579-240-17  
: Sequence 17, Application US/09579240  
: GENERAL INFORMATION:  
: APPLICANT: John C. Reed  
: APPLICANT: Frederick Pio  
: APPLICANT: Adam Godzik  
: TITLE OF INVENTION: Novel Card-Domain Containing  
: FILE REFERENCE: P-LJ 4211  
: CURRENT APPLICATION NUMBER: US/09/579, 240  
: CURRENT FILING DATE: 2000-05-24  
: NUMBER OF SEQ ID NOS: 79  
: SOFTWARE: FastSeq for Windows Version 4.0  
: SEQ ID NO 17  
: LENGTH: 2415  
: TYPE: DNA  
: ORGANISM: Homo Sapien  
: FEATURE:  
: NAME/KEY: CDS  
: LOCATION: (1)...(2412)  
US-09-579-240-17

## Alignment Scores:

Pred. No.: 2,33e-94  
Score: 829.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
DB: 22

Length: 2415  
Matches: 163  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Gaps: 0

US-09-697-089-2\_COPY\_161\_323 (1-163) x US-09-579-240-17 (1-2415)

OY 1 LeuGlnSerProCysIleIleGlnGlyGluSerGlyLysGlyLysSerThrLeuLeuGln 20

```
|||||
Db 508 CTGAGAGCCCTCGATCATGTAAGGGGAATCTGGCAAGGCAAGTCACCTGCTGCAG 567
OY 21 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40
    |||
Db 568 CGCATTTGCATGCTCTGGGGGCTCCGGAAAGTGCAGAGGCTTGACCAATTAAATTCGTC 627
OY 41 PhePheLeuArgLeuSerArgAlaGlnGlyLysLeuPheGluThrLeuCysAspGlnLeu 60
    |||
Db 628 TTCTTCTCCGCTTCAGAGAGGGCCAGGGTGAGCTTTTGAACCCCTGTGATCACTC 687
OY 61 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 80
    |||
Db 688 CTGATATACCTGGACACATCAGGAAGCAGACATTCATGGCCATGCTGAAAGCTGGGG 747
OY 81 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 100
    |||
Db 748 CAGAGGGTCTTTTCCCTTCTTGATGGCTACATGATTCAGCCCAACTGCCACAGA 807
OY 101 IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThrThr 120
    |||
Db 808 ATCGAAGCCCTGATTAAGAAACACCGCTTCAAGACATGTCATGTCACACCTACC 867
OY 121 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 140
    |||
Db 868 ACTAGTCTCTGAGGACACATAGCGAGTTTGTCCTGAGCTGAGAGTGGGGATATG 927
OY 141 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 160
    |||
Db 928 ACAGAAGACAGCGCCAGAGCTCTCATCCGAGAAGTGTGATCAAGAGACTTGTCAAGGC 987
OY 161 LeuLeuLeu 163
    |||
Db 988 TTGTTGCTC 996
```

## RESULT 10

US-09-577-408-3077  
: Sequence 3077, Application US/09577408  
: GENERAL INFORMATION:  
: APPLICANT: Tang, Y. Tom  
: APPLICANT: Tillinghast, John  
: APPLICANT: Slinku, Ankura  
: APPLICANT: Liu, Chenghua  
: APPLICANT: Drmanac, Radoje T.  
: TITLE OF INVENTION: Novel Nucleic Acids and  
: FILE REFERENCE: 792  
: CURRENT APPLICATION NUMBER: US/09/577,408  
: CURRENT FILING DATE: 2000-05-18  
: NUMBER OF SEQ ID NOS: 8502  
: SOFTWARE: PL\_GCT\_genes Version 1.0  
: SEQ ID NO 3077  
: LENGTH: 3018  
: TYPE: DNA  
: ORGANISM: Homo sapiens  
: FEATURE:  
: NAME/KEY: misc\_feature  
: LOCATION: (682)...(2040)  
: OTHER INFORMATION: similar to g13688110 in the genepept database release 115,  
US-09-577-408-3077

## Alignment Scores:

Pred. No.: 3,15e-94  
Score: 829.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
DB: 22

Length: 3018  
Matches: 163  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Gaps: 0

US-09-697-089-2\_COPY\_161\_323 (1-163) x US-09-577-408-3077 (1-3018)

OY 1 LeuGlnSerProCysIleIleGlnGlyGluSerGlyLysGlyLysSerThrLeuLeuGln 20

```
|||||
Db 715 CTTGAGAGCCCTGCATGATGAAGGGAATCTGCGAAGCAAGCAATCTGCTGCGAG 774
Qy 21 Arg1leAlaMetLeuThrPglYserGlyScyLysAlaLeuThrLysPheLysPheVal 40
Db 775 CGCATTTGCCATGCTCTGGGGCTCCGGAAAGTGCAGAGGCTGTGACCAAGTTCAAATTGCTG 834
Qy 41 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuCysAspGlnLeu 60
Db 835 TTCTTCCCTCCGCTCAGAGAGGCCGAGGCTGACTTTTGAACCCCTCTGTATCACTC 894
Qy 61 LeuAsp1leProGlyThr1leArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 80
Db 895 CTGGATATACCTGGCACAATCAGAGAAAGCAGACATCATGCCATCTGCTGAAGCTGCGG 954
Qy 81 GlnArgValLeuPheLeuLeuAspGlyTyraSngLupheLysProGlnAsnScyProGlu 100
Db 955 CAGAGGGTCTTTCTCTTCTTGATGGCTACAAATGAATTCAGCCCAAGAACTGCCAGAA 1014
Qy 101 lIeGluAlaLeu1leLysGluAsnHisArgPheLysAsnMetVal1leValThrThrThr 120
Db 1015 ATCGAAGCCCTGATTAAGAAACCAACCGCTTCAGAAACATGTCATGCTCACCACTACC 1074
Qy 121 ThrGluCysLeuArgHis1leArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 140
Db 1075 ACTGAGTCCCTGAGGACATACAGCGAGTTTGCTGCCCTGACTGCTGAGGTGGGGATATG 1134
Qy 141 ThrGluAspSerAlaGlnAlaLeu1leArgGluValLeu1leLysGluLeuAlaGluGly 160
Db 1135 ACAGAAAGACAGCGCCAGGCTCTCATCCGAGAAAGTGTGATCAAGAGAGCTTGCTGAAGGC 1194
Qy 161 LeuLeuLeu 163
Db 1195 TTGTTGCTC 1203
```

```
RESULT 11
PCT-US00-29643-3
: Sequence 3, Application PC/RTUS0029643
: GENERAL INFORMATION:
```

```
: APPLICANT: Millennium Pharmaceuticals, Inc.
: TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
: FILE REFERENCE: 07334-136MO1
: CURRENT APPLICATION NUMBER: PCT/US00/29643
: PRIOR FILING DATE: 2000-10-26
: PRIOR APPLICATION NUMBER: US 60/161,822
: PRIOR FILING DATE: 1999-10-27
: NUMBER OF SEQ ID NOS: 11
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 3
: LENGTH: 3072
: TYPE: DNA
: ORGANISM: Homo sapiens
PCT-US00-29643-3
```

## Alignment Scores:

```
Pred. No.: 3,23e-94
Score: 829.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
```

```
Length: 3072
Matches: 163
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0
```

US-09-697-089-2\_COPY\_161\_323 (1-163) x PCT-US00-29643-3 (1-3072)

```
Qy 1 LeuGlnSerProCys1le1leGluGlyLusSerGlyLysSerThrLeuLeuGln 20
Db 481 CTTGAGAGCCCTGCATGATGAAGGGAATCTGCGAAGCAAGCAATCTGCTGCGAG 540
Qy 21 Arg1leAlaMetLeuThrPglYserGlyScyLysAlaLeuThrLysPheLysPheVal 40
Db 541 CGCATTTGCCATGCTCTGGGGCTCCGGAAAGTGCAGAGGCTGTGACCAAGTTCAAATTGCTC 600
```

```
Qy 41 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuCysAspGlnLeu 60
Db 601 TTCTTCCCTCCGCTCAGAGAGGCCGAGGCTGACTTTTGAACCCCTCTGTATCACTC 660
Qy 61 LeuAsp1leProGlyThr1leArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 80
Db 661 CTGGATATACCTGGCACAATCAGAGAAAGCAGACATCATGCCATCTGCTGAAGCTGCGG 720
Qy 81 GlnArgValLeuPheLeuLeuAspGlyTyraSngLupheLysProGlnAsnScyProGlu 100
Db 721 CAGAGGGTCTTTCTCTTCTTGATGGCTACAAATGAATTCAGCCCAAGAACTGCCAGAA 780
Qy 101 lIeGluAlaLeu1leLysGluAsnHisArgPheLysAsnMetVal1leValThrThrThr 120
Db 781 ATCGAAGCCCTGATTAAGAAACCAACCGCTTCAGAAACATGTCATGCTCACCACTACC 840
Qy 121 ThrGluCysLeuArgHis1leArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 140
Db 841 ACTGAGTCCCTGAGGACATACAGCGAGTTTGCTGCCCTGACTGCTGAGGTGGGGATATG 900
Qy 141 ThrGluAspSerAlaGlnAlaLeu1leArgGluValLeu1leLysGluLeuAlaGluGly 160
Db 901 ACAGAAAGACAGCGCCAGGCTCTCATCCGAGAAAGTGTGATCAAGAGAGCTTGCTGAAGGC 960
Qy 161 LeuLeuLeu 163
Db 961 TTGTTGCTC 969
```

```
RESULT 12
US-09-697-089-3
: Sequence 3, Application US/09697089
: GENERAL INFORMATION:
```

```
: APPLICANT: Bertin, John
: TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
: FILE REFERENCE: 07334-136001
: CURRENT APPLICATION NUMBER: US/09/697,089
: PRIOR FILING DATE: 2000-10-26
: PRIOR APPLICATION NUMBER: US 60/161,822
: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 3
: LENGTH: 3072
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-697-089-3
```

## Alignment Scores:

```
Pred. No.: 3,23e-94
Score: 829.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
```

```
Length: 3072
Matches: 163
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0
```

US-09-697-089-2\_COPY\_161\_323 (1-163) x US-09-697-089-3 (1-3072)

```
Qy 1 LeuGlnSerProCys1le1leGluGlyLusSerGlyLysSerThrLeuLeuGln 20
Db 481 CTTGAGAGCCCTGCATGATGAAGGGAATCTGCGAAGCAAGCAATCTGCTGCGAG 540
Qy 21 Arg1leAlaMetLeuThrPglYserGlyScyLysAlaLeuThrLysPheLysPheVal 40
Db 541 CGCATTTGCCATGCTCTGGGGCTCCGGAAAGTGCAGAGGCTGTGACCAAGTTCAAATTGCTC 600
Qy 41 PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuCysAspGlnLeu 60
Db 601 TTCTTCCCTCCGCTCAGAGAGGCCGAGGCTGACTTTTGAACCCCTCTGTATCACTC 660
Qy 61 LeuAsp1leProGlyThr1leArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 80
```



Db	661	CTGGATTACTGGCACAAATCAGGAGGACAGCATTCATGGCCATGCTGCTGAACCTGGG	720
Qy	81	GLNArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu	100
Db	721	CAGAGGGTCTCTTTCCTCTTGATGGCTACATGATATTCAGGCCCAAAACCTGCCGAA	780
Qy	101	ILleguAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThrThr	120
Db	781	ATCGAAGCCCTGATAAAGGAAGAAACACCGCTTCAAGAACATGCTCATGTCACCACTAC	840
Qy	121	ThrGluCysLeuAlaArgHisIleArgGluPheGlyAlaLeuThrAlaGluValGlyAspMet	140
Db	841	ACTGATGCTCCCTGAGGCACATACGGCAGCTTGCTGCTCCCTGACTGCTGAGTGGGGATATG	900
Qy	141	ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly	160
Db	901	ACAGAAAGACAGCCGCCAGCTCTCATCCGAGAAAGTGCTGATCAAGGAGACTGCTGAAAGC	960
Qy	161	LeuLeuLeu 163	
Db	961	TTGTGTGCTC 969	

```

RESULT 13
US-09-841-739-3
: Sequence 3, Application US/09841739
: GENERAL INFORMATION:
: APPLICANT: Berlin, John
: TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF
: FILE REFERENCE: 07334-328001
: CURRENT APPLICATION NUMBER: US/09/841,739
: PRIOR FILING DATE: 2001-08-29
: PRIOR APPLICATION NUMBER: US 09/697,089
: PRIOR FILING DATE: 2000-10-26
: PRIOR APPLICATION NUMBER: US 60/161,822
: PRIOR FILING DATE: 1999-10-27
: NUMBER OF SEQ ID NOS: 16
: SOFTWARE: fastseq for Windows Version 4.0
: SEQ ID NO 3
: LENGTH: 3072
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-841-739-3

```

Alignment Scores:	
Pred. No.:	3, 23e-94
Score:	829.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	32
Length:	3072
Matches:	163
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-697-089-2\_COPY\_161\_323 (1-163) x US-09-841-739-3 (1-3072)

Oy	1	leqinsrprocylllellleqinslgvlsersgilylsglylsrserrlleuqln	20
Db	481	cttcagaccctccatattgaagggaattcgacagagcaagctcaccttccctcag	540
Oy	21	arglleaamelletrpglyserglylscylsalsaleuthrlyspheylsphenal	40
Db	541	cgcattggccatgctctggggcctcggaagagtcgaagcctcgaccagattcaattcgctc	600
Oy	41	phepelleuargleuserargalaglnlglyllyleuuphegiuphrilleucysasglnleu	60
Db	601	ttcttcctccgcgtcagcagggccagggctgacattttgaaacccctctgtgatacactc	660
Oy	61	leuaspileproglythrllearglyslgnhrphemetalamelleuleuylsleuarg	80
Db	661	ctggattataccctggcacatcaggaagacagacattcatggccatgctgtaaacctcgcg	720
Oy	81	glnatgvalleupheuleuaspqlyllyrnsnlgupheylsproglinaaspcproglu	100
Db	721	cagagggttcttcttcttgatggctacacatgaattcaagcccccgaactgcccgaa	780

QY	101	ILLEGUALLALEUILLIETVSGIASHNIIARGPHELYSINMETVALLIEVLIITHRITHR	120
QY	781	ATCGAGGCCCTGGATTAAGGAAAACCACCCTCTCAAGAACATGGTCATCGTCACACTAAC	840
Db	121	ThrgIucYsLeuArgHsIIeArgGInPheGlyAlaLeuThraGluValIglYasPmet	140
QY	841	ACTGATGCTCCCGAAGGCACATCGCGACAGTTGGTGCCTCGATCGTCGAGGAGGGGGATATG	900
Db	141	ThrgIuAspSerAlaGlnAlaLeuIIeArgGluValLeuIIeIysGluLeuAlaGluGly	160
QY	901	ACAGAGACACAGCCCGCAGGCTCTCATCCGAGAAAGTCTGATCAAGAGAGCTTGGCTGAAGGC	960
Db	161	LeuLeuLeu 163	
QY	961	TGTGTGCTC 969	

```

1  APPLICANT: Alimenti, Emad S.
2  TITLE OF INVENTION: IPAF, AN ICE-PROTEASE ACTIVATING
3  TITLE OF INVENTION: FACTOR
4  FILE REFERENCE: 480140, 477
5  CURRENT APPLICATION NUMBER: US/10/156, 733
6  CURRENT FILING DATE: 2002-05-24
7  NUMBER OF SEQ ID NOS: 14
8  SOFTWARE: FASTSEQ for Windows Version 4.0
9  SEQ ID NO 1
10 LENGTH: 3075
11 TYPE: DNA
12 ORGANISM: Homo sapiens
13 FEATURE:
14 NAME/KEY: CDS
15 LOCATION: (1)...(3075)
16 US-10-156-733-1

```

Alignment Scores:	
Pred. No.:	3,246-94
Score:	829.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	41
Length:	3075
Matches:	163
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-697-089-2\_COPY\_161\_323 (1-163) x US-10-156-733-1 (1-3075)

QY 1 LeuGlnSerProCysIleIleGlnGlnGlnSerGlySerGlyLysSerThrLeuGln 20  
DB 481 CTTCCAGACCCCTGCATCATTTGAAGGGGAATCTGGCAAGCAAGTCATCTGCTCGAG 540  
QY 21 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheAla 40  
DB 541 CCAATTGCCAGTCTCTGGGGCTCCGGAAAGTGCAGAGCCTTGACCAAGTTCCAAATTCCGTC 600  
QY 41 PhePheLeuArgLysSerArgAlaGlnGlyGlyLeuPheGlnThrLeuCysAspGlnLeu 60  
DB 601 TTCTTCCTCCGCTCTCAGCAGGGGCCCAAGGTGGACTTTTGAACCCCTGTGATCAACTC 660  
QY 61 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 80  
DB 661 CTGGGATATACCTGGCAGACATGAGGAACGACATTCATGGGCATGCTGCTGAAGTCGCGG 720  
QY 81 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGlnPheLysProGlnAsnCysProGlu 100  
DB 721 CAGAGGGTCTTTCTTCCTTGATGGCTGACAAATGAATTCAAAGCCCCAGACTGCCAGAA 780  
QY 101 IleGlnAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValThrThrThr 120  
DB 781 ATCGAAGCCGTGATTAAGGAAGAACACCGCTTCAAGAACATGTCATCGTCACACACTACC 840  
QY 121 ThrGlnCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGlnValGlyAspMet 140

Db 841 ACTGATGCTCGAGGCACATACGCGAGTTTGGTGCCCTGACTGCTGAGGTGGGGATATG 900  
QY 141 ThrGluAspSerAlaGlnAlaLeuIleArgGluValIleLysGluLeuAlaGluGly 160  
|||||  
Db 901 ACAGAGACAGCGCCAGGCTCTCATCCGAGAGTGTGATCAAGAGCTTGTGAAGGC 960  
QY 161 LeuLeuLeu 163  
|||||  
Db 961 TTGTTGCTC 969

## RESULT 15

PCT-US00-29643-1  
; Sequence 1, Application PC/TUS0029643  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
; FILE REFERENCE: 07334-136WO1  
; CURRENT APPLICATION NUMBER: PCT/US00/29643  
; CURRENT FILING DATE: 2000-10-26  
; PRIOR APPLICATION NUMBER: US 60/161,822  
; PRIOR FILING DATE: 1999-10-27  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 3133  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (36) ... (3107)  
PCT-US00-29643-1

## Alignment Scores:

Pred. No.: 3.32e-94 Length: 3133  
Score: 829.00 Matches: 163  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 1 Gaps: 0

US-09-697-089-2\_copy\_161\_323 (1-163) x PCT-US00-29643-1 (1-3133)

QY 1 LeuGlnSerProCysIleIleGluGlySerGlyLysSerThrLeuLeuGln 20  
|||||  
Db 516 CTTGAGACCCCTGCATATGTAAGGGGAATCTGGCANAAGCAAGTCCACTTGTCTGCG 575  
QY 21 ArgIleAlaMetLeuTyrPGLysSerGlyLysCysIleAlaLeuThrLysPheLysPheVal 40  
|||||  
Db 576 CGCATGGCCATGCTCTGGGGCTCCGGAAAGTGCANAGGCTGTGACCAAGTCAATTGCTG 635  
QY 41 PhePheLeuAlaGlyLeuSerArgAlaGlnGlyLeuPheGluThrLeuCysAspGlnLeu 60  
|||||  
Db 636 TTCTTCCCTCCGTCAGAGAGGGCCAGGGTGACTTTTGAACCCCTGTGATCAACTC 695  
QY 61 LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg 80  
|||||  
Db 696 CTGGATATACCTGGACACAATCAGAGACACATTCATGGCCATGCTCTGAAGCTGCGG 755  
QY 81 GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu 100  
|||||  
Db 756 CAGAGGGTTCTTTCCTCTTGATGGCTACAAATGAAATTCAGACCCAGACAGTCCAGAG 815  
QY 101 IleGlnAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIleValThrThrThr 120  
|||||  
Db 816 ATCGAAGCCCTGATAAAGAAACACCGCTTCAAGACATGTCATGTCACCACTAC 875  
QY 121 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 140  
|||||  
Db 876 ACTGATGCTCGAGGCAATACGCGAGTTTGGTGGCTGACTGCTGAGGTGGGGATATG 935  
QY 141 ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly 160  
|||||

Db 936 ACAGAGACAGCGCCAGGCTCTCATCCGAGAGTGTGATCAAGAGCTTGTGAAGGC 995  
QY 161 LeuLeuLeu 163  
|||||  
Db 996 TTGTTGCTC 1004

Search completed: January 31, 2003, 17:55:31  
Job time : 2076.15 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

## OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 31, 2003, 13:24:32 : Search time 153.327 Seconds  
(without alignments)  
1295.994 Million cell updates/sec

Title: US-09-697-089-2\_COPY\_161\_323  
Perfect score: 829  
Sequence: 1 LQSPCIEGSGKGSFLD.....SAQALIREVLKEALAEHL 163

Scoring table:  
BLOSUM62  
Xgapop 10.0, Ygapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 2500250 segs, 609544256 residues

Total number of hits satisfying chosen parameters: 5000500

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Command line parameters:

-MODEL=frame\_plus\_p2n.model -DEV=xlh  
-Q=/cgn2\_1/USPTO.spool/US09697089/runat\_29012003\_092755\_19775/app\_query.fasta\_1.981  
-DB=Pending\_Patents\_NA\_New -QFMT=fastlap -SUFFIX=p2n.rnpn -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HAPSIZE=500 -MILEN=0  
-MAILEN=2000000000 -USER=US09697089\_@cgn\_1\_1\_91.érunal\_29012003\_092755\_19775  
-NCPU=6 -ICPU=3 -NO\_XLIFY -NO\_MMAP -LARGQUERY -NEG\_SCORES=0 -WAIT -LONLOG  
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

## Database :

1: Pending\_Patents\_NA\_New:\*  
2: /cgn2\_6/ptodata/2/pna/PCT\_NEW\_COMB.seq:\*  
3: /cgn2\_6/ptodata/2/pna/US06\_NEW\_COMB.seq:\*  
4: /cgn2\_6/ptodata/2/pna/US07\_NEW\_COMB.seq:\*  
5: /cgn2\_6/ptodata/2/pna/US08\_NEW\_COMB.seq:\*  
6: /cgn2\_6/ptodata/2/pna/US09\_NEW\_COMB.seq:\*  
7: /cgn2\_6/ptodata/2/pna/US60\_NEW\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Length	ID	Description
1	829	100.0	3075	1 PCT-US02-21946A-1
2	829	100.0	3219	1 PCT-US02-21946A-14
3	829	100.0	3545	6 US-10-276-781-111
4	236.5	28.5	5984	6 US-10-285-408-2
5	236.5	28.5	6133	5 US-09-949-002-84
6	236.5	28.5	6133	5 US-09-949-002-125
7	236.5	28.5	60194	5 US-09-949-002-656
8	236.5	28.5	60195	5 US-09-949-002-697
9	235.5	28.4	3210	5 US-09-724-676-6819
10	235.5	28.4	3210	5 US-09-724-676A-6819
11	235.5	28.4	3597	5 US-09-724-676-6801

12	235.5	28.4	3597	5	US-09-724-676A-6801	Sequence 6801, Ap
13	235.5	28.4	4143	5	US-09-724-676-6810	Sequence 6810, Ap
14	235.5	28.4	4143	5	US-09-724-676A-6810	Sequence 6810, Ap
15	235.5	28.4	4259	5	US-09-724-676-6816	Sequence 6816, Ap
16	235.5	28.4	4259	5	US-09-724-676A-6816	Sequence 6816, Ap
17	235.5	28.4	4268	5	US-09-724-676-6824	Sequence 6824, Ap
18	235.5	28.4	4268	5	US-09-724-676A-6824	Sequence 6824, Ap
19	235.5	28.4	4280	5	US-09-724-676-6818	Sequence 6818, Ap
20	235.5	28.4	4280	5	US-09-724-676A-6818	Sequence 6818, Ap
21	235.5	28.4	4646	5	US-09-724-676-6798	Sequence 6798, Ap
22	235.5	28.4	4646	5	US-09-724-676A-6798	Sequence 6798, Ap
23	235.5	28.4	4667	5	US-09-724-676-6800	Sequence 6800, Ap
24	235.5	28.4	4667	5	US-09-724-676A-6800	Sequence 6800, Ap
25	235.5	28.4	5189	5	US-09-724-676-6815	Sequence 6815, Ap
26	235.5	28.4	5189	5	US-09-724-676A-6815	Sequence 6815, Ap
27	235.5	28.4	5192	5	US-09-724-676-6807	Sequence 6807, Ap
28	235.5	28.4	5192	5	US-09-724-676A-6807	Sequence 6807, Ap
29	235.5	28.4	5210	5	US-09-724-676-6817	Sequence 6817, Ap
30	235.5	28.4	5210	5	US-09-724-676A-6817	Sequence 6817, Ap
31	235.5	28.4	5213	5	US-09-724-676-6809	Sequence 6809, Ap
32	235.5	28.4	5213	5	US-09-724-676A-6809	Sequence 6809, Ap
33	235.5	28.4	5576	5	US-09-724-676-6797	Sequence 6797, Ap
34	235.5	28.4	5576	5	US-09-724-676A-6797	Sequence 6797, Ap
35	235.5	28.4	5597	5	US-09-724-676-6799	Sequence 6799, Ap
36	235.5	28.4	5597	5	US-09-724-676A-6799	Sequence 6799, Ap
37	235.5	28.4	6122	5	US-09-724-676-6806	Sequence 6806, Ap
38	235.5	28.4	6122	5	US-09-724-676A-6806	Sequence 6806, Ap
39	235.5	28.4	6143	5	US-09-724-676-6808	Sequence 6808, Ap
40	235.5	28.4	6143	5	US-09-724-676A-6808	Sequence 6808, Ap
41	111	13.4	4141	6	US-10-295-981-42	Sequence 42, Appl
42	107	12.9	1470	6	US-10-295-981-27	Sequence 27, Appl
43	107	12.9	2859	6	US-10-295-981-9	Sequence 9, Appl
44	107	12.9	3080	1	PCT-US02-38606-94	Sequence 94, Appl
45	107	12.9	3080	6	US-10-295-981-25	Sequence 25, Appl

## ALIGNMENTS

RESULT 1  
PCT-US02-21946A-1  
: Sequence 1, Application PC/TUS0221946A  
: GENERAL INFORMATION:  
: APPLICANT: Thomas Jefferson University  
: APPLICANT: Alnemri, Emdad S.  
: TITLE OF INVENTION: IPAF, AN ICE-PROTEASE ACTIVATING  
: TITLE OF INVENTION: FACTOR  
: FILE REFERENCE: 480140.477PC  
: CURRENT APPLICATION NUMBER: PCT/US02/21946A  
: CURRENT FILING DATE: 2002-05-24  
: NUMBER OF SEQ ID NOS: 14  
: SOFTWARE: FastSeq for Windows Version 4.0  
: SEQ ID NO 1  
: LENGTH: 3075  
: TYPE: DNA  
: ORGANISM: Homo sapiens  
: FEATURE:  
: NAME/KEY: CDS  
: LOCATION: (1)...(3075)  
PCT-US02-21946A-1

## Alignment Scores:

Pred. No.: 5.62e-96  
Score: 829.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
DB: 1  
Matches: 3075  
Conservative: 163  
Mismatch: 0  
Indels: 0  
Gaps: 0

US-09-697-089-2\_COPY\_161\_323 (1-163) x PCT-US02-21946A-1 (1-3075)

Qy 1 LeuGlnSerProCysIleIleGlnGlyGluSerGlyGlyGlySerThrLeuGln 20  
DB 481 CTTGAGCCCTGATCATTCATGAGGGAATCTGCAAGGCAAGTCACCTCTGCGAG 540

Qy	21	ArglllellamelleuTrpglySerGlyLysCysLysAlaIeuthrLysPheLysPheVal	40
Db	541	CGATTCGCCATGCTCTTGGGGCTCCGGAAGTCGAAGCTCTGACCAAGTCAATTCTGC	600
Qy	41	PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuCysAspGlnLeu	60
Db	601	TTCTTCCTCCGTCTCACACAGGGCCCAAGGGGAGACTTTTCAAAACCCCTGTGATCAACTC	660
Qy	61	LeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg	80
Db	661	CTGATATACCTGGCCACAAATCAGGAACCAACATTCATGGCCATGCTGCTGAAGCTGGG	720
Qy	81	GlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu	100
Db	721	CAGAGGGTCTTTTCCCTCTTGATGGCTACAAATCAATTAAGGCCCACTGGACGCCAGAA	780
Qy	101	IleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValIleThrThr	120
Db	781	ATCGAAGCCCGAATAAAGGAAMACACCGCTTCAAGAAACATGGTCATCGTCACCACTACC	840
Qy	121	ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet	140
Db	841	ACTGATGCTCCGAGGACACATACGCCAGTTTGCTGCTCTGACTGCTGAGGTGGGGGATATG	900
Qy	141	ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGlnGly	160
Db	901	ACAGAAAGACACGCCGCCAGGCTCTCATCTCGAAGAACTGCTGATCAAGAGAGCTTGCGAAGGC	960
Qy	161	LeuLeuLeu 163	
Db	961	TTGTGCTC 969	

## RESULT 2

```

PCT-US02-21946A-14
Sequence 14, Application PC/TUS0221946A
GENERAL INFORMATION:
APPLICANT: Thomas Jefferson University
APPLICANT: Altemurl, Emdad S.
TITLE OF INVENTION: IPAF, AN ICE-PROTEASE ACTIVATING
TITLE OF INVENTION: FACTOR
FILE REFERENCE: 480140, 477PC
CURRENT APPLICATION NUMBER: PCT/US02/21946A
CURRENT FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 3219
TYPE: DNA
ORGANISM: Homo sapiens
PCT-US02-21946A-14

```

Alignment Scores:

Pred. No.:	5,98e-96	Length:	3219
Score:	829.00	Matches:	163
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	1	Gaps:	0

US-09-697-089-2\_COPY-161-323 (1-163) x PCT-US02-21946A-14 (1-3219)

Oy 1 LeuGlnSerProGysIleIleGluGlyValSerGlyLysGlySerThrLeuGln 20

Db 625 CTTGAGACCCCTGCATATTGAAGGGGAATCTGGCAAGCAAGTCACCTCTGTCAG 688

Oy 21 ArgIleIleMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40

Db 685 CGAATGGCCATGCTCTGGGGCTCCGGAAAGTCGAAGGCTCTGACCAAGTCAATTTGCTC 744

Oy 41 PhePheLeuArgLeuSerArgAlaGlnGlyLysLeuPheGluThrLeuGlyAspGlnLeu 60

Db 745 TTCTTCCTCCGCTCAGCAGGGCCAGGGTGGACTTTTGAACCCCTCTGGATCAACTC 804

QY	61	LeuAsp1LeuProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArg	80
Db	805	CTGAGTATTACCTGGCAAAATCAGAGAGCAGACATTATGCGCATGCTGGTAGACTGGG	864
QY	81	GlnArgValIleuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnCysProGlu	100
Db	865	CAGAGGCTTCTTTTCCCTCTTGATGGCTCAAAATGAATTCAACCCAGAACAGCCCAAA	924
QY	101	IleLeuAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThrThr	120
Db	925	ATCCAAACCCCTGATTAAAGGAAAAACACCCCTTCAAAGACATGGTATCTCTACCCACTAC	984
QY	121	ThrGluGlyLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValAlaGlyAspMet	140
Db	985	ACTAGAGTCCGTGAGGCAATACGGCAGATTGGTGGCTTACTGCTGAGGTGGGGGATATG	1044
QY	141	ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeuAlaGluGly	160
Db	1045	ACAAGACAGCAGCGCCAGGCTCTCATTCGAGAAGTCTGATCAAGAGCTTCTGTAAAGC	1104
QY	161	LeuLeuLeu 163	
Db	1105	TTGTGTGCTC 1113	

### RESULT 3

```

US-10-2/6-781-111
? Sequence 111, Application US/10276781
? GENERAL INFORMATION:
? APPLICANT: Hyseq, Inc.
? APPLICANT: Tang et al.
? TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
? FILE REFERENCE: 21272-018 (785 cont'g)
? CURRENT APPLICATION NUMBER: US/10/2767,81
? CURRENT FILING DATE: 2002-11-18
? PRIOR APPLICATION NUMBER: 09/491,404
? PRIOR FILING DATE: 2000-01-25
? NUMBER OF SEQ ID NOS: 2018
? SOFTWARE: fastseq for Windows Version 3.0
? SEQ ID NO 111
? LENGTH: 3545
? TYPE: DNA
? ORGANISM: Homo sapiens
US-10-2/6-781-111

```

**Alignment Scores:**

Pred. No.:	6.82e-96	Length:	3545
Score:	829.00	Matches:	163
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-09-697-089-2\_COPY\_161\_323 (1-163) x US-10-276-781-111 (1-3545)

QY	1	LeuGlnSerProCysIleIleGluGluSerGlyLeuGlyLeuSerThrLeuGln	20
Db	712	CTTCAGACCCCTGCATATTGAAGGGAATCTGGCAAGCAGTCACTCTGCTCAG	7712
QY	21	ArgIlealaMetLeuTrpGlySerGlyLysCysLysalalaLeuThrLysPheVal	40
Db	772	GCATATGCCAATGCTCTGGGGCTCCGGAAATGCACAGGCTCGACCAAGTTCAAATTTGTC	8312
QY	41	PhePheLeuArgLeuSerArgAlaGlnGlyLeuPheGluThrLeuCysAspGlnLeu	60
Db	832	TTCTTCCTCCGCTCTGAGCAGGGCCCAAGGCTGACTTTTGAACCTCTGTGATCAACTC	8912
QY	61	LeuAspIleProGlyThrIleArgLysGlnThrPheMetalaMetLeuLeuLysLeuArg	80
Db	892	CTGGATATACCTGGCAGACATCAGCAAGCAGCAATTCATCAGCCCACTGCTGTAACCTCGG	9512
QY	81	GlnArgValIleuPheLeuLeuAspGlyLysGlnGluPheLysProGlnAsnCysProGlu	100

```
Db 952 CAGAGGCTTTTCCTTCCTGATGGCTACAAATGATTCAGCCCGAGAACTGCCAGAA 1011
QY 101 IIEGLUALaleuIlelysgluasnHsArgPheLysAsnMetValIleValThrThr 120
Db 1012 ATCGAAGCCCTGATTAAGAAACACCGCTTCAGAACATGCTATCTCCCTACCTACC 1071
QY 121 ThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMet 140
Db 1072 ACTGATGGCTGAGCAGCATACGAGCAGTTGGTGGCTGACCTGCTGAGGTGGGGATATG 1131
QY 141 ThrGluAspSerAlaGlnAlaLeuIleArgGluValIleLysGluLeuAlaGluGly 160
Db 1132 ACAGAAAGCAGCGCCAGGCTCTACCGAGAAAGTGATCAAGAGAGCTGCTGAAGGC 1191
QY 161 LeuLeuLeu 163
Db 1192 TTGTTGCTC 1200

RESULT 4
US-10-285-408-2
; Sequence 2, Application US/10285408
; GENERAL INFORMATION:
; APPLICANT: IKEDA, Johe
; TITLE OF INVENTION: Monoclonal Antibodies Against Human Apoptosis Inhibitory Protein
; FILE REFERENCE: 2002-1440/MMC/00653
; CURRENT APPLICATION NUMBER: US/10/285,408
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 09/830,338
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: PCT/JP99/05841
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 5984
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDC
; LOCATION: (292)..(4500)
US-10-285-408-2

Alignment Scores:
Pred. No.: 2,17e-19 Length: 5984
Score: 236.50 Matches: 53
Percent Similarity: 58.96% Conservative: 26
Best Local Similarity: 39.55% Mismatches: 48
Query Match: 28.53% Indels: 7
Gaps: 3
DB: 6

US-09-697-089-2_COPY_161_323 (1-163) x US-10-285-408-2 (1-5984)
QY 1 LeuGlnSerProCysIleIleGluGlyGlnSerGlyLysGlyLysSerThrLeuLeuGln 20
Db 1675 TTGAACCTGTCATGTGTGGAGGTGAAGCTGGAAGGAAAGCGGCTCCTCGAAG 1734
QY 21 ArgIleAlaMetLeuThrPheGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40
Db 1735 AAAAATGACTTTCCTGTGGCATCTGATGCTGCCCTGTGTAACAGGTTCACGCTGGTT 1794
QY 41 PhePheLeuArgLysSer-----ArgAlaGlnGlyLysLeuPheGluThrLeuLeuLys 58
Db 1795 TTCTACCTCTCCCTTAGTTCACACAGACACAGAGGGGCTGCCAGATCATCTGTGTAC 1854
QY 59 GlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLys 78
Db 1855 CAGCTCCCTAGAGAAAGAGATCTGTACTGAATGTGATGAGAACATATTCACAGCAG 1914
QY 79 LeuArgGlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPhe-----LysProGln 96
Db 1915 TTAAAGATCAGGCTCTATCTCTTTAGATGACTCAAAAGAAATATGTTCATCCCTCAA 1974
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QY 97 AsnCysProGluIleGluAlaLeuIleLysGluAsnHsArgPheLysAsnMetValIle 116
Db 1975 -----GTCATAGGAAGAAACTGATTCAAAAAACCACTTATCCCGAGACCTGCTATTG 2025
QY 117 ValThrThrThrThrGluCysLeuArgHisIleArgGlnPhe 130
Db 2026 ATTGCTGTCCGTACAAACAGGCGCAGGACATCCGCCGATAC 2067

RESULT 5
US-09-949-002-84
; Sequence 84, Application US/09949002
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; FILE REFERENCE: CLO00790
; CURRENT APPLICATION NUMBER: US/09/949,002
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 6133
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-84

Alignment Scores:
Pred. No.: 2,24e-19 Length: 6133
Score: 236.50 Matches: 53
Percent Similarity: 58.96% Conservative: 26
Best Local Similarity: 39.55% Mismatches: 48
Query Match: 28.53% Indels: 7
Gaps: 3
DB: 5

US-09-697-089-2_COPY_161_323 (1-163) x US-09-949-002-84 (1-6133)
QY 1 LeuGlnSerProCysIleIleGluGlyGlnSerGlyLysGlyLysSerThrLeuLeuGln 20
Db 1684 TTGAACCTGTCATGTGTGGAGGTGAAGCTGGAAGGAAAGCGGCTCCTCGAAG 1743
QY 21 ArgIleAlaMetLeuThrPheGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40
Db 1744 AAAAATGACTTTCCTGTGGCATCTGATGCTGCCCTGTAAACAGGTTCACAGCTGTT 1803
QY 41 PhePheLeuArgLysSer-----ArgAlaGlnGlyLysLeuPheGluThrLeuLysAsp 58
Db 1804 TTCTACCTCTCCCTTAGTTCACACAGACACAGAGGGGCTGCCAGATCATCTGTGTAC 1863
QY 59 GlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLys 78
Db 1864 CAGCTCCCTAGAGAAAGAGATCTGTACTGAATGTGATGAGAACATATTCACAGCAG 1923
QY 79 LeuArgGlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPhe-----LysProGln 96
Db 1924 TTAAAGATCAGGCTCTATCTCTTTAGATGACTCAAAAGAAATATGTTCATCCCTCAA 1983
QY 97 AsnCysProGluIleGluAlaLeuIleLysGluAsnHsArgPheLysAsnMetValIle 116
Db 1984 -----GTCATAGGAAGAAACTGATTCAAAAAACCACTTATCCCGAGACCTGCTATTG 2034
QY 117 ValThrThrThrThrGluCysLeuArgHisIleArgGlnPhe 130
Db 2035 ATTGCTGTCCGTACAAACAGGCGCAGGACATCCGCCGATAC 2076

RESULT 6
US-09-949-002-125
; Sequence 125, Application US/09949002
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
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; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; FILE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 6133
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-125

Alignment Scores:
Pred. No.: 2,24e-19 Length: 6133
Score: 236.50 Matches: 53
Percent Similarity: 58.96% Conservative: 26
Best Local Similarity: 39.55% Mismatches: 48
Query Match: 28.53% Indels: 7
Gaps: 3

US-09-697-089-2_COPY_161_323 (1-163) x US-09-949-002-125 (1-6133)
QY 1 LeuGlnSerProCysIleIleGluGlySerGlyLysGlyLysSerThrLeuGln 20
    ||| ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1684 TTGAACCTGTCATGTCGTGTGGAGGTCGAGCTGGAAGTGAAGAGCGTCTCTGAG 1743

QY 21 ArgIleAlaMetLeuThrPglSerGlyLysGlyLysAlaLeuThrLysPheVal 40
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1744 AAAATACCTTTTCTGTGGCATCTGAGTGTCCCTGTTAAACAGGTCTCAGCTGTT 1803

QY 41 PhePheLeuArgLeuSer-----ArgAlaGlnGlyLeuPheGluThrLeuCysAsp 58
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1804 TTCTACTCTCTCCTTAAGTCCACAGACAGACAGAGGGCTGGCCAGATATCTGTAC 1863

QY 59 GlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLys 78
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1864 CAGCTCCTAGAGAAAGAGAGATCTGTACTGAAATGTGCATGAGAACATATTCACGAG 1923

QY 79 LeuArgGlnArgValLeuPheLeuLeuAspGlyTyrAsnGlnPhe-----LysProGln 96
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1924 TTAAAGAATCAGGCTTATCTTTCCTTTAGATGACTACAAAGAAATATGTCAATCCCTCA 1983

QY 97 AsnCysProGluIleGluAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIle 116
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1984 -----GTCATAGGAAACATGATTCAAAAAACCCATTATCCCGGACCTGCCTATTG 2034

QY 117 ValThrThrThrThrGluCysLeuArgHisIleArgGlnPhe 130
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2035 ATTGCTGTCCGTACAAACAGGCGCACGAGCATCCGCCCATAC 2076

RESULT 7
US-09-949-002-656
; Sequence 656, Application US/09949002
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 656
; LENGTH: 60194
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-656
```

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Alignment Scores:
Pred. No.: 5.1e-18 Length: 60194
Score: 236.50 Matches: 53
Percent Similarity: 58.96% Conservative: 26
Best Local Similarity: 39.55% Mismatches: 48
Query Match: 28.53% Indels: 7
Gaps: 3

US-09-697-089-2_COPY_161_323 (1-163) x US-09-949-002-656 (1-60194)
QY 1 LeuGlnSerProCysIleIleGluGlySerGlyLysGlyLysSerThrLeuGln 20
    ||| ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 41011 TTGAACCTGTCATGTCGTGTGGAGGTCGAGCTGGAAGTGAAGAGCGTCTCTGAG 41070

QY 21 ArgIleAlaMetLeuThrPglSerGlyLysGlyLysAlaLeuThrLysPheVal 40
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 41071 AAAATACCTTTTCTGTGGCATCTGAGTGTCCCTGTTAAACAGGTCTCAGCTGTT 41130

QY 41 PhePheLeuArgLeuSer-----ArgAlaGlnGlyLeuPheGluThrLeuCysAsp 58
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 41131 TTCTACTCTCTCCTTAAGTCCACAGACAGAGGGCTGGCCAGATATCTGTGAC 41190

QY 59 GlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLys 78
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 41191 CAGCTCCTAGAGAAAGAGAGATCTGTACTGAAATGTGCATGAGAACATATTCACGAG 41250

QY 79 LeuArgGlnArgValLeuPheLeuLeuAspGlyTyrAsnGlnPhe-----LysProGln 96
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 41251 TTAAAGAATCAGGCTTATCTTTCCTTTAGATGACTACAAAGAAATATGTCAATCCCTCA 41310

QY 97 AsnCysProGluIleGluAlaLeuIleLysGlnAsnHisArgPheLysAsnMetValIle 116
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 41311 -----GTCATAGGAAACATGATTCAAAAAACCCATTATCCCGGACCTGCCTATTG 41361

QY 117 ValThrThrThrThrGluCysLeuArgHisIleArgGlnPhe 130
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 41362 ATTGCTGTCCGTACAAACAGGCGCACGAGCATCCGCCCATAC 41403

RESULT 8
US-09-949-002-697
; Sequence 697, Application US/09949002
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 697
; LENGTH: 60195
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-697

Alignment Scores:
Pred. No.: 5.1e-18 Length: 60195
Score: 236.50 Matches: 53
Percent Similarity: 58.96% Conservative: 26
Best Local Similarity: 39.55% Mismatches: 48
Query Match: 28.53% Indels: 7
Gaps: 3

US-09-697-089-2_COPY_161_323 (1-163) x US-09-949-002-697 (1-60195)
QY 1 LeuGlnSerProCysIleIleGluGlySerGlyLysGlyLysSerThrLeuGln 20
    ||| ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 41011 TTGAACCTGTCATGTCGTGTGGAGGTCGAGCTGGAAGTGAAGAGCGTCTCTGAG 41070
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OY 21 Arg1Leu1aMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40
    :::::::::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
Db 41071 AAAATAGCTTTCTGTGGGCACTGATGCTCTCCCTTTAAACAGGTTCCAGCTGGTT 41130
OY 41 PhePheLeuArgLeuSer-----ArgAlaGlnGlyGlyLeuPheGluThrLeuCysasp 58
    :::::::::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
Db 41131 TTCTACTCTCTCCCTTAGTTCACACAGACAGAGGGGCTGGCAGTATCTGTGAC 41190
OY 59 GlnLeuLeuAsp1LePProGlyThr1LeaGlySglnThrPheMetAlaMetLeuLeuLys 78
    :::::::::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
Db 41191 CAGCTCCTAGAGAAAGAAAGATCTGTACTGAAATGTGCATAGAGAAACATTTCCAGCAG 41250
OY 79 LeuArgGlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPhe-----LysProGln 96
    :::::::::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
Db 41251 TTAAAGAATCAGGCTGTATTCTTTAGTAGTACTACAAAGAATATGTTCATCCCTCAA 41310
OY 97 AsnCysProGlu1LeGluAlaLeu1Leu1LeuLysGlnAsnHisArgPheLysAsnMetVal11e 116
    :::::::::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
Db 41311 -----GTCATAGGAAAACTGATTCAAAAAACCACTTATCCCGACCTGCTATTG 41361
OY 117 ValThrThrThrThrGluCysLeuArgHis1LeaArgGlnPhe 130
    :::::::::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
Db 41362 ATTGCTGTCCTAGCAACAGGCGCAGGACATCCCGCATAC 41403

RESULT 9
US-09-724-676-6819
; Sequence 6819, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6819
; LENGTH: 3210
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-6819

Alignment Scores:
Pred. No.: 1,24e-19 Length: 3210
Score: 235.50 Matches: 53
Percent Similarity: 58.96% Conservative: 26
Best Local Similarity: 39.55% Mismatches: 48
Query Match: 28.41% Indels: 7
DB: 5 Gaps: 3

US-09-697-089-2_COPY_161_323 (1-163) x US-09-724-676-6819 (1-3210)
OY 1 LeuGlnSerProCys1Le1LeGlnGlyLysSerGlyLysGlyLysSerThrLeuLeuGln 20
    :::::::::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
Db 726 TTGACTCTGTCATGTCGTGGAGGAGTGAGCTGGAGTGAAGACAGCTCTCTCGAAG 785
OY 21 Arg1Leu1aMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40
    :::::::::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
Db 786 AAAATAGCTTTCTGTGGGCACTGATGCTCTCCCTTTAAACAGGTTCAGCTGGTT 845
OY 41 PhePheLeuArgLeuSer-----ArgAlaGlnGlyGlyLeuPheGluThrLeuCysasp 58
    :::::::::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
Db 846 TTCTACTCTCTCCCTTAGTTCACACAGACAGAGGGGCTGGCAGTATCTGTGAC 905
OY 59 GlnLeuLeuAsp1LePProGlyThr1LeaGlySglnThrPheMetAlaMetLeuLeuLys 78
    :::::::::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
Db 906 CAGCTCCTAGAGAAAGAAAGATCTGTACTGAAATGTGCTAGAGAAACATTTCCAGCAG 965
OY 79 LeuArgGlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPhe-----LysProGln 96
    :::::::::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
Db 966 TTAAAGAATCAGGCTGTATTCTTTAGTAGTACTACAAAGAATATGTTCATCCCTCAA 1025
OY 97 AsnCysProGlu1LeGluAlaLeu1Leu1LeuLysGlnAsnHisArgPheLysAsnMetVal11e 116
    :::::::::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
Db 1026 -----GTCATAGGAAAACTGATTCAAAAAACCACTTATCCCGGACCTGCTATTG 1076
OY 117 ValThrThrThrThrGluCysLeuArgHis1LeaArgGlnPhe 130
    :::::::::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
Db 1077 ATTGCTGTCCTAGCAACAGGCGCAGGACATCCCGCATAC 1118

RESULT 11
US-09-724-676-6801
; Sequence 6801, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
```

```
Db 1026 -----GTCATAGGAAAACTGATTCAAAAAACCACTTATCCCGGACCTGCTATTG 1076
OY 117 ValThrThrThrThrGluCysLeuArgHis1LeaArgGlnPhe 130
    :::::::::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
Db 1077 ATTGCTGTCCTAGCAACAGGCGCAGGACATCCCGCATAC 1118

RESULT 10
US-09-724-676A-6819
; Sequence 6819, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6819
; LENGTH: 3210
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-6819

Alignment Scores:
Pred. No.: 1,24e-19 Length: 3210
Score: 235.50 Matches: 53
Percent Similarity: 58.96% Conservative: 26
Best Local Similarity: 39.55% Mismatches: 48
Query Match: 28.41% Indels: 7
DB: 5 Gaps: 3

US-09-697-089-2_COPY_161_323 (1-163) x US-09-724-676A-6819 (1-3210)
OY 1 LeuGlnSerProCys1Le1LeGlnGlyLysSerGlyLysGlyLysSerThrLeuLeuGln 20
    :::::::::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
Db 726 TTGACTCTGTCATGTCGTGGAGGAGTGAGCTGGAGTGAAGACAGGCTCTCTCGAAG 785
OY 21 Arg1Leu1aMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40
    :::::::::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
Db 786 AAAATAGCTTTCTGTGGGCACTGATGCTCTCCCTTTAAACAGGTTCAGCTGGTT 845
OY 41 PhePheLeuArgLeuSer-----ArgAlaGlnGlyGlyLeuPheGluThrLeuCysasp 58
    :::::::::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
Db 846 TTCTACTCTCTCCCTTAGTTCACACAGACAGAGGGGCTGGCAGTATCTGTGAC 905
OY 59 GlnLeuLeuAsp1LePProGlyThr1LeaGlySglnThrPheMetAlaMetLeuLeuLys 78
    :::::::::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
Db 906 CAGCTCCTAGAGAAAGAAAGATCTGTACTGAAATGTGCTAGAGAAACATTTCCAGCAG 965
OY 79 LeuArgGlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPhe-----LysProGln 96
    :::::::::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
Db 966 TTAAAGAATCAGGCTGTATTCTTTAGTAGTACTACAAAGAATATGTTCATCCCTCAA 1025
OY 97 AsnCysProGlu1LeGluAlaLeu1Leu1LeuLysGlnAsnHisArgPheLysAsnMetVal11e 116
    :::::::::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
Db 1026 -----GTCATAGGAAAACTGATTCAAAAAACCACTTATCCCGGACCTGCTATTG 1076
OY 117 ValThrThrThrThrGluCysLeuArgHis1LeaArgGlnPhe 130
    :::::::::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
Db 1077 ATTGCTGTCCTAGCAACAGGCGCAGGACATCCCGCATAC 1118

RESULT 11
US-09-724-676-6801
; Sequence 6801, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
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SEQ ID NO 6801  
LENGTH: 3597  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-724-676-6801

Alignment Scores:  
Pred. No.: 1,45e-19  
Score: 235.50  
Percent Similarity: 58.96%  
Best Local Similarity: 39.55%  
Query Match: 28.41%  
Matches: 53  
Conservative: 26  
Mismatches: 48  
Indels: 7  
Gaps: 3

US-09-697-089-2\_COPY\_161\_323 (1-163) x US-09-724-676-6801 (1-3597)

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Db 1113 TTGAACCTGTCATGTCGTGTGGAGGTCGAACTGGAAAGACGCTCCTGAG 1172  
OY 21 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40  
Db 1173 AAAATAGCTTTCTGTGTGGGCACTGATGCTGCTCCCTGTTAAACAGGTTCCAGCTGTT 1232  
OY 41 PhePheLeuArgLeuSer-----ArgAlaGlnGlyGlyLeuPheGluThrLeuCysAsp 58  
Db 1233 TTCTACCTCTCCCTTAGTTCACACGACGAGGCGGCGGCGCATCATCTGTGAC 1292  
OY 59 GlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLys 78  
Db 1293 CAGCTCCCTAGAGAAAGAGATCTTACTGAAATGTCRGTGAGGAAACATTATCCAGCAG 1352  
OY 79 LeuArgGlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPhe-----LysProGln 96  
Db 1353 TTAAAGATCAGGTCCTTATCTCTTTAGATGACTCAAAAGAAATATGTTCAATCCCTCAA 1412  
OY 97 AsnCysProGluIleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIle 116  
Db 1413 -----GTCATAGAGAAACTGATTCAAAAGAACACTTATCCGACCTGCTATTG 1463  
OY 117 ValThrThrThrThrGluCysLeuArgHisIleArgGlnPhe 130  
Db 1464 ATTGCTGTCCGTACAAACAGGCGCCAGGACATCCGCCCATAC 1505

RESULT 12  
US-09-724-676A-6801  
Sequence 6801, Application US/09724676A  
GENERAL INFORMATION:  
APPLICANT: Compugen LTD  
TITLE OF INVENTION: Variants of alternative splicing  
FILE REFERENCE: 129181.4 Compugen  
CURRENT APPLICATION NUMBER: US/09/724,676A  
CURRENT FILING DATE: 2000-11-28  
NUMBER OF SEQ ID NOS: 97222  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 6801  
LENGTH: 3597  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-724-676A-6801

Alignment Scores:  
Pred. No.: 1,45e-19  
Score: 235.50  
Percent Similarity: 58.96%  
Best Local Similarity: 39.55%  
Query Match: 28.41%  
Length: 3597  
Matches: 53  
Conservative: 26  
Mismatches: 48  
Indels: 7  
Gaps: 3

US-09-697-089-2\_COPY\_161\_323 (1-163) x US-09-724-676A-6801 (1-3597)

OY 1 LeuGlnSerProCysIleIleGluGlyLysSerGlyLysSerThrLeuGln 20  
Db 1113 TTGAACCTGTCATGTCGTGTGGAGGTCGAACTGGAAAGACGCTCCTGAG 1172

Db 1113 TTGAACCTGTCATGTCGTGTGGAGGTCGAACTGGAAAGACGCTCCTGAG 1172  
OY 21 ArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal 40  
Db 1173 AAAATAGCTTTCTGTGTGGGCACTGATGCTGCTCCCTGTTAAACAGGTTCCAGCTGTT 1232

OY 41 PhePheLeuArgLeuSer-----ArgAlaGlnGlyGlyLeuPheGluThrLeuCysAsp 58  
Db 1233 TTCTACCTCTCCCTTAGTTCACACGACGAGGCGGCGGCGCATCATCTGTGAC 1292  
OY 59 GlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLys 78  
Db 1293 CAGCTCCCTAGAGAAAGAGATCTTACTGAAATGTCRGTGAGGAAACATTATCCAGCAG 1352

OY 79 LeuArgGlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPhe-----LysProGln 96  
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OY 97 AsnCysProGluIleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMetValIle 116  
Db 1413 -----GTCATAGAGAAACTGATTCAAAAGAACACTTATCCGACCTGCTATTG 1463  
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RESULT 13  
US-09-724-676-6810  
Sequence 6810, Application US/09724676  
GENERAL INFORMATION:  
APPLICANT: Compugen LTD  
TITLE OF INVENTION: Variants of alternative splicing  
FILE REFERENCE: 129181.4 Compugen  
CURRENT APPLICATION NUMBER: US/09/724,676  
CURRENT FILING DATE: 2000-11-28  
NUMBER OF SEQ ID NOS: 97222  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 6810  
LENGTH: 4143  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-724-676-6810

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Pred. No.: 1,76e-19  
Score: 235.50  
Percent Similarity: 58.96%  
Best Local Similarity: 39.55%  
Query Match: 28.41%  
Length: 4143  
Matches: 53  
Conservative: 26  
Mismatches: 48  
Indels: 7  
Gaps: 3

US-09-697-089-2\_COPY\_161\_323 (1-163) x US-09-724-676-6810 (1-4143)

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OY 41 PhePheLeuArgLeuSer-----ArgAlaGlnGlyGlyLeuPheGluThrLeuCysAsp 58  
Db 1779 TTCTACCTCTCCCTTAGTTCACACGACGAGGCGGCGGCGCATCATCTGTGAC 1838  
OY 59 GlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMetLeuLys 78  
Db 1839 CAGCTCCCTAGAGAAAGAGATCTTACTGAAATGTCRGTGAGGAAACATTATCCAGCAG 1898  
OY 79 LeuArgGlnArgValLeuPheLeuLeuAspGlyTyrAsnGluPhe-----LysProGln 96  
Db 1899 TTAAAGATCAGGTCCTTATCTCTTTAGATGACTCAAAAGAAATATGTTCAATCCCTCAA 1958



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GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus.p2n model

Run on: January 31, 2003, 11:41:11 : Search time 2961.36 seconds  
(without alignments)  
2004.811 Million cell updates/sec

Title: US-09-697-089-2\_COPY\_762\_965

Perfect score: 1046  
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Scoring table:

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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-DOCCALIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NOEM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
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Database :

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2: gb\_htg:\*  
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6: gb\_pat:\*  
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11: gb\_sts:\*  
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13: gb\_un:\*  
14: gb\_vl:\*  
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23: em\_pat:\*  
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25: em\_pl:\*  
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31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htg\_mus:\*  
34: em\_htg\_pln:\*  
35: em\_htg\_rnd:\*  
36: em\_htg\_mam:\*  
37: em\_htg\_vrt:\*  
38: em\_sy:\*  
39: em\_htgo\_hum:\*  
40: em\_htgo\_mus:\*  
41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1046	100.0	618	6 AX318176	AX318176 Sequence
2	1046	100.0	1355	6 IR2005417	AL389934 Homo sapi
3	1046	100.0	1395	6 AX318093	AX318093 Sequence
4	1046	100.0	1395	9 AY027788	AY027788 Homo sapi
5	1046	100.0	3133	9 AY032589	AY032589 Homo sapi
6	1046	100.0	3219	9 AY035391	AY035391 Homo sapi
7	1046	100.0	3360	9 BC031555	BC031555 Homo sapi
8	1046	100.0	3396	6 AX318091	AX318091 Sequence
9	1046	100.0	3396	9 AY027787	AY027787 Homo sapi
10	1046	100.0	3581	9 AF376061	AF376061 Homo sapi
11	1042	99.6	3335	9 AK095467	AK095467 Homo sapi
12	331	31.6	138909	9 CNS01DS3	AL121653 BAC sequ
13	331	31.6	185281	2 AC011232	AC011232 Homo sapi
14	326	31.2	160583	2 AC010968	AC010968 Homo sapi
15	298	28.5	553	11 G55568	G55568 SHGC-100923
16	238	22.8	185469	2 AC010193	AC101793 Mus muscu
17	202	19.3	162692	2 CNS01DS8	AL11668 BAC sequ
18	176	16.8	8366	2 AC131423	AC131423 Rattus no
19	147.5	14.1	3447	6 AX427592	AX427592 Sequence
20	147.5	14.1	3447	10 AF074018	AF074018 Mus muscu
21	124.5	11.9	3162	3 AY113398	AY113398 Drosophill
22	124	11.9	202431	2 AC116395	AC116395 Mus muscu
23	122.5	11.7	61107	2 AC017941	AC017941 Drosophill
24	122.5	11.7	191466	3 AC008348	AC008348 Drosophill
25	122.5	11.7	307363	3 AE003457	AE003457 Drosophill
26	121.5	11.6	3069	6 AX459879	AX459879 Sequence
27	121	11.6	4550	3 AY128499	AY128499 Drosophill
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30	121	11.6	217756	3 AE003717	AE003717 Drosophill
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32	120	11.5	2470	9 AK000338	AK000338 Homo sapi
33	120	11.5	2754	9 BC003407	BC003407 Homo sapi
34	120	11.5	2826	6 AX405866	AX405866 Sequence
35	120	11.5	2846	9 BC008586	BC008586 Homo sapi
36	120	11.5	2847	9 AK022951	AK022951 Homo sapi
37	120	11.5	76170	25 ATAC2329	AC002329 Arabidops
38	120	11.5	121848	2 AC098833	AC098833 Oryza sat
39	118.5	11.3	2400	9 AK026912	AK026912 Homo sapi
40	118	11.3	1573	6 BC011186	BC011186 Homo sapi
41	118	11.3	1514	6 E62970	E62970 Recombinant
42	118	11.3	1682	9 HUM1HRP	M2414 Human place
43	118	11.3	1682	11 G28528	G28528 human STS S
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RESULT 1

#### ALIGNMENTS

AX318176	LOCUS	AX318176	618 bp	DNA	linear	PAT 14-DEC-2001
DEFINITION	Sequence 181 from Patent WO0190156.					
ACCESSION	AX318176					
VERSION	AX318176.1	GI:17900867				
KEYWORDS	.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
AUTHORS	1					
TITLE	Reed, J.C., Plo, F.F., Godzik, A., Stehlik, C., Damiano, J.S., Lee, S.H., Oliveira, V.A., Hayashi, H. and Pawlowski, K.					
JOURNAL	Card domain containing polypeptides, encoding nucleic acids, and methods of use					
FEATURES	Patent: WO 0190156-A 181 29-NOV-2001; The Burnham Institute (US)					
source	location/Qualifiers					
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	/db_xref="taxon:9606"					
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Best Local Similarity:	100.00%
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DB:	6
	Gaps:
	618
	Matches:
	204
	Conservative:
	0
	Mismatches:
	0
	Indels:
	0
	Gaps:
	0

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Db	67	AAACTACTGAAGCCCGTAAGAAACCTGAAGAGATGTGTTATTATTCATTGACCACTTG	128
QY	41	SerAspIleGlyGluGlyMetAspTyrTleValLysSerLeuSerSerGluProCysAsp	60
Db	127	TCTGACATTTGAGAGGGAATGCATATACATAGTCAAGTCTGTGCATGAACCTGTGAC	186
QY	61	LeuGluGluIleGluLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAla	80
Db	187	CTTGAAAGAAATTCATTAGTCTCTCTGCTGCTTCCTGCAATGACGTAAGAAATCTAGCT	248
QY	81	GlnAsnLeuHisAsnLeuValLysLeuSerTleLeuAspLeuSerGluAsnTyrLeuGlu	100
Db	247	CAGATCTTACACATTTGGTCAAACTGAGCATCTTATATTATTCAGAAATTAACCTGGAA	306
QY	101	LysAspCysAsnGluAlaLeuHisGluLeuIleLysAspArgMetAsnValLeuGluGlnLeu	120
Db	307	AAAGATGGAATGAAGCTCTTCATGAACCTATGACAGGATGAAGACGTGCTAGAACACCTC	366
QY	121	ThrAlaLeuMetLeuProTyrGlyCysAspValGlnIysSerLeuSerSerLeuLeuLys	140
Db	367	ACCGCACTGATGCTGCGCCCTGGGCTGTGACCTGCAGAGCGACCTGACCACTGTGTGAAA	428
QY	141	HisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrArgLeuThrAsp	160

Db	427	CATTGGAGGAGGTC	CCACCAACTGCTAACCTTGCTGAAAAAACTGGACATCCACGAT	486
QY	161	ThrcGulllearglleu	glYalaphheglYlYsbnProleuYsasnphegInGln	180
Db	487	ACAGAGATTGAAATTTTAGGTGCATTTTTTGGAAAGAACCCCTCGAAAAA	CTCCAGCAG	546
QY	181	LeuasnLeuAlaGlyasnArGValSerSerAspGlyrrProleuAlaPheMetGlyValPhe		200
Db	547	TTGCAATTTGGGGGGAATTCGTGTACGACGTAGATGAGGCTTGCTTCATGAGGTGATTT		606
QY	201	gluasnLeuYs	204	
Db	607	GAGATCTTAAG	618	

LOCUS	IR2005417	1355 bp	mRNA	linear	PRI 16-JUL-2000
DEFINITION	Homo sapiens mRNA full length	cdna	clone	EUROIMAGE	2005417.
ACCESSION	AF389934				
VERSION	AF389934.1	GI:9367839			
KEYWORDS	FLI-CDNA.				
SOURCE	human.				
ORGANISM	Homo sapiens				

REFERENCE AUTHORS	TITLE	JOURNAL REFERENCE AUTHORS
1 (bases 1 to 1355) Auffray, C., Ansoorge, W., Ballabio, A., Estivall, X., Gibson, K., Lehrach, H., Postula, A. and Underberg, J.	The European IMAC consortium for integrated Molecular analysis of human gene transcripts	unpublished 2 (bases 1 to 1355) Pluvigne, R., Estivall, X., Escarceller, M. and Sumoy, L.

COMENT  
EURO-IMAGE Consortium Contact: Aulfiy C  
http://www.iro.es e-mail enquiries: lsumoy@iro.es  
SPAIN. Tel: ++34-93-260-7775 Fax: ++34-93-260-7776 WWW site:  
s/n Km 2,7 L'Hospitalet de Llobregat, 08907 Barcelona, Catalunya,  
Recerca Oncologica (IRO), Hospital Duran i Reynals, Av. Gran Via  
Barcelona (15-062 20097) Spain. Contact: Hospital de

CNRS upr 420 - Genetique Moléculaire et Biologie du Développement  
IFR 1221 - Rue Guy Moquet 19, Batiment G - Bp 8  
94801 Villejuif Cedex, FRANCE  
Tel: ++33-1-49 58 34 98  
Fax: ++33-1-49 58 35 09  
E-mail: [auffray@infobiogen.fr](mailto:auffray@infobiogen.fr)  
This clone is available royalty-free through IMAGE Consortium  
Distributors.  
IMPORTANT: This sequence represents the full insert of this IMAGE  
cDNA clone. No attempt has been made to verify whether this  
corresponds to the full-length of the original mRNA from which it  
was derived.

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/db_xref="taxon:9606"
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BASE COUNT 416 a 265 c 312 g 362 t

ORIGIN

Alignment Scores:

Pred. No.:	2,52e-95	Length:	1355
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Best Local Similarity:	100.00%	Mismatches:	0
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		Gaps:	0

US-09-697-089-2\_COPY\_762\_965 (1-204) x IR2005417 (1-1355)

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|||||  
Db 550 AAACAGCTGAAGGCGCTGAAAAACCTGAAGAAGATGTGTTATTCATTGACCCACTTG 649

Qy 41 SerAspIleGluGluGluMetAspTyrIleValLysSerLeuSerSerGluProCysAsp 60  
|||||  
Db 650 TCTGCATTTGGAGAGGAGGATGATACATAGTCAGTCTCTGCAAGTGAACCTGTGAC 709  
Qy 61 LeuGluGluIleGluLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAla 80  
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Qy 201 GluAsnLeuLys 204  
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RESULT 3  
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DEFINITION Sequence 98 from Patent WO0190156.  
ACCESSION AX318093  
VERSION AX318093.1 GI:17900822  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Reed,J.C., Plo,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H.,  
Oliveira,V.A., Hayashi,H. and Pawlowski,K.

TITLE Card domain containing polypeptides, encoding nucleic acids, and  
methods of use  
JOURNAL Patent: WO 0190156-A 98 29-NOV-2001;  
The Burnham Institute (US)

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US-09-697-089-2\_COPY\_762\_965 (1-204) x IR2005417 (1-1355)

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Db 635 AAACAGCTGAAGGCGCTGAAAAACCTGAAGAAGATGTGTTATTCATTGACCCACTTG 684

Qy 41 SerAspIleGluGluGluMetAspTyrIleValLysSerLeuSerSerGluProCysAsp 60  
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Db 685 TCTGCATTTGGAGAGGAGGATGATACATAGTCAGTCTCTGCAAGTGAACCTGTGAC 744

Qy 61 LeuGluGluIleGluLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAla 80  
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Db 745 CTTGAAGAAATTCATTAAGTCTCCTGCTGCTGCTGCAAAATGACAGTAAATCTTACCT 804

Qy 81 GlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu 100  
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Db 805 CAGAACTTCCACAAATTTGGTCAAACTGAGCATTTGATTTATTCAGAAAATTAACCTGGAA 864

Qy 101 LysAspGluAsnGluAlaLeuHisGluLeuLleAspArgMetAsnValLeuGluGluLeu 120  
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Qy 121 ThrAlaLeuMetLeuProTirpGlyCysAspValGlnGlySerLeuSerSerLeuLeuLys 140  
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Db 925 ACCGACATGATGCTCCCTCGGGCGTGTGACGTGCAAGCAGCCTGACAGCCTGTTGAAA 984

Qy 141 HisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTirpArgLeuThrAsp 160  
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Qy 161 ThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGln 180  
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Qy 181 LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTirpLeuAlaPheMetGlyAlaPhe 200  
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Db 1105 TTGAATTTGGGGGGAATCGTGTGAGCAGTATGATGATGCTTGGCTTCATGGGTATATT 1164

QY 201 GluAsnLeuLys 204  
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Db 1165 GAGAACTCTTAAG 1176

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LOCUS AY027788 1395 bp mRNA linear PRI 20-JUL-2001  
DEFINITION Homo sapiens CIANB (CIAN1) mRNA, complete cds.  
ACCESSION AY027788  
VERSION AY027788.1 GI:14324114  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 1395)  
AUTHORS Damiano,J.S., Stehlik,C., Plo,F., Godzik,A. and Reed,J.C.  
TITLE CJan, a novel human ced-4-like gene  
JOURNAL Genomics 75 (1-3), 77-83 (2001)  
MEDLINE 21365712  
PUBMED 11472070  
REFERENCE 2 (bases 1 to 1395)  
AUTHORS Stehlik,C., Damiano,J.S., Plo,F., Godzik,A. and Reed,J.C.  
TITLE Direct Submission  
JOURNAL Submitted (21-FEB-2001) Program on Apoptosis and Cell Death  
Research, The Burnham Institute, 10901 North Torrey Pines Road, La  
Jolla, CA 92037, USA

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Pred. No.: 2,61e-95 Length: 1395  
Score: 1046.00 Matches: 204  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-697-089-2\_COPY\_762\_965 (1-204) x AY027788 (1-1395)

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QY 21 LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu 40  
|||||  
Db 625 AAACCTAGCTGAAGCGCTGAAGAAACCTGAAGAAGATGTATTATTCAATTCACCCACTTG 684

QY 41 SerAspIleGlyGlyGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAsp 60  
|||||

Db 685 TCTCACATTGGAGAGCGAATGATATACATAGTCTCTGTCACAGTGAACCTGTGAC 744

QY 61 LeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAla 80  
|||||  
Db 745 CTTGAAGAATAATTCAATTAGTCTCTGCTGCTGCTGCTCAATGACGAGAAATCTGAGT 804

QY 81 GluAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu 100  
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QY 101 LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeu 120  
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QY 121 ThrAlaLeuMetLeuPorrPglCysAspValGlnGlySerLeuSerSerLeuLys 140  
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QY 201 GluAsnLeuLys 204  
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RESULT 5  
AY032589

LOCUS AY032589 3133 bp mRNA linear PRI 25-MAY-2001  
DEFINITION Homo sapiens caspase recruitment domain protein 12 mRNA, complete  
cds.  
ACCESSION AY032589  
VERSION AY032589.1 GI:13899172  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 3133)  
AUTHORS Geddes,B.J., Wang,L., Huang,W.-J., Lavellee,M., Manji,G.A.,  
Brown,M., Jurman,M., Morganstern,J., Merriam,S., Glucksmann,A.,  
Distefano,P.S. and Bertin,J.  
TITLE Human CARD12 is a novel CED4/Apaf-1 family member that induces  
apoptosis  
JOURNAL Biochem. Biophys. Res. Commun. 284 (1), 77-82 (2001)  
MEDLINE 21268963  
PUBMED 11374873  
REFERENCE 2 (bases 1 to 3133)  
AUTHORS Bertin,J.  
TITLE Direct Submission  
JOURNAL Submitted (15-APR-2001) Neurobiology, Millennium Pharmaceuticals  
Inc., 640 Memorial Drive, Cambridge, MA 02139, USA

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Score: 1046.00 Matches: 204
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

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DB 2379 AAACGACGAGGAGGCGCTGAAAAAAGCTGAAAGAGATGTTTATTCATTGACCCACTTG 2438
QY 41 SerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAsp 60
DB 2439 TCTGCATTTGCGAGAGGAGATGATACATGCAAGTCTCTCTCAAGTGAACCTGTGAC 2498
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QY 121 ThrAlaLeuMetLeuProTyrPglCysAspValGlnGlySerLeuSerSerLeuLeuYs 140
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QY 201 GlnAsnLeuLys 204
DB 2919 GAGAACTCTTAAG 2930

RESULT 6
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LOCUS
DEFINITION Homo sapiens ICE-protease activating factor mRNA, complete cds.
ACCESSION AY035391
VERSION AY035391.1 GI:1434214
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
Poyet,J.L., Srinivasula,S.M., Tianl,M., Raznara,M.,
Fernandes-Alnemri,T. and Alnemri,E.S.
Identification of Ipa1, a human caspase-1-activating protein
related to Apa1-1
J. Biol. Chem. 276 (30), 28309-28313 (2001)
MEDLINE 21359454
PUBMED 11390368
REFERENCE
2 (bases 1 to 3219)
Poyet,J.-L., Srinivasula,S.M., Fernandez-Alnemri,T. and
Alnemri,E.S.
Direct Submission
Submitted (16-May-2001) Microbiology and Immunology, Thomas
Jefferson University, 233 S. 10th Street, Philadelphia, PA 19107,
USA

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BASE COUNT 934 a 696 c 748 g 841 t
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Alignment Scores:
Pred. No.: 6.83e-95 Length: 3219
Score: 1046.00 Matches: 204
Percent Similarity: 100.00% Conservative: 0
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Query Match: 100.00% Indels: 0
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RESULT 7  
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LOCUS BC031555  
DEFINITION Homo sapiens, caspase recruitment domain protein 12, clone  
HMC:35330 IMAGE:5179909, mRNA, complete cds.  
ACCESSION BC031555  
VERSION BC031555.1 GI:21594975  
KEYWORDS MGC.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 3360)  
AUTHORS Strausberg, R.  
TITLE Direct Submission  
JOURNAL Submitted (06-JUN-2002) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
NIR-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Baylor College of Medicine Human Genome  
Sequencing Center

Center code: BCM-HGSC  
Web site: <http://www.bhsc.bcm.tmc.edu/cdna/>  
Contact: [amgdbcm.tmc.edu](mailto:amgdbcm.tmc.edu)  
Gonartne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,  
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,  
Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAC Plate: 50 Row: a Column: 10  
This clone was selected for full length sequencing because it  
passed the following selection criteria: Hexamer frequency ORF  
analysis.

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BASE COUNT 1011 a 718 c 768 g 863 t

ORIGIN

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Score: 1046.00 Matches: 204  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
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US-09-697-089-2\_COPY\_762\_965 (1-204) x BC031555 (1-3360)

QY 1 LeuysasnlleuthThrlsleuilemetaspasniileysmetasngluculaspalalle 20  
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QY 21 LysleualagluglyLeuylsasnleuylslysmetCysleuphehisleuthrlisleu 40  
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Db 2575 AAACAGCTGAAGGCCCTGAAAAAAGAGAGATGTGTTATTTTCATTGGACCACTTG 2634

QY 41 SeraspillegluglyCylmetaspyrillevalylsSerleuSerSerGluProcysasp 60  
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QY 61 LeuglugliuleglnleuValserCysCysleuSerAlaasnAlaValylsleuAla 80  
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Db 2695 CTTGAGAAATTCATTAAGTCTCTCTGCTCTGCAAAATGCAAGTGAATTCCTAGCT 2754  
QY 81 GlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnIleuGlu 100  
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QY 101 LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeu 120  
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QY 121 ThrAlaLeuMetLeuProTropGlyCysAspValGlnGlySerLeuSerSerLeuLeuLys 140  
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QY 141 HisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThrAsp 160  
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QY 181 LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGlyValPhe 200  
Db 3055 TTGAATTTGGCGGAAATCGTGTGACAGTGTGATGATGCTTGCCTTCATGGGTGATTT 3114  
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RESULT 8  
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LOCUS AX318091  
DEFINITION Sequence 96 from Patent WO0190156.  
ACCESSION AX318091  
VERSION AX318091.1 GI:17900820  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Reed,J.C., Plo,F.F., Godzik,A., Stehlik,C., Damiano,J.S., Lee,S.H.,  
Oliveira,Y.A., Hayaishi,H. and Pawlowski,K.  
TITLE Card domain containing polypeptides, encoding nucleic acids, and  
JOURNAL methods of use  
Patent: WO 0190156-A 96 29-NOV-2001;  
The Burnham Institute (US)  
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BASE COUNT 992 a 737 c 793 g 874 t  
ORIGIN

Alignment Scores:  
Pred. No.: 7.26e-95 Length: 3396  
Score: 1046.00 Matches: 204  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

US-09-697-089-2\_COPY\_762\_965 (1-204) x AX318091 (1-3396)

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QY 201 GluAsnLeuLys 204  
Db 3160 GAGAAATCTTAAG 3171

RESULT 9  
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LOCUS AY027787  
DEFINITION Homo sapiens CLIAN1 (CLIAN1) mRNA, complete cds.  
ACCESSION AY027787  
VERSION AY027787.1 GI:14324112  
KEYWORDS  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 3396)  
AUTHORS Damiano,J.S., Stehlik,C., Plo,F., Godzik,A. and Reed,J.C.  
TITLE Clam, a novel human ced-4-like gene

JOURNAL Genomics 75 (1-3), 77-83 (2001)  
 MEDLINE 21365712  
 PUBMED 11472070  
 REFERENCE 2 (bases 1 to 3396)  
 AUTHORS Stehlik,C., Damiano,J.S., Pio,F., Godzik,A. and Reed,J.C.  
 TITLE Direct Submission  
 JOURNAL Submitted (21-FEB-2001) Program on Apoptosis and Cell Death  
 Research, The Burnham Institute, 10901 North Torrey Pines Road, La  
 Jolla, CA 92037, USA

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BASE COUNT 992 a 737 c 793 g 874 t

ORIGIN

Alignment Scores:  
 Pred. No.: 7.26e-95 Length: 3396  
 Score: 1046.00 Matches: 204  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0

US-09-697-089-2\_COPY\_762\_965 (1-204) x AY027787 (1-3396)

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QY 41 SerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAsp 60  
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 DB 3100 TTGAATTTGGCGGGAATTCGTGTGACAGTATGATGATGCTGCTTCATGGGTGATATT 3159

QY 201 GluAsnLeuLys 204  
 DB 3160 GAGAACTTTAAG 3171

RESULT 10  
 LOCUS AF376061  
 DEFINITION Homo sapiens caspase recruitment domain protein 12 mRNA, complete cds.

ACCESSION AF376061  
 VERSION AF376061.1 GI:14040074  
 KEYWORDS

SOURCE  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 1 (bases 1 to 3581)  
 Gingras,M.-C., Olin,J. and Margolin,J.F.  
 Differential expression of the caspase recruitment domain protein 12 (CARD12) during monocytic differentiation

AUTHORS  
 TITLE  
 JOURNAL  
 REFERENCE  
 2 (bases 1 to 3581)  
 Gingras,M.-C., Olin,J. and Margolin,J.F.  
 Submitted (03-MAY-2001) Pediatric/Texas Children's Cancer Center,  
 Baylor College of Medicine, 6621 Fannin St. MC3-3320, Houston, TX  
 77030, USA

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/note="Region: caspase recruitment domain"

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ORIGIN

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Percent Similarity: 100.00% Conservative: 0  
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Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-697-089-2\_COPY\_762\_965 (1-204) x AF376061 (1-3581)

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Oy 41 SerAspIleGlyGluGlyMetAspTyrTrileValLysSerLeuSerSerGluProCysasp 60  
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Oy 201 GlnAsnLeuLys 204  
Db 3373 GAGATCTTAAG 3384

RESULT 11  
LOCUS AK095467 3355 bp mRNA linear PRI 15-JUL-2002  
DEFINITION Homo sapiens cDNA FLJ38148 fis, clone D90ST2003791, highly similar  
to Homo sapiens ICE-protease activating factor mRNA.

ACCESSION AK095467  
VERSION AK095467.1 GI:21754727  
KEYWORDS Oligo capping; fts (full insert sequence).  
SOURCE Homo sapiens CD34+ Cells cDNA to mRNA, clone\_lib:D90ST2  
clone:D90ST2003791.

#### ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

#### REFERENCE

##### AUTHORS

1 Ninomiya, K., Wagatsuma, M., Kanda, K., Kondo, H., Yokoi, T., Kodaira, H., Furuya, T., Takahashi, M., Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Murakawa, K., Kanenori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuo, Y., Nagai, K. and Isogai, T.  
NEDO human cDNA sequencing project

##### REFERENCE

2 (bases 1 to 3355)

##### AUTHORS

Isogai, T. and Yamamoto, J.

##### JOURNAL

Submitted (04-JUL-2002) Takao Isogai, FRI Project(HRI Team); 2-6-7

#### COMMENT

(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)  
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'-63'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.

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BASE COUNT 986 a 726 c 774 g 869 t

#### ORIGIN

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DB: 9 Gaps: 0

US-09-697-089-2\_COPY\_762\_965 (1-204) x AK095467 (1-3355)

Oy 1 LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAlaIle 20  
Db 2545 TTGAAGAAGACCTTACAAACCTCATATAGATTAACATTAAGAGATGAAGAAACATCTATA 2604  
Oy 21 LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu 40  
Db 2605 AAACAGCTGAAGGCTGAAAAACCTGGAGAGAGATGTTTATTTTCATTGACCCACTTG 2664  
Oy 41 SerAspIleGlyGluGlyMetAspTyrTrileValLysSerLeuSerSerGluProCysasp 60  
Db 2665 TCTGACATTGGAGAGGATGATTAACATAGCAAGTCTCTGCAAGTGAAGAACCTGTCAG 2724  
Oy 61 LeuGluGluIleGlnLeuValSerCysLeuSerSerAlaAsnAlaValLysIleLeuAla 80  
Db 2725 CTGGAAGAATTCATTAATGCTCTCGCTGCTGTCTGCAAAAGCAGTGAATAATCTTACT 2784  
Oy 81 GlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu 100

```

|||||
Db 2785 CACAATCTTACAAATTTGGTCAAACTGAGCATCTTGTATTATCAGAAATTTACTCTGAA 2844
QY 101 LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValIleGluGlnLeu 120
Db 2845 AAAGATGGAATGATGAGCTCTTCATGAACTGATGCACAGATGAACTGCTGTAAGAACACTC 2904
QY 121 ThrAlaLeuMetLeuProTrrpGlyCysAspValGlnGlySerLeuSerSerLeuLeuLys 140
Db 2905 ACCGACTGATGCTGCCCTGGGCTGTGAGCTGCAGAGCAGCCGTGACAGAGCTGTGAA 2964
QY 141 HisLeuGlnGluValProGlnLeuValIleGluGlyLeuLysAsnTrrpArgLeuThrAsp 160
Db 2965 CATTTGAGAGGAGGTCACACACTGCTCAAGCTTGAGTGAAGAACTGAGACTCAGAT 3024
QY 161 ThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPhelGln 180
Db 3025 ACAGAGATTTGAATTTTAGTGCGATTTTGGAAAGAACCTCGAAGAAATTCACAGAG 3084
QY 181 LeuAsnLeuAlaGlyAsnAlaValSerSerAspGlyTrrpLeuAlaPheMetGlyValPhe 200
Db 3085 TTGAAATTTGGCGGGAATCGTGTGAGCAGATGATGATGGCTTGCCTCATGCGTATTT 3144
QY 201 GluAsnLeuLys 204
Db 3145 GAGATCTTAAG 3156

RESULT 12
CNS01DS3 138909 bp DNA linear PRI 18-APR-2002
LOCUS CNS01DS3/c
DEFINITION BAC sequence from the SPG4 candidate region at 2p21-2p22 BAC 164M19
of library CITB_978_SKB from chromosome 2 of Homo sapiens (Human).
ACCESSION AL121653
VERSION AL121653.2 GI:7159616
KEYWORDS SPG4 genomic DNA interval.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 138909)
Hazan,J., Fonknechten,N., Mavel,D., Paternotte,C., Samson,D.,
Artiguenave,F., Dayoche,C.S., Cruaud,C., Durr,A., Wincker,P.,
Brotier,P., Gattolico,L., Barde,V., Burgunder,J.M.,
Prud'Homme,J.F., Brice,A., Fontaine,B., Heilig,R. and
Weissenbach,J.
Spastin, a novel AAA protein, is altered in the most frequent form
of autosomal dominant spastic paraplegia
Nat. Genet. (1999) in press
2 (bases 1 to 138909)
Genoscope.
JOURNAL Direct Submission
REFERENCE Submitted (18-APR-2002) Genoscope - Centre National de Sequencage :
AUTHORS BP 161 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
JOURNAL - Web : www.genoscope.cns.fr)
COMMENT On Mar 6, 2000 this sequence version replaced gi:6002386.
FEATURES
source
Location/Qualifiers
1..138909
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
/clone="164M19"
/clone_lib="CITB_978_SKB"
BASE COUNT 39243 a 28424 c 29121 g 42121 t
ORIGIN
Alignment Scores:
Pred. No.: 1.53e-21 Length: 138909
Score: 331.00 Matches: 91
Percent Similarity: 28.10% Conservative: 2
Best Local Similarity: 27.49% Mismatches: 6
Query Match: 31.64% Indels: 232
DB: 9 Gaps: 2

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US-09-697-089-2_COPY_762_965 (1-204) x CNS01DS3 (1-138909)
QY 80 AlaGlnAsnLeuHisAsnLeuValIleLeuSerIleLeuAspLeuSerGluAsnTrrpLeu 99
Db 60048 GCTGAGATCTTTCACAAATTTGGTCAAACTGAGCATCTTGTATTATCAGAAATTTACTCTG 59989
QY 100 GluLysAspGlyAsnGluAlaLeuHisGluLeu----- 110
Db 59988 GAAAAGATGGAATGAAATGAAAGCTTCATGAACTGTAAGAAATGCAATTCAGCCMAAAT 59929
QY 110 ----- 110
Db 59928 AGATACCTGAATATGATCTAGGCTAGTCCGAATACATACCTGGTGGTCTGAGTCTTT 59869
QY 110 ----- 110
Db 59868 ATACCATGTGTGCTTACTAGATGACACCTCCTTAGAAGAAATCATTTAGGCTTCTTA 59809
QY 110 ----- 110
Db 59808 AACTGCCCTTAAGAACACAGGCCCATGTCTTTAAGTCACCACTTACATATGCTCACT 59749
QY 110 ----- 110
Db 59748 GCACTTGAGCGGCTATCCACCTGCTTCTCTCTTGAAGAGGCACTGCAAGAGTAG 59689
QY 110 ----- 110
Db 59688 CCGATGTGCAAGACAAATTTGCTTAAGGAATTTGGTATGATTTTATAGTGTGATAGT 59629
QY 110 ----- 110
Db 59628 GATATGTGATTATGTTAAAAAGAAAAAGAAAGAACTGATTCATATTGTCCATGATT 59569
QY 110 ----- 110
Db 59568 TGCTTTGAATTAATACAGAGGAATTAGTCAGATTAAAGCAATGCCATATTTAA 59509
QY 110 ----- 110
Db 59508 TGTTTTGAAGGTGCTTATTATGATATATATGTTTCAATTATATCTTCGATATATGTT 59449
QY 110 ----- 110
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QY 110 ----- 110
Db 59388 TGAGTAGGCTCAGAGCCACCAACATTAAGATCATTCCTCCCTAACACCCCTTGTTC 59329
QY 111 ----- 113
Db 59328 TTCTCAGATTTTGAGACCATCCAGTCCCTGAAGTCTTGTTCCTCCAGTCGACAGG 59269
QY 114 MetAsnValIleGluGlnLeuThrAlaLeuMetLeuProTrrpGlyCysAspValGlnGly 133
Db 59268 ATGAACGTGCTAGAACAGCTCACCGCATGATGTGCGCTGGGCTGTGAGAGTCAAGGC 59209
QY 134 SerLeuSerSerLeuLeuHisLeuGlnGluValProGlnLeuValIleLysLeuGlyLeu 153
Db 59208 AGCCTGAGCACCTGTTGAAACATTTGGAGGAGGTCCCAACACGTCGACCTGGGTTG 59149
QY 154 LysAsnTrrpArgLeuTrrpAspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsn 173
Db 59148 AAAAAGTGAAGACTCAGACAGATACAGAGATTGATTTAGTAGTAGTACACATACAGAG 59089
QY 174 Pro-----LeuLysAsnPhe 178
Db 59088 CCAAGATTAAGTGAATTTGGCCCTTAAGAAATTC 59056
RESULT 13
AC011232/c
LOCUS AC011232 185281 bp DNA linear HTG 10-MAR-2001

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DEFINITION Homo sapiens chromosome 2 clone RP11-78E13, WORKING DRAFT SEQUENCE
ACCESSION AC011232
VERSION AC011232.7
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE 1 (bases 1 to 185281)
JOURNAL Waterston,R.H.
REFERENCE The sequence of Homo sapiens clone
AUTHORS Unpublished
TITLE 2 (bases 1 to 185281)
JOURNAL Waterston,R.H.
REFERENCE Direct Submission
AUTHORS Submitted (04-OCT-1999) Genome Sequencing Center, Washington
TITLE University School of Medicine, 4444 Forest Park Parkway, St. Louis
JOURNAL MO 63108, USA
COMMENT On Mar 10, 2001 this sequence version replaced gi:9799811.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site:http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H.NH0078E13
----- Summary Statistics -----
Sequencing vector: M13; 57k
Sequencing vector: plasmid; 40k
Chemistry: Dye-primer ET; 48% of reads
Chemistry: Dye-terminator B1g Dye; 50% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 182798 bases at least Q40
Consensus quality: 183538 bases at least Q30
Consensus quality: 184045 bases at least Q20
Insert size: 168000; agarose-fp
Insert size: 184681; sum-of-contigs
Quality coverage: 7.07 in Q20 bases; agarose-fp
Quality coverage: 7.33 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 1985: contig of 1985 bp in length
* 1986 2085: gap of unknown length
* 2086 8183: contig of 6098 bp in length
* 8184 8283: gap of unknown length
* 8284 22741: contig of 14458 bp in length
* 22742 22841: gap of unknown length
* 22842 41446: contig of 18605 bp in length
* 41447 41546: gap of unknown length
* 41547 69182: contig of 27636 bp in length
* 69183 69282: gap of unknown length
* 69283 112331: contig of 42849 bp in length
* 112332 112231: gap of unknown length
* 112232 185281: contig of 73050 bp in length.
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1. 185281
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/db_xref="taxon:9606"
/chromosome="2"
/clone="RP11-78E13"
1. 1985
/note="assembly_name:Contig11"
2086. 8183
/note="assembly_name:Contig12"
8284. .22741

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[illegible]

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 Db 170949 ATGAACGTGTAAGAACAGCTACCGCACTGATGCTGCCCTGGGGCTGTGAGCTGAAGAC 170890  
 QY 134 SerleuserSerleuLeuLysHisleuGluValProGlnleuValLysleuGlyLeu 153  
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 Db 170889 AGCCTGAGACCCCTGTGAAACATTTTGAGAGAGTCCCAACATCTGTCACACTTGCGTTG 170830  
 QY 154 LysasnPrpAgtleuThAspThrGluileArgileuGlyAlaPhePhgLyLysasn 173  
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 Db 170829 AAAAAGTGAGACTCACAGATACAGATTGAAATTTTAGTAGTACACATACAGAG 170770  
 QY 174 Pro-----LeuLysasnPhe 178  
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 Db 170769 CCAAGATPACTGATTTGGCCCTTAAAAAATTC 170737

RESULT 14  
 AC010968 160583 bp DNA linear HTG 18-AUG-2000  
 LOCUS Homo sapiens chromosome 2 clone RP11-9302, WORKING DRAFT SEQUENCE,  
 DEFINITION 11 unordered pieces.  
 AC010968  
 VERSION AC010968.5 GI:9845170  
 KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
 SOURCE Homo sapiens.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 1 (bases 1 to 160583)  
 Waterston, R.H.  
 The sequence of Homo sapiens clone  
 Unpublished  
 2 (bases 1 to 160583)  
 Waterston, R.H.  
 Direct Submission  
 Submitted (28-SEP-1999) Genome Sequencing Center, Washington  
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
 MO 63108, USA  
 On Aug 18, 2000 this sequence version replaced g1:8439959.

COMMENT

----- Genome Center -----  
 Center: Washington University Genome Sequencing Center  
 Center code: WUGSC  
 Web site: http://genome.wustl.edu/gsc/index.shtml  
 ----- Project Information -----  
 Center project name: H\_NH0093002  
 ----- Summary Statistics -----  
 Sequencing vector: M13; 598  
 Sequencing vector: plasmid; 418  
 Chemistry: Dye-primer ET; 47% of reads  
 Chemistry: Dye-terminator Big Dye; 53% of reads  
 Assembly program: Phrap; version 0.990319  
 Consensus quality: bases at least Q40  
 Consensus quality: bases at least Q30  
 Consensus quality: bases at least Q20  
 Insert size: 14700; agarose-fp  
 Insert size: 159583; sum-of-contigs  
 Quality coverage: 6.64 in Q20 bases; agarose-fp  
 Quality coverage: 6.38 in Q20 bases; sum-of-contigs  
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 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 11 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.  
 \* 1 1080: contig of 1080 bp in length  
 \* 1081 1180: gap of unknown length  
 \* 1181 2476: contig of 1296 bp in length  
 \* 2477 2576: gap of unknown length

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 vector\_side:right"  
 116936. 160583  
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 Score: 326.00 Matches: 91  
 Percent Similarity: 28.10% Conservative: 2  
 Best local Similarity: 27.49% Mismatches: 6  
 Query Match: 31.17% Indels: 232  
 DB: 2 Gaps: 2  
 US-09-697-089-2\_COPY\_762\_965 (1-204) x AC010968 (1-160583)  
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 Db 64448 GTGAGATCTTTCACATTTTGTCAAACTGAGCATTTCTGTATTATCAGAAATTTACTCG 64507  
 QY 100 GluLysAspGluAsnGluAlaLeuHisGluLeu----- 110  
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 Db 64508 GAAAGATGGAATGGAAGCTCTTCATGACACTGATAGATGACAAATTCAGCCAAAT 64567  
 QY 110 ----- 110  
 Db 64568 AGATPACTGATPACTGAGTGGTACTGGAATPACTAGCCCTGGTCTGAGTCTTTT 64627



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Oy 110 ----- 110
Db 6468 ATACCATTGTCCTTACTAGATGACCCCTCTTAGGAAATCATTTAGGCTTTCTTA 64687
Oy 110 ----- 110
Db 6468 AACGCCCTTAGGAAACAGAGCCCATGCTTTTAAGTACACAGTTTACATATGCTCACT 64747
Oy 110 ----- 110
Db 64748 GCACCTTGAGCGGTATCCACCTGCTTCTCTTGAGAGGCACTGTCAAGAGTAG 64807
Oy 110 ----- 110
Db 64808 CCGATGTGCAAGACAAATTTGCTTAGGAATTTGGATATGATTTTGTAGTGTGATGCT 64867
Oy 110 ----- 110
Db 64868 GATATGTATGTATGTTAAAGAAAAAGAAAGAAAGAACTATTCATATTTGTCACGATT 64927
Oy 110 ----- 110
Db 64928 TGCTTTAGAAATATACAGAGGAATTAGTCAAGATTAAGCAACATGCCCCATGATTTAA 64987
Oy 110 ----- 110
Db 64988 TGTTTTGAAGCTGCTTATATATATATATATAGTTTCATATATTTCTTCCATTAATGTTT 65047
Oy 110 ----- 110
Db 65048 GATATGCTTGAATACTTTCCAAAAAACCAAAATTAAGTAGATTCTCATTTACAGAT 65107
Oy 110 ----- 110
Db 65108 TGAGTAGCTGACAGACCAACAAATTAAGATCATTCCTCCACACCCCTTTGTTC 65167
Oy 111 ----- 113
Db 65168 TTCCATGTTTGGAGACCATTCAGTCCCTGAACTGCTTTGTTTCTTCCAGTGCACAGG 65227
Oy 114 MetasValLeuGlugInLeuThrAlaLeuMetLeuProTprGlyCysAspValGlnGly 113
Db 65228 ATGAACGTGTAGAACACCTACCGCACTGATGCTGCCCTGGGCTGTGAGCTGCAAGG 65287
Oy 134 SerLeuSerSerLeuLeuLysHisLeuGluValProGlnLeuValLysLeuGlyLeu 153
Db 65288 AGCCTGAGCAGCCTGTTGAAACATTTGGAGAGGATCCCAACTGCTCAAGCTTGGTTG 65347
Oy 154 LysAsnTrpArgLeuThrAspThrGluIleArgTlleLeuGlyAlaPhePheGlyLysAsn 173
Db 65348 AAAAAGTGGAGACTCACAGATACAGATTAAGATTTAGGTAGGTACACACATACAGAG 65407
Oy 174 Pro-----LeuLysAsnPhe 178
Db 65408 CCAAGATTAACCTGATTTGGCCCTTAATAAAATTC 65440
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DEFINITION SHGC-100923 Human Homo sapiens STS genomic, sequence tagged site.
ACCESSION G55568
VERSION G55568.1 GI:6120887
KEYWORDS STS.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 553)
AUTHORS Olivier,M. and Cox,D.R.
TITLE Unpublished, Olivier, M., Cox, D.R. (2000)
JOURNAL Unpublished (2000)
COMMENT

```

Contact: Michael Olivier, David R. Cox  
Stanford Human Genome Center  
Stanford University School of Medicine  
4005 Miranda Ave., 2nd Fl., Palo Alto, CA 94025, USA  
Tel: (650) 320-5800  
Fax: (650) 320-5801  
Email: olivier@shgc.stanford.edu  
Primer A: AATAGAGGGGCAAAATAGCAAA  
Primer B: TACACCCCTTGTCTCTCTCA  
STS size: 322

PCR Profile:  
Initial incubation: 95 degrees C for 10 minutes  
Denaturation: 94 degrees C for 30 seconds  
Annealing: 60 degrees C for 30 seconds  
Polymerization: 72 degrees C for 23 seconds  
PCR Cycles: 30  
Thermal Cycler: Perkin Elmer 9700

Protocol:  
Template: 25 ng  
Primer: each 1 uM  
dNTPs: each 200 uM  
AmpliTaq Gold Polymerase: 0.07 units/uL  
Total Vol: 5 uL

Buffer:  
MgCl2: 2.5 mM  
KCl: 50 mM  
Tris-HCl: 10 mM  
pH: 8.3

BAC ends sequenced at TIGR from the RPC11 BAC library. Designed and developed at the Stanford Human Genome Center.

FEATURES  
Location/Qualifiers  
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STS  
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BASE COUNT 170 a complement(304..326)  
ORIGIN

Alignment Scores:  
Pred. No.: 5.24e-21 Length: 553  
Score: 298.00 Matches: 60  
Percent Similarity: 83.78% Conservative: 2  
Best Local Similarity: 81.08% Mismatches: 6  
Query Match: 28.49% Indels: 6  
DB: 11 Gaps: 1

US-09-697-089-2\_COPY-762\_965 (1-204) x G55568 (1-553)

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Oy 111 IleaSPArGMeTAsnValLeuGluInLeuThrAlaLeuMetLeuProTprGlyCysAsp 130
Db 259 GTCCACAGATGACGCTCTAGAACAGCTCACCGCATGATGCTCCCTGGGCTGTAC 200
Oy 131 ValGlnGlySerLeuSerSerLeuLeuLysHisLeuGluValProGlnLeuValLys 150
Db 139 GTGCAGAGCAGCCTGAGCAGCTGTTGAACATTTGGAGAGGATCCCAACTGCTCAAG 140
Oy 151 LeuGlyLeuLysAsnTrpArgLeuThrAspThrGluIleArgTlleLeuGlyAlaPhePhe 170
Db 139 CTGGGTGAAAAAACTGAGACTCACAGATACAGATTAAGATTTAGGTAGGTACACA 80
Oy 171 GlyLysAsnPro-----LeuLysAsnPhe 178
Db 79 CATACAGAGCCACAGATTAACGATTTGGCCCTTAATAAAATTC 38

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Search completed: January 31, 2003, 15:16:30  
Job time : 3019.36 secs





Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES						
Result No.	Score	% Query Match	Length	DB	ID	Description
1	1046	100.0	618	24	ABK22767	Human cDNA encoding
2	1046	100.0	1395	24	AAK22732	Human cDNA encoding
3	1046	100.0	2950	22	AAN9581	Human protein encod
4	1046	100.0	3133	22	AAS03945	Human caspase recr
5	1046	100.0	3213	22	AAH78219	Nucleotide sequenc
6	1046	100.0	3396	24	ABK22731	Human cDNA encodin
7	1046	100.0	3545	22	AAH98254	Murine EST-derived
8	1046	100.0	3615	22	AAS03946	Human caspase recr
9	626	59.8	2735	22	AAH34171	Human colon cancer
10	202	19.3	421	22	ABA45612	Human breast cell
11	202	19.3	421	22	ABA56119	Human foetal liver
12	202	19.3	421	22	ABA25770	Probe #4236 for ge
13	202	19.3	421	22	AAK04305	Human brain express
14	202	19.3	421	22	AAK29801	Human bone marrow
15	202	19.3	421	22	AAI14389	Probe #4322 for ge
16	202	19.3	421	22	AAI35764	Probe #4450 used t
17	202	19.3	421	22	AAI04213	Probe #4204 used t
18	202	19.3	421	24	ABS04362	Human genome-deriv
19	147.5	14.1	3447	24	AAH48611	Mouse MATR cDNA.
20	124.5	11.9	2748	23	ABL10007	Drosophila melanog
21	122.5	11.7	4936	23	ABL10006	Drosophila melanog
22	121.5	11.6	3069	24	AAI47134	Pyrin domain conta
23	121	11.6	2614	23	ABL09367	Drosophila melanog
24	121	11.6	7324	23	ABL09366	Drosophila melanog
25	120	11.5	2826	24	AAN59870	Novel human coding
26	120	11.5	2840	22	AAH24250	Human Ras-binding
27	120	11.5	3847	22	AAH17735	Human cDNA sequenc
28	119.5	11.4	3525	20	AAH91788	Porphorymonas ging
29	119.5	11.4	3636	20	AAH91787	Porphorymonas ging
30	119.5	11.4	3798	20	AAH91786	Porphorymonas ging
31	119.5	11.4	3807	20	AAH91646	Porphorymonas ging
32	118	11.3	1386	19	AAV18082	Human liver ribonnu
33	118	11.3	1426	17	AAH33115	Human placental ri
34	118	11.3	1614	11	AAH77394	Human placental ri
35	118	11.3	1698	9	AAN81083	Encodes human plac
36	116.5	11.1	2479	22	AAH55219	Protein PRO265 cDN
37	116.5	11.1	2479	22	AAH52144	Human cDNA sequenc
38	116.5	11.1	2479	22	AAH87044	Nucleotide sequenc
39	116.5	11.1	2479	22	AAH72377	Human PRO265 cDNA
40	116.5	11.1	2479	24	AAH95853	Human angiogenesi
41	116.5	11.1	2479	24	AAH88094	Human PRO265 cDNA
42	116.5	11.1	2545	22	AAS36059	Human cardiovascu
43	116.5	11.1	2545	22	AAS34358	DNA encoding human
44	115	11.0	220	22	ABA50734	Human breast cell
45	115	11.0	220	22	ABA66704	Human foetal liver

RESULT 1  
ABK22767

ID ABR22767 standard; cDNA; 618 BP.

AC ABR22767;

DT 26-MAR-2002 (first entry)

DE Human cDNA encoding CLAN LRR.

KX Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;  
KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;  
KW autoimmune disease; inflammation; keratinocyte hyperplasia;  
KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;  
KW ballooning angiolysis; restenosis; glioma; carcinoma; sarcoma; melanoma;  
KW leukemia; allergy; arthritis; lupus; Schistosomiasis syndrome;  
KW Crohn's disease; graft-versus-host disease; stroke;  
KW myocardial infarction; heart failure; neurodegenerative disease;

KW Parkinson's disease; Alzheimer's disease; HIV;  
 XX human immunodeficiency virus infection.  
 OS Homo sapiens.  
 XX MO200190156-A2.  
 XX 29-NOV-2001.  
 XX 24-MAY-2001; 2001WO-US17158.  
 XX 24-MAY-2000; 2000US-0579240.  
 PR 10-OCT-2000; 2000US-0686347.  
 PR 14-MAR-2001; 2001US-275980P.  
 PR 23-MAY-2001; 2001US-0864921.  
 XX (BURN-) BURHAM INST.  
 XX Reed JC, Plo FF, Godzik A, Stehlik C, Damiano JS, Lee SH;  
 PI Oliveira VAM, Hayashi H, Pawlowski K;  
 XX WPI: 2002-083086/11.  
 DR P-PSDB; AAU80873.  
 XX New caspase recruitment domain (CARD)-containing polypeptides and  
 PT encoding nucleic acids, useful for treating abnormal cell proliferation  
 PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,  
 PT arthritis or stroke -  
 XX Claim 1; Page 202-203; 216pp; English.  
 XX The invention relates to an isolated caspase recruitment domain (CARD)  
 CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain  
 CC from it, and the polynucleotides encoding them. Also included are a  
 CC recombinant vector comprising the polynucleotide, recombinant cells  
 CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian  
 CC and insect cells) and an anti-CARD antibody. The CARD-containing  
 CC polypeptide and CARD-encoding nucleic acid are useful for treating a  
 CC pathology characterised by abnormal cell proliferation (e.g. cancer),  
 CC abnormal cell death (apoptosis), autoimmune diseases or inflammation.  
 CC Particular, the polypeptide and nucleic acid are useful for treating  
 CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth  
 CC muscle cell proliferation in arteries following balloon angioplasty  
 CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,  
 CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,  
 CC graft-versus-host disease, stroke, myocardial infarction, heart failure,  
 CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's  
 CC disease) or immunodeficiency associated disease (e.g. human  
 CC immunodeficiency virus (HIV) infection). The nucleic acids are useful  
 CC in a variety of diagnostic applications. The present sequence is a  
 CC cDNA encoding a CARD domain containing protein.  
 XX Sequence 618 BP; 194 A; 113 C; 148 G; 163 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 1,09e-106 Length: 618  
 Score: 1046.00 Matches: 204  
 Percent Similarity: 100.00% Conservative: 0  
 Best local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 24 Gaps: 0  
 US-09-697-089-2\_COPY\_762\_965 (1-204) x ABR22767 (1-618)  
 QY 1 LeuysAsnLeuThrIysLeuIleMerAspAsnIleYsMeTasGluAspAlaIle 20  
 DB 7 TTGAAGAACCCTTACAAAGCTCATATGATACATAAAGATGAAGAAGAGCTATTA 66  
 QY 21 LysleuAgluGluLeuIysAsnLeuYsIysMeCysleuPheHisLeuThrHisIeu 40  
 DB 67 AAAGTAGCTGAAGGCTGAAAACCTGAGAAAGATGCTTTATTTCATTGACCCACTTG 126  
 QY 41 SeraspIleGlyGluGlyMetaspTyrIleValYsSerLeuSerSerGluProCysasp 60

DB 127 TCTACATTGGAGAGGGAATGATTACATAGTCAAGCTCTGTCAAGTGAACCTGGAC 186  
 QY 61 LeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValIysIleLeuAla 80  
 DB 187 CTTGAAGAAATTCATTAGTCTCTGCTGCTGTCTCCAAATGACGAGAAATCTTAGCT 246  
 QY 81 GlnAsnLeuHisAsnLeuValIysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu 100  
 DB 247 CAGAAATCTTCACATTTTGGTCAAACTGACATCTTGTATTATTCAGAAATTAACCTGGA 306  
 QY 101 LysAspGlyAsnGluAlaLeuHisGlnLeuIleAspArgMetAsnValIleGluGlnLeu 120  
 DB 307 AAAGATGGAATGAAAGCTCTTCATGAACCTGACACGAGATGAACCGTGTAAGAACACTC 366  
 QY 121 ThrAlaLeuMetLeuProTppGlyCysAspValGlnIleSerLeuSerSerLeuIys 140  
 DB 367 ACCGCACTGATGCTGCCCTGGGCTGTGACGTGCAAGGCAAGCTGACACCTGTTGAAA 426  
 QY 141 HisLeuGluGluValProGlnLeuValIysLeuGlyLeuIysAsnTyrArgLeuThrAsp 160  
 DB 427 CATTGGAGGAGGTCCCAACACTGTCAGCTTGCTGTAAGAACTGAGACTCAGAGAT 486  
 QY 161 ThrGluIleArgIleLeuGlyAlaPhePheGlyIysAsnProLeuIysAsnPheGlnGln 180  
 DB 487 ACAGAGATTGAATTTAGTGCAATTTTGGAAAAGAACCTTGAAAACCTTCACAGAG 546  
 QY 181 LeuAsnLeuAlaGlyAsnArgValSerSerAspIlyTyrLeuAlaPheMetGlyValPhe 200  
 DB 547 TTGAATTTGGCGGGAATTCGTGTGACGATGATGATGATGGCTTGCCTTCATGGGTATT 606  
 QY 201 GluAsnLeuIys 204  
 DB 607 GAGATCTTTAAG 618  
 RESULT 2  
 ABR22732  
 ID ABR22732 standard; cDNA; 1395 BP.  
 XX ABR22732;  
 XX 26-MAR-2002 (first entry)  
 DE Human cDNA encoding CIAN B.  
 XX Caspase recruitment domain; CARD; ss; NB-ARC; ANGIO-R; LRR; SAM;  
 KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;  
 KW autoimmune disease; inflammation; keratinocyte hyperplasia;  
 KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;  
 KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;  
 KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;  
 KW Crohn's disease; graft-versus-host disease; stroke;  
 KW myocardial infarction; heart failure; neurodegenerative disease;  
 KW Parkinson's disease; Alzheimer's disease; HIV;  
 KW human immunodeficiency virus infection.  
 KW Homo sapiens.  
 OS MO200190156-A2.  
 XX 29-NOV-2001.  
 XX 24-MAY-2001; 2001WO-US17158.  
 XX 24-MAY-2000; 2000US-0579240.  
 PR 10-OCT-2000; 2000US-0686347.  
 PR 14-MAR-2001; 2001US-275980P.  
 PR 23-MAY-2001; 2001US-0864921.  
 XX (BURN-) BURHAM INST.  
 XX Reed JC, Plo FF, Godzik A, Stehlik C, Damiano JS, Lee SH;  
 PI Oliveira VAM, Hayashi H, Pawlowski K;

XX WPI: 2002-083086/11.  
DR P-PSDB: AAU80862.  
XX New caspase recruitment domain (CARD)-containing polypeptides and  
PT encoding nucleic acids, useful for treating abnormal cell proliferation  
PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,  
XX arthritis or stroke  
XX  
PS Claim 1; Page 174-176; 216pp; English.  
XX  
CC The invention relates to an isolated caspase recruitment domain (CARD)  
CC -containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain  
CC from it, and the polynucleotides encoding them. Also included are a  
CC recombinant vector comprising the polynucleotide, recombinant cells  
CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian  
CC and insect cells) and an anti-CARD antibody. The CARD-containing  
CC polypeptide and CARD-encoding nucleic acid are useful for treating a  
CC pathology characterised by abnormal cell proliferation (e.g. cancer),  
CC abnormal cell death (apoptosis), autoimmune diseases or inflammation. In  
CC particular, the polypeptide and nucleic acid are useful for treating  
CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth  
CC muscle cell proliferation in arteries following balloon angioplasty  
CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukaemias,  
CC allergies, arthritis, lupus, Schrogen's syndrome, Crohn's disease,  
CC graft-versus-host disease, stroke, myocardial infarction, heart failure,  
CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's  
CC disease) or immunodeficiency associated disease (e.g. human  
CC immunodeficiency virus (HIV) infection). The nucleic acids are useful  
CC in a variety of diagnostic applications. The present sequence is a  
CC cDNA encoding a CARD domain containing protein.  
XX  
SQ Sequence 1395 BP; 436 A; 248 C; 327 G; 384 T; 0 other;

Alignment Scores:  
Pred. No.: 3,28e-106 Length: 1395  
Score: 1046.00 Matches: 204  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 24

US-09-697-089-2\_COPY\_762\_965 (1-204) x ABK22732 (1-1395)

OY 1 LeuysaenleuThryleuilemetaspasnielysmetAsnleuGluAsnparalle 20  
DB 565 TTGAAGAAGCTTACAAACCTCATATATGATACATTAAGATGAAGAAACATGCTATA 624  
OY 21 LysleuAlaGluGlyLeuLysAsnleuLysLysMetCysLeuPheHisLeuThrHisleu 40  
DB 625 AAACAGCTGAAGGCGCTGAAAAACCTGAAGAAGATGTTTATTTCATTGACCCACTTG 684  
OY 41 SeraspIleGlyGluGlyMetaspTyrIleValLysSerLeuSerSerGluProCysasp 60  
DB 685 TCTGACATTGAGAGGAGGATGATACATACATGCTCTGTCAGTGAAGCAACCCGTGAC 744  
OY 61 LeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleleuAla 80  
DB 745 CTTGAGAAATTCATTAATGCTCCGTGCTGCTGTCGAAATGACGTAAAAATCCTACT 804  
OY 81 GlnAsnLeuHisAsnleuValLysLeuSerIleLeuAspLeuSerGluAsnTyrleuGlu 100  
DB 805 CAGAAATCTTCACAAATTTGGTCAAACTGAGCATTTCTTGATTTATCGAAATAATTAACCTGGA 864  
OY 101 LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValleuGluGlnleu 120  
DB 865 AAAGTGGAAATGAAGCTCTTCATGAACTGATCGACAGAGTGAAGAGTCTGAAACAGCTC 924  
OY 121 ThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerLeuSerSerleuLeuLys 140  
DB 925 ACCGACATGATGCTGCTCCCTGGGGCTGTGACGTGCAAGGACAGCTTGAGCAAGCCCTGTGAAA 984  
OY 141 HisleuGluGluValProGlnleuValLysleuGlyLeuLysAsnTyrArgLeuThrAsp 160

DB 985 CATTTGGAGAGAGTCCCAACACTCGTCAAGCTTGAGTGAAGAAACGAGACTCACAGAT 1044  
OY 161 ThrGluIleArgIleleuGlyAlaPhePheGlyLysAsnProleuLysAsnPheGlnGln 180  
DB 1045 ACAGAGATTGAAATTTAGTGCATTTTGGAAAAAGAACCCCTGAAAAAATCCAGCAG 1104  
OY 181 LeuAsnleuAlaGlyAsnArgValSerSerAspGlyTyrPleuAlaPheMetGlyAlaPhe 200  
DB 1105 TTGAATTTGGCGGGAATTCGTGAGCAGTGTGATGCTGCTTCAATGGGTGATATT 1164  
OY 201 GluAsnleuLys 204  
DB 1165 GAGAAATCTTAAG 1176  
RESULT 3  
AAH99581  
ID AAH99581 standard; cDNA: 2950 BP.  
XX  
AC AAH99581;  
XX  
DE 16-OCT-2001 (first entry)  
XX  
XX Human protein encoding cDNA sequence SEQ ID NO:416.  
KW Human: cancer; HIV infection; human immunodeficiency virus;  
KW antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;  
KW antibacterial; endocrine; cardiac; central nervous system; virucide;  
KW anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;  
KW antiagregant; haemostatic; vulnerary; antulcer; osteopathic; eczema;  
KW dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;  
KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;  
KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;  
KW antiaphylactic; rheumatoid arthritis; septic shock; pancreatitis;  
KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;  
KW genetic disease; haematopoietic disorder; platelet disorder; asthma;  
KW thrombocytopenia; osteoporosis; severe combined immunodeficiency;  
KW allergic rhinitis; diabetes; multiple sclerosis; depression;  
KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;  
KW neurological disorder; ss.  
XX  
OS Homo sapiens.  
XX  
PN MO200153455-A2.  
XX  
PD 26-JUL-2001.  
XX  
XX 22-DEC-2000; 2000WO-US35017.  
PF  
XX 23-DEC-1999; 99US-0471275.  
PR 21-JAN-2000; 2000US-0488725.  
PR 25-APR-2000; 2000US-0552317.  
XX  
XX (HXSE-) HXSEQ INC.  
PA  
PI Tang YT, Liu C, Drmanac RT;  
XX  
XX WPI: 2001-457603/49.  
DR P-PSDB: AAM25640.  
XX  
XX Isolated human polynucleotides encoding polypeptides, useful for the  
PT treatment and diagnosis of e.g. cancer, ulcers and HIV infection -  
PT  
XX  
PS Claim 1; Page 511-512; 1217pp; English.  
XX  
XX AAH99166 to AAH99904 encode the human proteins given in AAM25225 to  
CC AAM25963. The proteins can have activities based on the tissues and  
CC cells they are expressed in, such as: antiinflammatory; antirheumatic;  
CC antiarthritic; immunosuppressive; antibacterial; endocrine; cardiac;  
CC central nervous system; virucide; anti-HIV; fungicide; antimutagen;  
CC cardiovascular; antianaemic; antiagregant; haemostatic; vulnerary;  
CC antilicer; osteopathic; dermatological; antiallergic; antiasthmatic;  
CC antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;

CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides  
 CC encoding them can be used in gene therapy, antisense therapy and vaccine  
 CC production. The proteins and polynucleotides are useful for screening for  
 CC agonists or antagonists of a protein and for the treatment and diagnosis  
 CC of disorders associated with the activity of a protein e.g. inflammation,  
 CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,  
 CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal  
 CC infections, autoimmunity, genetic diseases, haematopoietic disorders,  
 CC anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,  
 CC osteoporosis, severe combined immunodeficiency, eczema, allergic  
 CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,  
 CC Alzheimer's disease, Parkinson's disease, neurodegenerative and  
 CC neurological disorders.

XX Sequence 2950 BP; 915 A; 592 C; 628 G; 815 T; 0 other;

#### Alignment Scores:

Pred. No.:	9.04e-106	Length:	2950
Score:	1046.00	Matches:	204
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	22	Gaps:	0

US-09-697-089-2\_COPY\_762\_965 (1-204) x AAH99581 (1-2950)

QY 1 LeutysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluuAspAlaIle 20  
 DB 1139 TTGAAGAAGCTTACAAACCTATATGATGATACATAAAGATGAAAGATGATCTATA 1198  
 QY 21 LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu 40  
 DB 1199 AAACGTAGCTGAAGGCTGAAACCTGAAAGAGATGTGTATTATTATTGATGACCCACTG 1258  
 QY 41 SerAspIleGlyGluGlyMetAspPylrIleValLysSerLysSerSerGluAsnProCysasp 60  
 DB 1259 TCTGCATTTGAGAGGAGGATGATTACATGACATCTGTCTGTCAGTGAACCCCTGTAAC 1318  
 QY 61 LeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAla 80  
 DB 1319 CTTGAGAGAAATTCATATTGTCCTCGCTGCTGTCTGCAATGCGATGAAATCCTACT 1378  
 QY 81 GlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu 100  
 DB 1379 CAGAACTCTTCAACATTTGTCGTAACCTGAGACATTTCTGATTATATCAGAAATTAACCTCGAA 1438  
 QY 101 LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeu 120  
 DB 1439 AAAGATGGAAATGAAAGCTTCTCATGAACTGATCGACAGATGAAAGCTGTAAGAACAGCTC 1498  
 QY 121 ThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerLeuSerSerLeuLeuLys 140  
 DB 1499 ACCGACACTGATCTCCCTCGGGGCTGTACGTGCAGAGCAGCCTGAGACCTGTTGAAA 1558  
 QY 141 HisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrArgLeuThrAsp 160  
 DB 1559 CATTGGAGGAGGCTCCACCACTGCTCAAGCTGGGTTGAAAACTGGAGACTCAGACT 1618  
 QY 161 ThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGln 180  
 DB 1619 ACAGAGATTAGAAATTTTGGGTCATTTTGGAAAAAGAACCTCTGAAAAAAGCTTCAGCAG 1678  
 QY 181 LeuAsnLeuAlaGlyLysAsnArgValSerSerAspGlyTyrPheAlaPheMetGlyValPhe 200  
 DB 1679 TTGAATTTGGGGGGAATCGTGTAGCAGTGTGATGCTTGGCTTCATGGGTATATT 1738  
 QY 201 GluAsnLeuLys 204  
 DB 1739 GAGAAATCTTAAG 1750

RESULT 4  
 AAS03945  
 ID AAS03945 standard; cDNA; 3133 BP.

XX AAS03945;  
 AC 12-SEP-2001 (first entry)  
 DE Human caspase recruitment domain 12 (CARD-12) cDNA.

XX Caspase recruitment domain: CARD-12; apoptosis; stress-related pathway;  
 XX cancer; viral infection; poxvirus; adenovirus; autoimmune disorder;  
 XX systemic lupus erythematosus; arthritis; neurological disorder; stroke;  
 XX Alzheimer's disease; amyotrophic lateral sclerosis; haematologic disease;  
 XX aplastic anaemia; myocardial infarction; inflammatory disorder;  
 XX Crohn's disease; insulin-dependent diabetes; contact dermatitis;  
 XX psoriasis; graft rejection; bacterial infection; lepromatous leprosy;  
 XX tuberculosis; ischemic brain injury; hypoxic brain injury; ss;  
 XX kidney ischaemia; reperfusion injury; acute bacterial meningitis;  
 XX excitotoxic brain damage; liver disease.

XX Homo sapiens.

XX Key Location/Qualifiers  
 XX CDS 36..3110  
 XX /tag= a  
 XX /product= "Human CARD-12"

XX W0200130971-A2.

XX 03-MAY-2001.

XX 26-OCT-2000; 2000WO-US29643.

XX 27-OCT-1999; 99US-0161822.

XX (MILL-) MILENTRIUM PHARM INC.

XX Bertin J, Robison KE;

XX WPI; 2001-308628/32.

XX P-PSDB; AAU02880.

XX Isolated caspase recruitment domain-12 polypeptide and nucleic acids  
 XX encoding them, useful for treating and diagnosing disorders associated  
 XX with abnormal apoptosis such as cancer, arthritis and Alzheimer's  
 XX disease -

XX Claim 2; Fig 1; 93pp; English.

XX The sequence represents a cDNA which encodes the human caspase  
 XX recruitment domain 12 (CARD-12) polypeptide. CARD domains are found in a  
 XX number of proteins that transmit signals that activate apoptosis and  
 XX inflammatory pathways in response to stress and other stimuli. Therefore,  
 XX CARD-12 and its corresponding nucleic acid may be used in treatment and  
 XX diagnosis of patients suffering from disorders associated with an  
 XX abnormal level (an increase or a decrease) of apoptotic cell death or  
 XX abnormal activity of stress-related pathways. The disorders include  
 XX cancer, viral infections (e.g. caused by poxviruses, adenoviruses),  
 XX autoimmune disorders (e.g. systemic lupus erythematosus, arthritis),  
 XX neurological disorders (e.g. Alzheimer's disease, amyotrophic lateral  
 XX sclerosis), haematologic diseases (e.g. aplastic anaemia, myocardial  
 XX infarction, stroke), inflammatory and immune system disorders (e.g.  
 XX Crohn's disease, insulin-dependent diabetes, contact dermatitis,  
 XX psoriasis, graft rejection), bacterial infections (e.g. tuberculosis,  
 XX lepromatous leprosy), ischemic and hypoxic brain injury, kidney  
 XX ischaemia/reperfusion injury, excitotoxic brain damage, acute bacterial  
 XX meningitis and liver disease.

XX Sequence 3133 BP; 903 A; 691 C; 729 G; 810 T; 0 other;

#### Alignment Scores:

Pred. No.:	9.81e-106	Length:	3133
Score:	1046.00	Matches:	204
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0

Query Match: 100.00% Indels: 0  
DB: 22 Gaps: 0  
US-09-697-089-2\_COPY\_762\_965 (1-204) x AAS03945 (1-3133)

QY 1 LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluLysAlaIle 20  
DB 2319 TTGAAGAACCCTTACAAACCTCATATAGATTAACATAAAGATGAAGATGATCTTATA 2378  
QY 21 LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu 40  
DB 2379 AAACCTAGCTGAAGGCCCTGAAAACCTGAAGAAGATGCTTTATTTCAATTGACCCACTTG 2438  
QY 41 SerAspIleGlyGluGlyMetAspTyrIleValLysSerLysSerLysSerGluProCysAsp 60  
DB 2439 TCTGACATTGGAGAGGGAATGATTAATCAAGTCTCTGTCAGTGAACCTCTGTAC 2498  
QY 61 LeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAla 80  
DB 2499 CTTGAAGAATTTCAATTAGTCTCCTGCTGCTGCTGCAAAATGACGTAATAATCTTACT 2558  
QY 81 GlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu 100  
DB 2559 CAGATCTTCAACAATTTGGTCAAACTGAGCATCTTGATTTATCAGAAATTTACTCTGGA 2618  
QY 101 LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeu 120  
DB 2619 AAAGTGGAAATGANGCTCTTCATGACTGATCGACAGGATGAGCTGCTAGAACAGCTC 2678  
QY 121 ThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerLeuSerSerLeuLeuLys 140  
DB 2679 ACCGACATGATGCTGCCCTCGGGGCTGTGACGTCGCAAGCAGCCTGAGCCTGTTGAA 2738  
QY 141 HisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrArgLeuThrAsp 160  
DB 2739 CATTTGGGAGGCTCCCAACCTGCTCAAGCTTGGGTGAAAACCTGAGACTCACAAT 2798  
QY 161 ThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnIle 180  
DB 2799 ACAGAGATTAAATTTTGGTGGCATTTTGGAAAGAACCTCTGTAATAAACTCCAGCAG 2858  
QY 181 LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrPheAlaPheMetGlyAlaPhe 200  
DB 2859 TTGAATTTGGCGGGAATCGTGTGAGCAGTATGATGCTTGCTTCATGGGTATATT 2918  
QY 201 GluAsnLeuLys 204  
DB 2919 GAGAACTTTAAG 2930

RESULT 5  
AAH78219  
ID AAH78219 standard; DNA: 3213 BP.

AC AAH78219;

XX 26-NOV-2001 (first entry)

DE Nucleotide sequence of a human secreted polypeptide.

XX Human; secreted polypeptide; nervous disease; muscular disease; tumour;  
KW gastrointestinal ulceration; spinal cord disease; trachea disease;  
KW thyroid gland disease; ovary disease; prostate disease; heart disease;  
KW renal gland disease; small intestine disease; thymus disease;  
KW lymph node disease; muscular system disease; colon disease;  
KW lipase deficiency; cystic fibrosis; pancreatitis; clot formation;  
KW myocardial infarction; angiodysplasia; liver disease; coagulation disorder;  
KW microbial disease; immune disorder; inflammation; transplant rejection;  
KW bone thickness; bone density; ferroxidase loss; apoptosis;  
KW vascular smooth cell proliferation; vaccine; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..3213  
FT /tag= a  
FT /product= "secreted polypeptide"

PN WO200166690-A2.

PD 13-SEP-2001.

XX 05-MAR-2001; 2001WO-US07143.

XX 06-MAR-2000; 2000US-0187107.

PR 13-MAR-2000; 2000US-0188916.

PR 03-OCT-2000; 2000US-0236874.

PR 03-OCT-2000; 2000US-0237846.

PA (SMIK ) SMITHKLINE BEECHAM CORP.

PI (SMIK ) SMITHKLINE BEECHAM PLC.

PI Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;

DR WPI: 2001-570768/64.

DR P-PSDB; AAG67527.

XX Novel isolated secreted polypeptide useful for treating nervous and

PT muscular diseases, gastrointestinal ulceration, coagulation and immune

PT disorders, microbial diseases, inflammation and transplant rejection -

PS Claim 2; Page 53-54; 102pp; English.

XX The present sequence encodes a human secreted polypeptide. The  
CC secreted polypeptides and polynucleotides are useful for treating  
CC nervous and muscular diseases, for inhibiting tumour formation and  
CC metastasis, for treating gastrointestinal ulceration, for preventing  
CC and treating diseases in spinal cord, thyroid gland, ovary, prostate,  
CC renal gland, small intestine, heart, trachea, thymus, lymph node,  
CC muscular system and colon, for treating lipase deficiency in cystic  
CC fibrosis and pancreatitis, for treating undesirable clot formation  
CC such as myocardial infarction, during angioplasty and all surgical  
CC procedures that require decreased blood clot formation, for treating  
CC liver diseases, coagulation disorders and microbial diseases, for  
CC treating immune disorders, for treating inflammation and transplant  
CC rejection, for enhancing bone thickness and increasing bone density,  
CC for reducing the loss of essential ferroxidases, for suppressing  
CC apoptosis, and for regulating vascular smooth cell proliferation. They  
CC may also be used as vaccines.

XX Sequence 3213 BP, 916 A; 704 C; 756 G; 837 T; 0 other:

Alignment Scores:

Pred. No.: 1.01e-105 Length: 3213  
Score: 1046.00 Matches: 204  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 22

US-09-697-089-2\_COPY\_762\_965 (1-204) x AAH78219 (1-3213)

QY 1 LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluLysAlaIle 20

DB 2422 TTGAAGAACCCTTACAAACCTCATATAGATTAACATAAAGATGAAGAAGATGCTTATA 2481

QY 21 LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu 40

DB 2482 AAACCTAGCTGAAGGCCCTTAAAAACCTGAAGAAGATGCTTTATTTTCAATTGACCCACTTG 2541

QY 41 SerAspIleGlyGluGlyMetAspTyrIleValLysSerLysSerSerGluProCysAsp 60

DB 2542 TCTGACATTGGAGAGGGAATGATTAATCAAGTCTCTGTCAGTGAAGAACCTCTGTAC 2601

QY 61 LeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAla 80

DB 2602 CTTGAAGAATTTCAATTAGTCTCCTGCTGCTTGTCTGCAAAATGACGTAATAATCTTACT 2661

QY 81 GlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu 100  
Db 2662 CAGATCTTCACAAATTTGGTCAAACTGACATCTTGTATATGAGAAATTAACCTGAAA 2721  
QY 101 LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeu 120  
Db 2722 AAAAGATGGAATGAAAGCTCTTCATGAACTGATCGACAGAGAAAGAGCTGTGAAACAGCTC 2781  
QY 121 ThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerIleSerLeuLeuLys 140  
Db 2782 ACCGCACTGATGCTGCTCCCTGGGCTGTGACGTGCAAGGACAGCTGAGAGCTGTGAAA 2841  
QY 141 HisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrArgLeuThrAsp 160  
Db 2842 CATTGGAGGAGGTGCCCAACACTGCTCAAGCTTGGCTTGAAAACTGGAGACTCACAAT 2901  
QY 161 ThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGln 180  
Db 2902 ACAGAGATTAGAAATTTTGTGTCATTTTGTGAAAGAACCTCTGAAAACTTCACAGCAG 2961  
QY 181 LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrPheAlaPheMetGlyValPhe 200  
Db 2962 TTGAATTTGGCGGGAATCGTGTGAGCAGTATGATGATGCTTGCCTTCATGGGTATATT 3021  
QY 201 GluAsnLeuLys 204  
Db 3022 GAGAAATCTTAAG 3033

## RESULT 6

ABK22731  
ID ABK22731 standard; CDNA: 3396 BP.

AC ABK22731:

XX 26-MAR-2002 (first entry)

DE Human CDNA encoding CLAN A.

XX Caspase recruitment domain; CARD; ss: NB-ARC; ANGIO-R; LRR; SAM;  
KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;  
KW autoimmune disease; inflammation; keratinocyte hyperplasia;  
KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;  
KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;  
KW leukemia; allergy; arthritis; lupus; Schlegel's syndrome;  
KW Crohn's disease; graft-versus-host disease; stroke;  
KW myocardial infarction; heart failure; neurodegenerative disease;  
KW Parkinson's disease; Alzheimer's disease; HIV;  
KW human immunodeficiency virus infection.

XX Homo sapiens.

PN W0200190156-A2.

PD 29-NOV-2001.

PF 24-MAY-2001: 2001WO-US17158.

PR 24-MAY-2000: 2000US-0579240.

PR 10-OCT-2000: 2000US-0686347.

PR 14-MAR-2001: 2001US-275980P.

PR 23-MAY-2001: 2001US-0864921.

PA (BURN-) BURNHAM INST.

PI Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;

PI Oliveira VM, Hayashi H, Pawlowski K;

DR WPI: 2002-083086/11.

DR P-PSDB: AAU080861.

XX New caspase recruitment domain (CARD)-containing polypeptides and

PT encoding nucleic acids, useful for treating abnormal cell proliferation

PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,  
PT arthritis or stroke  
PS Claim 1; Page 166-171; 216pp; English.

XX The invention relates to an isolated caspase recruitment domain (CARD)  
CC containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain  
CC from it, and the polynucleotides encoding them. Also included are a  
CC recombinant vector comprising the polynucleotide, recombinant cells  
CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian  
CC and insect cells) and an anti-CARD antibody. The CARD-containing  
CC polypeptide and CARD-encoding nucleic acid are useful for treating a  
CC pathology characterised by abnormal cell proliferation (e.g. cancer),  
CC abnormal cell death (apoptosis), autoimmune diseases or inflammation.  
CC In particular, the polypeptide and nucleic acid are useful for treating  
CC keratinocyte hyperplasia, inflammatory hyperplasia, fibrosis, smooth  
CC muscle cell proliferation in arteries following balloon angioplasty  
CC (restenosis), gliomas, carcinomas, sarcomas, melanomas, leukemias,  
CC allergies, arthritis, lupus, Schlegel's syndrome, Crohn's disease,  
CC graft-versus-host disease, stroke, myocardial infarction, heart failure,  
CC neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's  
CC disease) or immunodeficiency associated disease (e.g. human  
CC immunodeficiency virus (HIV) infection). The nucleic acids are useful  
CC in a variety of diagnostic applications. The present sequence is a  
CC CDNA encoding a CARD domain containing protein.

XX Sequence 3396 BP; 992 A; 737 C; 793 G; 874 T; 0 other;

## Alignment Scores:

Pred. No.: 1,09e-105 Length: 3396  
Score: 1046.00 Matches: 204  
Percent Similarity: 100.00% Conservative: 0  
Best local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Dbs: 24 Gaps: 0

US-09-697-089-2\_COPY\_762\_965 (1-204) x ABK22731 (1-3396)

QY 1 LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluAspAlaIle 20  
Db 2560 TTGAAGAACCTTCAAAAGCTATATGATGATACATTAAGATGAAAGAGATGCTATA 2619  
QY 21 LysLeuAlaGluGlyLeuLysAsnLeuLysMetCysLeuPheHisLeuThrHisLeu 40  
Db 2620 AAACAGCTGAGGCGCTGAAAGAACCTGAGAGAAAGTGTATTATTCATTGACCACTG 2679  
QY 41 SerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAsp 60  
Db 2680 TCTGACATTTGAGAGGGAATGATTTACATGCTCAAGTCTGTCAAGTGAACCTGTGAC 2739  
QY 61 LeuGluGluIleGlnLeuValSerCysCysLeuSerIleAsnAlaValLysIleLeuAla 80  
Db 2740 CTTGAGAGAAATTCATTAATGATCTCTGCTGCTTGTCTGCAAAATGCAAGAAATCTTAC 2799  
QY 81 GlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu 100  
Db 2800 CAGAACTTTCACAAATTTGGTCAAACTGAGCATCTTGTATATGAGAAATTAACCTGAAA 2859  
QY 101 LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeu 120  
Db 2860 AAAAGATGGAATGAAAGCTCTTCATGAACTGATCGACAGAGAAAGAGCTGTGAAACAGCTC 2919  
QY 121 ThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerIleSerLeuLeuLys 140  
Db 2920 ACCGCACTGATGCTGCTCCCTGGGCTGTGACGTGCAAGGACAGCTGAGAGCTGTGAAA 2979  
QY 141 HisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrArgLeuThrAsp 160  
Db 2980 CATTGGAGGAGGTGCCCAACACTGCTCAAGCTTGGCTTGAAAACTGGAGACTCACAAT 3039  
QY 161 ThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGln 180  
Db 3040 ACAGAGATTAGAAATTTTGTGTCATTTTGTGAAAGAACCTCTGAAAACTTCACAGCAG 3099

OY 181 LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetClyValAlphe 200  
Db 3100 TTGAATTGGGGGAAATCGTGTGACAGTGTGATGGCTTGCCTTCATGGGTATATT 3159  
OY 201 GluAsnLeuLys 204  
Db 3160 GAGAACTTTAAG 3171  
RESULT 7  
AAH98254  
ID AAH98254 standard; cDNA: 3545 BP.  
XX  
AC AAH98254;  
XX  
DT 12-OCT-2001 (first entry)  
XX  
DE Murine EST-derived coding sequence SEQ ID NO: 111.  
XX  
XX Human: sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;  
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;  
KW diagnostics; forensic test; gene mapping; genetic disorder;  
KW biodiversity; gene therapy; nutrition; ss.  
XX  
OS Mus musculus.  
XX  
PN WO200154477-A2.  
XX  
PD 02-AUG-2001.  
XX  
PF 25-JAN-2001; 2001WO-US02687.  
XX  
PR 25-JAN-2000; 2000US-0491404.  
PR 17-JUL-2000; 2000US-0617746.  
PR 03-AUG-2000; 2000US-0631451.  
PR 15-SEP-2000; 2000US-0663870.  
XX  
XX  
PA (HYSE-) HYSEQ INC.  
PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;  
PI Cao Y, Dzmanac RA, Zhang J, Werthman T;  
XX  
DR WPI: 2001-476164/51.  
DR P-PSDB: AAM23595.  
XX  
PT antilobes and research use -  
XX  
PS Claim 1; Page 250-251; 1275pp; English.  
XX  
CC The present invention provides the protein and coding sequences of novel  
CC proteins from a variety of organisms, including human, dog, cat, horse,  
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea  
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)  
CC from the organism of interest. They can be used in diagnostics,  
CC forensics, gene mapping, identification of mutations, to assess  
CC biodiversity and for nutritional purposes. The present sequence is a cDNA  
CC of the invention.  
XX  
SQ Sequence 3545 BP; 1038 A; 755 C; 816 G; 936 T; 0 other;  
Alignment Scores:  
Pred. No.: 1.16e-105 Length: 3545  
Score: 1046.00 Matches: 204  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 22 Gaps: 0  
US-09-697-089-2\_COPY\_762\_965 (1-204) x AAH98254 (1-3545)  
OY 1 LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAlaIle 20  
|||||

Db 2515 TTGAAGAACTTACCAAGCTCATATGATATACATTAAGATGATGAAAGATGCTATA 2574  
OY 21 LysLeuAlaGluGlyLeuLysAsnLeuLysMetCysLeuPheHisLeuThrHisLeu 40  
Db 2575 AAACATGCTGAAGGCGCTGAAAAACCTGAAGAAGATGTGTTTATTCATTGACCCACATGG 2634  
OY 41 SerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAsp 60  
Db 2635 TCTGACATTGGAGAGGAAATGATTCATAGTCMAAGTCTCTGTCAAGTGAACCTGTGAC 2694  
OY 61 LeuGluGluIleGlnLeuValSerCysLeuSerAlaAsnAlaValLysIleLeuAla 80  
Db 2695 CTTGAAGAAATTCATATGATCTCTGCTGCTGTCTGCAAAATGACGATAATCCTACCT 2754  
OY 81 GluAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu 100  
Db 2755 CAGAACTTCACAAATTTGGTCAAACTGAGCAATTCCTGATTATTCAGAAAATTAATCCTGGAA 2814  
OY 101 LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeu 120  
Db 2815 AAAGATGGAATGAAGAGCTTCTATGACTGACAGATGAAAGCTGTAGAACAGCTC 2874  
OY 121 ThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLys 140  
Db 2875 ACCGCACTGATGCTGCTGCGGGCTGTGACGTGCAAGGACGCTGAGCAGCTGTGAAA 2934  
OY 141 HisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThrAsp 160  
Db 2935 CATTTGGAGGAGGCTCCACAACTGCTCAAGCTTGGGTTGAAAACCTGAGACTCAAGAT 2994  
OY 161 ThrGluIleArgIleLeuGlyValaPhePheGlyLysAsnProLeuLysAsnPheGlnGln 180  
Db 2995 ACAGAGATTAGATTTAGAGTCTCATTTTGGAAAAGAACCTCTAATAAACTCCAGCAG 3054  
OY 181 LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetClyValAlphe 200  
Db 3055 TTGAATTTGGCGGAAATCGTGTGAGCAGTGTGATGATGGCTTGCCTTCATGGGTATATT 3114  
OY 201 GluAsnLeuLys 204  
Db 3115 GAGAACTTTAAG 3126  
RESULT 8  
AAS03946  
ID AAS03946 standard; DNA: 3615 BP.  
AC AAS03946;  
XX  
DT 12-SEP-2001 (first entry)  
XX  
DE Human caspase recruitment domain 12 (CARD-12) genomic DNA.  
XX  
CC Caspase recruitment domain: CARD-12; apoptosis; stress-related pathway;  
CC cancer; viral infection; poxvirus; adenovirus; autoimmune disorder;  
CC systemic lupus erythematosus; arthritis; neurological disorder; stroke;  
CC Alzheimer's disease; amyotrophic lateral sclerosis; haematologic disease;  
CC aplastic anaemia; myocardial infarction; inflammatory disorder;  
CC Crohn's disease; insulin-dependent diabetes; contact dermatitis;  
CC psoriasis; graft rejection; bacterial infection; lepromatous leprosy;  
KW tuberculosis; ischaemic brain injury; hypoxic brain injury; ds;  
KW kidney ischaemia; reperfusion injury; acute bacterial meningitis;  
KW excitotoxic brain damage; liver disease.  
XX  
XX Homo sapiens.  
OS  
XX  
FH Key Location/Qualifiers  
FT CDS 1..3615  
FT /tag= a  
FT /product= "Human CARD-12"  
PN WO200130971-A2.  
XX  
XX 03-MAY-2001.  
PD



XX 26-OCN-2000; 2000WO-US29643.  
 XX  
 XX 27-OCT-1999; 99US-0161822.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Bertin J, Robison KE;  
 XX  
 DR WPI: 2001-308628/32.  
 DR P-PSDB: AAU02881.  
 XX  
 PT Isolated caspase recruitment domain-12 polypeptide and nucleic acids  
 PT encoding them, useful for treating and diagnosing disorders associated  
 PT with abnormal apoptosis such as cancer, arthritis and Alzheimer's  
 PT disease -  
 XX  
 PS Disclosure; Fig 2; 93pp; English.  
 XX  
 CC The sequence represents a genomic DNA which encodes the human caspase  
 CC recruitment domain 12 (CARD-12) polypeptide. CARD domains are found in a  
 CC number of proteins that transmit signals that activate apoptosis and  
 CC inflammatory pathways in response to stress and other stimuli. Therefore,  
 CC CARD-12 and its corresponding nucleic acid may be used in treatment and  
 CC diagnosis of patients suffering from disorders associated with an  
 CC abnormal level (an increase or a decrease) of apoptotic cell death or  
 CC cancer, viral infections (e.g. caused by poxviruses, adenoviruses),  
 CC autoimmune disorders (e.g. systemic lupus erythematosus, arthritis),  
 CC neurological disorders (e.g. Alzheimer's disease, amyotrophic lateral  
 CC sclerosis), hematologic diseases (e.g. aplastic anaemia, myocardial  
 CC infarction, stroke), inflammatory and immune system disorders (e.g.  
 CC Crohn's disease, insulin-dependent diabetes, contact dermatitis,  
 CC psoriasis, graft rejection), bacterial infections (e.g. tuberculosis,  
 CC lepromatous leprosy), ischemic and hypoxic brain injury, kidney  
 CC ischemia/reperfusion injury, excitotoxic brain damage, acute bacterial  
 CC meningitis and liver disease.  
 CC  
 XX  
 XX Sequence 3615 BP; 1041 A; 811 C; 845 G; 918 T; 0 other;  
 XX  
 Alignment Scores:  
 Pred. No.: 1,19e-105 Length: 3615  
 Score: 1046.00 Matches: 204  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: Gaps: 0  
 US-09-697-089-2\_COPY\_762\_965 (1-204) x AAS03946 (1-3615)  
 QY 1 LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluAspAlaIle 20  
 DB 2755 TTGAAGAAGACCTTACAAACCTCATATGATTAACATAAGAGATGAGAAAGATCTCTATA 2814  
 QY 21 LysLeuAlaGluGlyLeuLysAsnLeuLysMetCysLeuPheHisLeuThrHisLeu 40  
 DB 2815 AAAGTAGCTGAAGCGCTGAAAAACCTGAAGAGATGTTTATTCATTGACCCACTTG 2874  
 QY 41 SerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAsp 60  
 DB 2875 TCTGACATGAGAGAGGAGATGATTACATCAAGTCTCTGTCAGAGAACCCCTGTAC 2934  
 QY 61 LeuGluGluIleGluLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAla 80  
 DB 2935 CTTGAAGAAGAAATTCATTAGTCTCTGCTGCTTGTCTGCAAAATGACGATGAATCTTACT 2994  
 QY 81 GluAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAspTyrIleGlu 100  
 DB 2995 CAGAAATCTTCACAAATTTGGTCAAACTGAGCATTTCTTGATTATATCGAAGAAATTAACCTG 3054  
 QY 101 LysAspGlyAsnGluAlaLeuHisGluLeuLeuAspArgMetAsnValLeuGluGluLeu 120  
 DB 3055 AAAAGTAGAAATGAAGAGCTTTCATGATGACTGATCGACAGAGATGAACGTCCTTAGAACGCTC 3114

QY 121 ThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerLeuSerSerLeuLys 140  
 DB 3115 ACCGACATGATGCTGCCCTGGGGCTGTGACGTGCAAGGACACCTGAGAGAGCTTTGAAA 3174  
 QY 141 HisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrPArgLeuThrAsp 160  
 DB 3175 CATTTGGAGGAGGTCGCCCAACTGCTCAAGCTTGAGTGAAGAACTGAGACCTCACAGAT 3234  
 QY 161 ThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln 180  
 DB 3235 ACAGAGATTAGAAATTTAGTGCAATTTTGGAAAAGAACCTCTGAAAACCTCCAGCAG 3294  
 QY 181 LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrLeuAlaPheMetGlyValPhe 200  
 DB 3295 TTGAATTTGGCGGGGAAATCGTGTGACAGCATGATGATGATGCTTGCTTCATGATGTTAT 3354  
 QY 201 GluAsnLeuLys 204  
 DB 3355 GAGAAATCTTAAG 3366  
 RESULT 9  
 AAH34171/C  
 ID AAH34171 standard; cDNA; 2735 BP.  
 XX  
 AC AAH34171;  
 XX  
 DT 03-SEP-2001 (first entry)  
 XX  
 DE Human colon cancer antigen encoding cDNA SEQ ID NO:1253.  
 XX  
 KW Human; colon cancer; colon cancer antigen; diagnosis; detection;  
 KW colorectal carcinoma; ss.  
 KW  
 OS Homo sapiens.  
 XX  
 PN WO200122920-A2.  
 PD  
 PP 05-APR-2001.  
 PF 28-SEP-2000; 2000WO-US26524.  
 XX  
 PR 29-SEP-1999; 99US-0157137.  
 PR 03-NOV-1999; 99US-0163280.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Ruden SM, Barash SC, Birse CE, Rosen CA;  
 XX  
 DR WPI: 2001-235357/24.  
 DR P-PSDB: AAG74766.  
 PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,  
 PT useful for preventing, diagnosing and/or treating colorectal cancers -  
 XX  
 PS Claim 1; Page 3017; 9803pp; English.  
 CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon  
 CC cancer-associated nucleic acid molecules (N) and proteins (P), where  
 CC the proteins are collectively known as colon cancer antigens. The colon  
 CC cancer antigens have cytostatic activity and can be used in gene  
 CC therapy and vaccine production. N and P may be used in the prevention,  
 CC diagnosis and treatment of diseases associated with inappropriate P  
 CC expression. For example, N and P may be used to treat disorders  
 CC associated with decreased expression by rectifying mutations or deletions  
 CC in a patient's genome that affect the activity of P by expressing  
 CC inactive proteins or to supplement the patients own production of P.  
 CC Additionally, N may be used to produce the colon cancer-associated Ps,  
 CC by inserting the nucleic acids into a host cell and culturing the cell  
 CC to express the proteins. N and P can be used in the prevention, diagnosis  
 CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204  
 CC and AAB77789 represent sequences used in the exemplification of the  
 CC present invention.



PR 30-JUN-2000; 2000US-0608408.  
PR 03-AUG-2000; 2000US-0632366.  
PR 21-SEP-2000; 2000US-0234687.  
PR 27-SEP-2000; 2000US-0234687.  
PR 04-OCT-2000; 2000US-0236359.  
PR 04-OCT-2000; 2000GB-0024263.  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
XX WPI; 2001-483447/52.  
XX  
XX  
XX Human genome-derived single exon nucleic acid probes useful for  
XX analyzing gene expression in human fetal liver -  
XX  
XX  
XX Claim 1; SEQ ID NO 4424; 639pp + sequence listing; English.  
XX  
XX The invention relates to a single exon nucleic acid probe for  
XX measuring human gene expression in a sample derived from human foetal  
XX liver. The single exon nucleic acid probes may be used for predicting,  
XX measuring and displaying gene expression in samples derived from human  
XX fetal liver. The present sequence is a single exon nucleic acid  
XX probe of the invention.  
XX Note: The sequence data for this patent did not form part of the  
XX printed specification, but was obtained in electronic format directly  
XX from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX Sequence 421 BP; 126 A; 69 C; 77 G; 149 T; 0 other;

Alignment Scores:  
Pred. No.: 2,49e-13 Length: 421  
Score: 202.00 Matches: 38  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 19.31% Indels: 0  
DB: 22 Gaps: 0

US-09-697-089-2\_COPY\_762\_965 (1-204) x ABA56119 (1-421)

QY 167 GtAaLaphePheGtLyAsnProLeuLyAsnPhenGInLeuAsnLeuAaGlyAsn 186  
DB 181 GGTGATTTTTTGGAAAGAACCCCTGGAACCTTCACAGCTTGAATTTGGCGGAAT 240  
QY 187 ArgValSerSerAspGlyTTrpLeuAlaPheMetGlyValPheGluAsnLeuLys 204  
DB 241 CGTGGAGCAGATGATGATGCTTCCTTCATGGGTGATTTGAGAACTTAAAG 294

#### RESULT 12

ABA25770  
ID ABA25770 standard; DNA; 421 BP.  
XX  
XX ABA25770;  
XX  
XX 23-JAN-2002 (first entry)  
XX  
XX Probe #4236 for gene expression analysis in human heart cell sample.  
XX  
XX Human; gene expression; heart; microarray; vascular system; probe;  
XX cardiovascular disease; hypertension; cardiac arrhythmia;  
XX congenital heart disease; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200157274-A2.  
XX  
XX 09-AUG-2001.  
XX  
XX 30-JAN-2001; 2001WO-US00666.  
XX  
XX 04-FEB-2000; 2000US-0180312.  
XX 26-MAY-2000; 2000US-0207456.  
XX 30-JUN-2000; 2000US-0608408.  
XX 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.  
PR 27-SEP-2000; 2000US-0236359.  
PR 04-OCT-2000; 2000GB-0024263.  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
XX WPI; 2001-488899/53.  
XX  
XX  
XX Single exon nucleic acid probes for analyzing gene expression in human  
XX hearts -  
XX  
XX  
XX Claim 1; SEQ ID NO 4236; 530pp; English.  
XX  
XX The present invention relates to single exon nucleic acid probes for  
XX measuring human gene expression in a sample derived from human heart. The  
XX present sequence is one such probe. The probes may be used for  
XX predicting, measuring and displaying gene expression in samples derived  
XX from the human heart via microarrays. By measuring gene expression, the  
XX probes are useful for predicting, diagnosing, grading, staging,  
XX monitoring and prognosing diseases of the human heart and vascular system  
XX e.g. cardiovascular disease, hypertension, cardiac arrhythmias and  
XX congenital heart disease.  
XX Note: The sequence data for this patent did not form part of the printed  
XX specification, but was obtained in electronic format directly from WIPO  
XX at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX Sequence 421 BP; 126 A; 69 C; 77 G; 149 T; 0 other;

Alignment Scores:  
Pred. No.: 2,49e-13 Length: 421  
Score: 202.00 Matches: 38  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 19.31% Indels: 0  
DB: 22 Gaps: 0

US-09-697-089-2\_COPY\_762\_965 (1-204) x ABA25770 (1-421)

QY 167 GtAaLaphePheGtLyAsnProLeuLyAsnPhenGInLeuAsnLeuAaGlyAsn 186  
DB 181 GGTGATTTTTTGGAAAGAACCCCTGGAACCTTCACAGCTTGAATTTGGCGGAAT 240  
QY 187 ArgValSerSerAspGlyTTrpLeuAlaPheMetGlyValPheGluAsnLeuLys 204  
DB 241 CGTGGAGCAGATGATGATGCTTCCTTCATGGGTGATTTGAGAACTTAAAG 294

#### RESULT 13

AAK04305  
ID AAK04305 standard; DNA; 421 BP.  
XX  
XX AAK04305;  
XX  
XX 05-NOV-2001 (first entry)  
XX  
XX Human brain expressed single exon probe SEQ ID NO: 4296.  
XX  
XX Human; brain expressed exon; gene expression analysis; probe;  
XX microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;  
XX epilepsy; cancer; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200157275-A2.  
XX  
XX 09-AUG-2001.  
XX  
XX 30-JAN-2001; 2001WO-US00667.  
XX  
XX 04-FEB-2000; 2000US-0180312.  
XX 26-MAY-2000; 2000US-0207456.  
XX 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.  
PR 21-SEP-2000; 2000US-0234687.  
PR 27-SEP-2000; 2000US-0236359.  
PR 04-OCT-2000; 2000GB-0024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2001-483446/52.  
DR  
XX Single exon nucleic acid probes for analyzing gene expression in human  
PT brains -  
XX  
PS Example 4; SEQ ID NO: 4296; 650pp + Sequence Listing; English.  
XX  
CC The present invention provides a number of single exon nucleic acid  
CC probes which are derived from genomic sequences expressed in the human  
CC brain. They can be used to measure gene expression in brain cell samples,  
CC which may enable the diagnosis and improved treatment of nervous system  
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,  
CC epilepsy and cancers. The present sequence is one of the probes of the  
CC invention.  
XX  
SQ Sequence 421 BP; 126 A; 69 C; 77 G; 149 T; 0 other;  
XX  
Alignment Scores:  
Pred. No.: 2,49e-13 Length: 421  
Score: 202.00 Matches: 38  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 19.31% Indels: 0  
DB: 22 Gaps: 0  
US-09-697-089-2\_COPY\_762\_965 (1-204) x AAK04305 (1-421)  
OY 167 GYAlaPhePhGlyLysAsnProLeuYsAsnPhGInGlnLeuAsnLeuAAGlyAsn 186  
DB 161 GGTGCATTTTGGAAAGAACCCCTGTGAAAACTTCACAGCACTTGAATTTGGCGGGAAT 240  
OY 187 ArgValSerSerAspGlyTTrpLeuAlaPheMetGlyValPheGluAsnLeuYs 204  
DB 241 CGTGTGACAGACGATGATGGCTTCCTTCATGGGTATTTGAGAACTCTTAAG 294  
RESULT 14  
AAK29801  
ID AAK29801 standard; DNA; 421 BP.  
XX  
AC AAK29801;  
XX  
DT 06-NOV-2001 (first entry)  
XX  
DE Human bone marrow expressed single exon probe SEQ ID NO: 4358.  
XX  
KW Human; bone marrow expressed exon; gene expression analysis; probe;  
KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200157276-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US00668.  
XX  
PR 04-FEB-2000; 2000US-0180312.  
PR 26-MAY-2000; 2000US-0207456.  
PR 30-JUN-2000; 2000US-0608408.  
PR 03-AUG-2000; 2000US-0632366.  
PR 21-SEP-2000; 2000US-0234687.  
PR 27-SEP-2000; 2000US-0236359.  
PR 04-OCT-2000; 2000GB-0024263.  
XX

PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2001-488900/53.  
DR  
XX Human genome-derived single exon nucleic acid probes useful for  
PT analyzing gene expression in human bone marrow -  
XX  
PS Example 4; SEQ ID NO: 4358; 658pp + Sequence Listing; English.  
XX  
CC The present invention provides a number of single exon nucleic acid  
CC probes which are derived from genomic sequences expressed in the human  
CC bone marrow. They can be used to measure gene expression in bone marrow  
CC samples, which may enable the improved diagnosis and treatment of cancers  
CC such as lymphoma, leukaemia and myeloma. The present sequence is one of  
CC the probes of the invention.  
XX  
SQ Sequence 421 BP; 126 A; 69 C; 77 G; 149 T; 0 other;  
XX  
Alignment Scores:  
Pred. No.: 2,49e-13 Length: 421  
Score: 202.00 Matches: 38  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 19.31% Indels: 0  
DB: 22 Gaps: 0  
US-09-697-089-2\_COPY\_762\_965 (1-204) x AAK29801 (1-421)  
OY 167 GYAlaPhePhGlyLysAsnProLeuYsAsnPhGInGlnLeuAsnLeuAAGlyAsn 186  
DB 161 GGTGCATTTTGGAAAGAACCCCTGTGAAAACTTCACAGCACTTGAATTTGGCGGGAAT 240  
OY 187 ArgValSerSerAspGlyTTrpLeuAlaPheMetGlyValPheGluAsnLeuYs 204  
DB 241 CGTGTGACAGACGATGATGGCTTCCTTCATGGGTATTTGAGAACTCTTAAG 294  
RESULT 15  
AA114389  
ID AA114389 standard; DNA; 421 BP.  
XX  
AC AA114389;  
XX  
DT 12-OCT-2001 (first entry)  
XX  
DE Probe #4322 for gene expression analysis in human cervical cell sample.  
XX  
KW Probe; human; microarray; gene expression; cervical epithelial cell;  
KW cervical cancer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200157278-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US00670.  
XX  
PR 04-FEB-2000; 2000US-0180312.  
PR 26-MAY-2000; 2000US-0207456.  
PR 30-JUN-2000; 2000US-0608408.  
PR 03-AUG-2000; 2000US-0632366.  
PR 21-SEP-2000; 2000US-0234687.  
PR 27-SEP-2000; 2000US-0236359.  
PR 04-OCT-2000; 2000GB-0024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2001-488901/53.  
XX

PT Human genome-derived single exon nucleic acid probes useful for  
PR analyzing gene expression in human cervical epithelial cells -

PS Claim 25; SEQ ID No 4322; 487bp; English.

XX  
CC The present invention relates to human single exon nucleic acid probes  
CC (SNP). The present sequence is one such probe. The SNPs are derived  
CC from human HeLa cells. The SNPs can be used to produce a single exon  
CC microarray, which can be used for measuring human gene expression in a  
CC sample derived from human cervical epithelial cells. By measuring gene  
CC expression, the probes are therefore useful in grading and/or staging  
CC of diseases of the cervix, notably cervical cancer.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX  
SQ Sequence 421 BP; 126 A; 69 C; 77 G; 149 T; 0 other;

Alignment Scores:

Pred. No.:	2.49e-13	Length:	421
Score:	202.00	Matches:	38
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	19.31%	Indels:	0
DB:	22	Gaps:	0

US-09-697-089-2\_COPY\_762\_965 (1-204) x AA114389 (1-421)

QY	167	GIYAlAPhEPheGlyLYsAsnProLeuLYsAsnPhEgInGInLeuAsnLeuAlaGlyAsn	186
DB	181	GGTGCATTTTTGGAAAGAACCCCTCTGAAAAACTTCACAGCACTTGAATTTGGCGGGAAT	240
QY	187	ArgValSerSerAspGlyTTrPLeuAlaPhMetGlyValPheGluAsnLeuLYs	204
DB	241	CGTGTGACGACATGATGATGGCTTCCTCATGCGGTATTTGAGAAATCTTAAG	294

Search completed: January 31, 2003, 13:24:27  
Job time : 245.662 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 31, 2003, 11:50:07 ; Search time 1666.97 Seconds

Title: US-09-697-089-2\_COPY\_762\_965

Perfect score:

Sequence: 1 LKNLTKLIMDNIKNEEDAI.....GNRVSSDGLAFMGVFENLK 204

### Scoring table:

Xgapop	10.0	Xgapext	0.5
Ygapop	10.0	Ygapext	0.5
Fgapop	6.0	Fgapext	7.0
Delop	6.0	Delext	7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000000

Post-processing: Minimum Match 0%

**Command line parameters:**

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-o/cgpn_1/USPTO.spool/US069697089/runat_29012003_092154.19729/app_query.fasta.1.981
-DB=EST -QMM=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -IOOPCL=0 -LOOEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blotsun6r -TRANS=hman4.0.cdi -LIST=45
-DICALIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-USEFM=pic -NORR=ext -HEAPSIZE=500 -MILLEN=200000000
-USER=US0697089.gcn1.1.1.985 -tunat_29012003_092754.19729 -NCPU=6
-NO.XLXY -NO.MAP -LARGEOUTERY -NEG.SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120
-WARN.TIMEOUT=30 -THREADS=1 -XGAOP=10 -XGAPEXT=0.5 -FGAOP=6 -FGAPEXT=7
-YGAOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

```
Database :

ESR: *
1: em_estba: *
2: em_esthum: *
3: em_estin: *
4: em_estmu: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_htc: *
9: gb_est1: *
10: gb_est2: *
11: gb_htc: *
12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
15: em_estfun: *
16: em_estom: *
17: gb_gss: *
18: em_gss_hum: *
19: em_gss_inv: *
20: em_gss_pln: *
21: em_gss_vrt: *
22: em_gss_fun: *
23: em_gss_mam: *
24: em_gss_mus: *
25: em_gss_other: *
26: em_gss_pro: *
27: em_gss_rtd: *
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	506	48.4	480	10	AV719179	AV719179 AV719179
2	347	33.2	775	13	B1854236	B1854236 603381263
3	313	29.9	637	7	AL782121	AL782121 AL782121
C 4	298	28.5	553	17	A0320928	A0320928 RPlC11-.93
C 5	290	27.7	364	9	AI263394	AI263394 Gx57b01.x
C 6	279	26.7	719	14	BQ264082	BQ264082 UT-R-DN1-
7	235	24.4	630	17	AQ112439	AQ112439 CIT-HSP-2
C 8	184.5	17.6	476	12	BG210375	BG210375 RST29913
C 9	176.5	16.9	728	17	A2720059	A2720059 RPlC1 -24-8
C 10	173	16.5	637	9	AL639997	AL639997 AL639997
11	142.5	13.6	577	13	BJ037401	BJ037401 B1037401
12	140.5	13.4	714	9	AL657756	AL657756 AL657756
13	137.5	13.1	1913	11	AK016782	AK016782 Mus muscu
14	127	12.1	805	12	BG684008	BG684008 602635613
15	126	12.0	619	13	BJ361756	BJ361756 B1361756
16	124.5	11.9	630	12	BG081770	BG081770 H3068040-
17	121.5	11.6	806	9	AI455014	AI455014 AI455014
18	121	11.6	1019	13	BM470084	BM470084 AGENCCOURT
19	120	11.5	961	13	BM458722	BM458722 AGENCCOURT
20	119.5	11.4	745	14	BM779763	BM779763 EST9590339
21	119.5	11.4	862	14	BM779781	BM779781 EST9590357
22	119.5	11.4	1490	11	AY103901	AY103901 Zee mays
23	119	11.4	893	12	BG831716	BG831716 602766010
24	118.5	11.3	985	14	BQ645517	BQ645517 AGENCCOURT
25	118	11.3	625	12	BF309088	BF309088 601890996
26	118	11.3	737	13	BM020728	BM020728 603644242
27	118	11.3	849	9	AL555302	AL555302 AL555302
28	118	11.3	883	13	B1761214	B1761214 603043447
29	118	11.3	892	9	AL540576	AL540576 AL540576
30	118	11.3	906	14	BQ961941	BQ961941 AGENCCOURT
31	118	11.3	924	9	AL541714	AL541714 AL541714
32	118	11.3	926	9	AL557388	AL557388 AL557388
33	118	11.3	1020	13	BM552397	BM552397 AGENCCOURT
34	118	11.3	1085	13	BM545249	BM545249 AGENCCOURT
35	118	11.3	1085	14	BM919092	BM919092 AGENCCOURT
36	117.5	11.2	733	14	BQ042443	BQ042443 UT-M-BMO-
37	117.5	11.2	803	12	BF384755	BF384755 602046246
38	117.5	11.2	1034	14	BQ059434	BQ059434 AGENCCOURT
39	117	11.2	586	12	BF718051	BF718051 f455905.y
40	116.5	11.1	543	9	AA426831	AA426831 vF20e04.s
41	116.5	11.1	848	9	AU118229	AU118229 AU118229
42	116	11.1	599	9	AL651084	AL651084 AL651084
43	116	11.1	667	12	BF718068	BF718068 f455h11.y
44	116	11.1	758	12	BG750840	BG750840 602707366
45	116	11.1	865	13	B1668326	B1668326 603295589

## ALIGNMENTS

RESULT 1	LOCUS	AV719179/c	480 bp	mRNA	linear	EST 16-OCT-2000
DEFINITION	AV719179	GLC Homo sapiens cDNA clone G1CEQA015', mRNA sequence.				
ACCESSION	AV719179					
VERSION	AV719179.1	GI:10816331				
KEYWORDS	EST.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.					
AUTHORS	Qian,B., Wu,T., Huang,O., Huang,C., Kang,B., Gao,X., Xu,Z., Xiao,H., Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z., Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Yang					

TITLE  
JOURNAL  
COMMENT

,Y., Gu,Y., Chen,Z. and Han,Z.  
Homo sapiens cDNA GLC clones  
Unpublished (2000)  
Contact: Zeguang Han  
Chinese National Human Genome Center at Shanghai  
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai  
201203, P. R. China  
Tel: 86-21-50801919(ex.45)  
Fax: 86-21-50801922  
Email: hanzg@chgc.sh.cn  
This clone is available at CHGC in Shanghai.

## FEATURES

## SOURCE

Location/Qualifiers

1..480

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="GLCE0A10"

/clone\_1lb="GLC"

/tissue\_type="corresponding non cancerous liver tissue"

/dev\_stage="adult"

/lab\_host="SOLR"

/note="Vector: pBluescript sk(-); Site\_1: EcoRI; Site\_2:

XhoI"

BASE COUNT 138 a 120 c 85 g 137 t

## ORIGIN

## Alignment Scores:

Pred. No.: 2,47e-52 Length: 480  
Score: 506.00 Matches: 97  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 48.37% Indels: 0  
DB: 10 Gaps: 0

US-09-697-089-2\_COPY\_762\_965 (1-204) x AV719179 (1-480)

QY 108 HisGlueuileaspargmetsValleugluInleuthralaleuemetleuprotpr 127  
Db 480 CATAACTGATGACAGAGATGACGTCTGACACAGCTCAGCTATCTGCTCGG 421  
QY 128 GGCCTGACGTCGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 147  
Db 420 GGCCTGACGTCGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 361  
QY 148 LeuVallysleuglyleuValysAsnTrpArgleuthrAspThrIleargIleu 167  
Db 360 CTCCTCAAGCTTGGTGAAGAACTGAGAGACTACAGATACAGAGATTAAGT 301  
QY 168 AlaPhePheglylyAsnProleuylsAsnPhedngluInleuAsnleuAlaGlyAsnArg 187  
Db 300 GCATTTTGGAAAGAACCTCTGAAAACTCCAGAGATTGGAATTGGCGGAATCGT 241  
QY 188 ValserSerAspGlyTrpLeuAlaPheMetGlyValPheGluAsnleuLys 204  
Db 240 GTGAGCAGTGTGATGAGCTTGCCTTCATGGGTGATTGAGAACTTAAG 190

RESULT 2 775 bp mRNA linear EST 10-OCT-2001  
BI854236 603381263F1 NCI\_GCAP\_Mam4 Mus musculus cDNA clone IMAGE:5389239 5',

LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

BI854236  
BI854236  
BI854236.1 GI:15994983  
EST.  
house mouse.  
Mus musculus

REFERENCE  
AUTHORS  
JOURNAL  
TITLE  
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NIH-MGC <http://mgs.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)

Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furch  
Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
Plate: L1AM11991 row: m column: 16  
High quality sequence stop: 764.

## FEATURES

## SOURCE

Location/Qualifiers

1..775

/organism="Mus musculus"

/strain="NMRI"

/db\_xref="taxon:10090"

/clone="IMAGE:5389239"

/clone\_1lb="NCI\_GCAP\_Mam4"

/tissue\_type="tumor, gross tissue"

/dev\_stage="5 months"

/lab\_host="DH10B"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site\_1: SalI;  
Site\_2: NotI; Cloned unidirectionally. Primer: oligo dT.  
Library constructed by Life Technologies, Inc. Investigators  
providing samples: Lothar Hennighausen/Priscilla Furch,  
NIH Reference for transgenic model: Li et al., Cell Growth  
and Differentiation 7, 3-11 (1996)."

BASE COUNT 226 a 162 c 196 g 191 t

## ORIGIN

## Alignment Scores:

Pred. No.: 2,64e-32 Length: 775  
Score: 347.00 Matches: 71  
Percent Similarity: 74.29% Conservative: 7  
Best Local Similarity: 67.62% Mismatches: 27  
Query Match: 33.17% Indels: 0  
DB: 13 Gaps: 0

US-09-697-089-2\_COPY\_762\_965 (1-204) x BI854236 (1-775)

QY 100 GluylsAspGlyAsnGluAlaLeuHisGluLeuileaspargmetsValleugluIn 119  
Db 2 GAAAAGATGGGAATGAAGAGCTCTACAGAGCTGACAGCTGGGCTTCTGGAGAG 61  
QY 120 LeuThrAlaLeuMetLeuProTrpGlyCysAspValGnglySerSerSerleu 139  
Db 62 CTCCTCAAGTGTGAGCTTCTGGGCTGGGATGACACAGAGCTGCCAAGCTGTG 121  
QY 140 LysHisleugluGluValProGluLeuValysleuglyleuLysAsnTrpArgleuthr 159  
Db 122 AAGCAGTTGGAGGGAGACCCAGAGACTTCCCAACTTGGATTGAAAACTGAGACTCAGA 181  
QY 160 AspThrGluIleArgIleleuGlyAlaPhePheglylyAsnProleuylsAsnPhednglu 179  
Db 182 GACGAGAGATTAAGAGTTAGTGAATTTCTGAGATGAATCTCTGAGAGACTTGCAG 241  
QY 180 GluLeuAsnleuAlaGlyAsnArgValserSerAspGlyTrpLeuAlaPheMetGlyVal 199  
Db 242 CAGTTGATTTAGGGGGGACCTGTGAGCAGTACGAGATGCTTACTTCATGATGTG 301  
QY 200 PheGluAsnleuLys 204  
Db 302 TTTGAGATCTGAAG 316

RESULT 3 637 bp mRNA linear EST 25-JUN-2002  
AL782121 AL782121 XGC-neurula silurana tropicalis cDNA clone TNeu076a12 5',

LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AL782121  
AL782121  
AL782121.1 GI:21567825  
EST.  
western clawed frog.  
Silurana tropicalis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae; Silurana.  
1 (bases 1 to 637)  
REFERENCE  
AUTHORS Taylor,R., Ashurst,J.L., Croning,M.D.R., Zorn,A.M. and Rogers,J.  
TITLE Sanger Xenopus tropicalis EST project 2002  
JOURNAL Unpublished (2001)  
COMMENT Contact: Taylor R  
Sanger Centre  
Hinxton, Cambridgeshire, CB10 1SA, UK  
Email: trop@sanger.ac.uk  
Sanger Xenopus tropicalis EST project 2001  
TROPICALIS\_SEQUENCE\_ID: TNeu076a12.p1csp6  
Sequencing primer: P1CSP6  
This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.

FEATURES  
source  
1..637  
/organism="Silurana tropicalis"  
/db\_xref="taxon:8364"  
/clone="TNeu076a12"  
/dev\_stage="neuraula"  
/lab\_host="Escherichia coli DH10B"  
/note="vector: pCS107; Site\_1: EcoRI; Site\_2: NotI; cDNA was oligo dT primed from 5ug of poly A+ RNA from neuraula. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end."

BASE COUNT 211 a 103 c 138 g 185 t

ORIGIN

Alignment Scores:  
Pred. No.: 3.14e-28 Length: 637  
Score: 313.00 Matches: 66  
Percent Similarity: 61.90% Conservative: 38  
Best Local Similarity: 39.29% Mismatches: 64  
Query Match: 29.92% Indels: 0  
DB: 9 Gaps: 0

US-09-697-089-2\_copy\_762\_965 (1-204) x AL782121 (1-637)

QY 1 LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluLysAlaIle 20  
DB 133 CTAGTAGGGCTTGAAGAAATGGTTTCCATTAATTAATAGACAGAAATGCAAAA 192  
QY 21 LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu 40  
DB 193 ACTCTGGCTGAGAGCATTTTAAGTCTGAAGAGATTAAAGAGTTATCCATATCTCATATC 252  
QY 41 SerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerLeuProCysAsp 60  
DB 253 TCCAACTATTGGAGATGGAGATGATGCAAGATCAATTTCTTATGTTCCATGAG 312  
QY 61 LeuGluGluIleGluLeuValSerCysLeuSerAlaAsnAlaValLysIleLeuAla 80  
DB 313 CTTAAGAACTGAATTAATTAATGCTTTGAGTGTGAAGCTCTCATGAGTCTTGA 372  
QY 81 GluAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu 100  
DB 373 TTCCTCTTAAATAATGTTCTCTAGCATTTGAATAATGATGTTCTGCAAAATATTACTA 432  
QY 101 LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGluLeu 120  
DB 433 CAGAAGGGAGAAATCAAGATAGAAAGAGCTGCCAACTGATATCTTATGATGCAATA 492  
QY 121 ThrAlaLeuMetLeuProTyrPheLysAspValGlnGlySerLeuSerSerLeuLys 140  
DB 493 AAGACACTTATGCTGCTGAGAGACATATGTAAGTTTGGCTGAGAGCAATATTACT 552  
QY 141 HisLeuGluGluValProGluLeuValLysLeuGlyLeuLysAsnTyrArgLeuThrAsp 160  
DB 553 ACATTGAGGCGCATTCCTACCTGTTCAGAACTTGTCTTAAAGATGAACTTGACCAAT 612

QY 161 ThrGluIleArgIleLeuGlyAla 168  
DB 613 GATGACTGATGACATTACCTTGG 636

RESULT 4  
LOCUS AO320928/c  
DEFINITION RPC111-93C9.TV RPC111 Homo sapiens genomic clone RPC11-93C9, DNA  
sequence.  
ACCESSION AO320928  
VERSION AO320928.1 GI:4053662  
KEYWORDS GSS.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.  
TITLE Use of human BAC End Sequences for Sequence-Ready Map Building  
JOURNAL Unpublished (1998)  
COMMENT Other GSSs: RPC111-93C9.TV  
Contact: Shaying Zhao, William Nierman, Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: hbe@tigr.org

Clones are derived from the human BAC library RPC11-1. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.bufileo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.bufileo.edu/ordering>) or from Research Genetics ([info@resgen.com](http://info@resgen.com)). BAC end search page: [http://www.tigr.org/tldb/hunguen/bac\\_end\\_search/bac\\_end\\_search.html](http://www.tigr.org/tldb/hunguen/bac_end_search/bac_end_search.html)  
Seq primer: 17  
Class: BAC ends.

FEATURES  
source  
1..553  
Location/Qualifiers

/organism="Homo sapiens"  
/db\_xref="GDB:7535384"  
/db\_xref="taxon:9606"  
/clone="RPC11-93C9"  
/clone\_1db="RPC11-11"  
/sex="Male"  
/cell\_type="Lymphocytes"  
/note="vector: pBACe3.6; site\_1: EcoRI; site\_2: EcoRI; RPC11 Human Male BAC library"  
BASE COUNT 170 a 107 c 114 g 162 t

Alignment Scores:  
Pred. No.: 1.8e-26 Length: 553  
Score: 298.00 Matches: 60  
Percent Similarity: 83.78% Conservative: 2  
Best Local Similarity: 81.08% Mismatches: 6  
Query Match: 28.49% Indels: 6  
DB: 17 Gaps: 1

US-09-697-089-2\_copy\_762\_965 (1-204) x AO320928 (1-553)

QY 111 IleAspArgMetAsnValLeuGluGluIleThrAlaLeuMetLeuProTyrPheLysAsp 130  
DB 259 GTGCAAGAGATGAGCTGTAGAACAGCTCACCGCATGATGCTGCGGCGCTGTAC 200  
QY 131 ValGlnGlySerLeuSerSerLeuLysHisLeuGluGluValProGluLeuValLys 150  
DB 199 GTGCAAGGAGCTGAGCAGCTGTGGAACACTTTGGAGAGAGCTCCACAACTGTCAG 140  
QY 151 LeuGlyLeuLysAsnTyrArgLeuThrAspThrGluIleArgIleLeuGlyAlaPhePhe 170  
DB 139 CTTGGGTTGAATAAGCTGAGACTCACAGATACAGAGATTAGTATTTAGTGTAGTACACA 80



QY 171 GlytysAsnPro-----LeutysAsnPro 178  
Db 79 CATACAGAGCCAGATAGTGGATTGGCCCTTAAATAATTC 38

RESULT 5  
AI263294/c  
LOCUS AI263294 364 bp mRNA linear EST 03-FEB-1999  
DEFINITION q57b01.x1 NCI\_CGAP\_Pan1 Homo sapiens cDNA clone IMAGE:2005417 3',  
ACCESSION AI263294  
VERSION AI263294  
KEYWORDS AI263294.1 GI:3871497  
SOURCE EST.  
ORGANISM human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
AUTHORS 1 (bases 1 to 364)  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
Life Technologies catalog #: 11548-013  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/ILMIL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
Insert length: 2146 Std Error: 0.00  
Seq primer: -40UP from Glibco  
High quality sequence stop: 364.  
Location/Qualifiers  
1. 364  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2005417"  
/clone\_lib="NCI\_CGAP\_Pan1"  
/tissue\_type="adenocarcinoma"  
/lab\_host="DH10B"  
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site:1: Salt;  
Site:2: NotI: Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.72 kb. Life Technologies catalog #:  
11548-013"

BASE COUNT 117 a 84 c 55 g 108 t  
ORIGIN

Alignment Scores:  
Pred. NO.: 9.05e-26 Length: 364  
Score: 290.00 Matches: 55  
Percent Similarity: 100.00% Conservative: 0  
Best local Similarity: 100.00% Mismatches: 0  
Query Match: 27.72% Indels: 0  
DB: Gaps: 0

US-09-697-089-2\_COPY\_762\_965 (1-204) x AI263294 (1-364)

QY 150 LysleuGlyLeuLysAsnTrpArgLeuThrAspThrGluIleArgIleLeuGlyAlaPhe 169  
Db 364 AAGCTGGGTTGAAAAAAGTGGAGCTCAGACATACAGATTAGATTTTACGTGCATTT 305

QY 170 PheGlyLysAsnProLeuLysAsnPheGlnGlnLeuAsnLeuAlaGlyAsnArgValSer 189  
Db 304 TTTTGAAAGAACCTCTGTAACCTTCACAGAGTTGATTTGGCGGAATCGTGTGAGC 245

QY 190 SeraspGlyTrpLeuAlaPheMetGlyValPheGluAsnLeuLys 204  
Db 244 AGTATGATGATGGCTTGCTTCATGGGTGTATTGAGATCTTTAAG 200

RESULT 6  
BQ204082/c  
LOCUS BQ204082 719 bp mRNA linear EST 02-MAY-2002  
DEFINITION UI-R-DNI-cmv-e-08-0-UI.s1 UI-R-DNI Rattus norvegicus cDNA clone  
UI-R-DNI-cmv-e-08-0-UI 3', mRNA sequence.

ACCESSION BQ204082  
VERSION BQ204082.1 GI:20420547  
KEYWORDS EST.  
SOURCE Norway rat.  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
REFERENCE 1 (bases 1 to 719)  
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.  
TITLE Normalization and subtraction: two approaches to facilitate gene  
discovery  
JOURNAL Genome Res. 6 (9), 791-806 (1996)  
MEDLINE 9704447  
COMMENT Contact: Soares, MB  
Program for Rat Gene Discovery and Mapping  
University of Iowa  
451 Eckstein Medical Research Building Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: [msaoures@blue.weeg.uiowa.edu](mailto:msaoures@blue.weeg.uiowa.edu)  
The sequence contained an oligo-dT track that was present in the  
oligonucleotide that was used to prime the synthesis of first  
strand cDNA and therefore this may represent a bonafide poly A  
tail. The sequence tag present in the cDNA between the NotI site  
and the oligo-dT track served to verify it as a clone from the  
normalized distal colon library cDNA library preparation: M.B.  
Soares lab clone distribution: clones will be available through  
Research Genetics ([www.resgen.com](http://www.resgen.com)) The following repetitive  
elements were found in this cDNA sequence: 12-210, >L1PB3#LINE/L1  
Seq primer: M13 Forward  
POLYA=yes.  
Location/Qualifiers  
1. 719  
/organism="Rattus norvegicus"  
/strain="Sprague-Dawley"  
/db\_xref="taxon:10116"  
/clone="UI-R-DNI-cmv-e-08-0-UI"  
/clone\_lib="UI-R-DNI"  
/dev\_stage="adult"  
/lab\_host="DH10B (Life Technologies)"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker; Site:1: Not I; Site:2: Eco RI; The UI-R-DNI  
library is a normalized Rat Distal Colon library (nRCC)  
constructed in pT37 PAC vector according to the procedure  
described by Bonaldo, Lennon & Soares (Normalization and  
Subtraction: Two Approaches to Facilitate Gene Discovery,  
Genome Research 6: 791-806, 1996). The oligonucleotide  
used to prime first strand synthesis contained the  
sequence tag GAAGTGTCTC between the Not I cloning site and  
DT8 stretch. The Rat Distal Colon tissue was provided by  
Tom Freeman of the Sanger Center.  
TAG\_LIB=UI-R-DNI  
TAG\_TISSUE=distal colon  
TAG\_SEQ=GAAGTGTCTC"

BASE COUNT 184 a 185 c 146 g 203 t 1 others  
ORIGIN

Alignment Scores:  
Pred. NO.: 6.2e-24 Length: 719  
Score: 279.00 Matches: 57  
Percent Similarity: 75.29% Conservative: 7  
Best local Similarity: 67.06% Mismatches: 21  
Query Match: 26.67% Indels: 0  
DB: Gaps: 0

US-09-697-089-2\_COPY\_762\_965 (1-204) x BQ204082 (1-719)

QY 120 LeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerLeuLeu 139  
Db 718 CTAAGCGGCTGATGCTCTTGGTGTGGGATGCGTACATCACTGTCTGCTG 659

QY 140 LysHisLeuGluGluValProGlnLeuValLysleuGlyLeuLysAsnTrpArgLeuThr 159

```

Db 658 AACCACTGAGGAGGAGCCAGGCGTTGTCAAACTTGATGAGAAAAGCTGAGGCTCAGA 599
QY 160 AAspThrGluIleArgIleLeuGlyAlaIlePheGlyLysAsnProLeuLysAsnPheGln 179
Db 598 GACGAGAGATTAAGATTGCGGTGTAATTTTGAGATGAATCACTCTGAGAGAGACTTCAG 539
QY 180 GlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyIrrPheLeuAlaPheMetGlyVal 199
Db 538 CAGTTGGATTTCAGCAGACAGCGGTGTGACAGATGATGAGCTTCTTCATCATGATGTG 479
QY 200 PheGluAsnLeuLys 204
Db 478 TTGAGACATCTTAAG 464

RESULT 7
LOCUS A0112439 630 bp DNA linear GSS 29-AUG-1998
DEFINITION CIT-HSP-2372C1.TR CIT-HSP Homo sapiens genomic clone 2372C1, DNA
sequence.
ACCESSION A0112439
VERSION A0112439.1 GI:3484599
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1 (bases 1 to 630)
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and
Venter,J.C.
TITLE Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building
JOURNAL Map Building (1998)
COMMENT Unpublished (1998)
Other-GSSs: CIT-HSP-2372C1.TR
Contact: Mark Adams
Department of Eukaryotic Genomics
7912 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.
FEATURES
Location/Qualifiers
source 1..630
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CIT-HSP"
/sex="Male"
/cell_type="Sperm"
/note="Vector: pBelobAC11; site_1: HindIII; site_2:
HindIII"
BASE COUNT 188 a 126 c 124 g 192 t
ORIGIN

Alignment Scores:
Pred. No.: 4,71e-21 Length: 630
Score: 255.00 Matches: 48
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 24.38% Indels: 0
DB: 17 Gaps: 0

US-09-697-089-2_COPY_762_965 (1-204) x A0112439 (1-630)
QY 23 AlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeuSerAsp 42
Db 486 GCTGAAGGCGCTGAAGAAACGTAAGAGATGTGTTTATTTCATTGACCCACTTGTCTGAC 545
```

```

QY 43 IlleGlyGluGlyMetAspTyrIleValLysSerLeuSerLeuProCysAspLeuGlu 62
Db 546 ATTGGAAAGGGAATGATGTTACATAGTCATCACTCTGTCAAGTAGAACCTGTGACCTTGA 605
QY 63 GluIleGlnLeuValSerCysCys 70
Db 606 GAAATTCATTTAGTCTCTCTCTGC 629

RESULT 8
LOCUS BG210375 476 bp mRNA linear EST 21-APR-2001
DEFINITION RST29913 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG210375
VERSION BG210375.1 GI:13732062
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1 (bases 1 to 476)
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramchandran,R., Whittington,J.,
Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith
E., Veloso,N., Kika,A., Hess,J., Cochren,K., Lo,K., Offenbacher
J., Danzig,J. and Ducat,M.
TITLE Creation of genome-wide protein expression libraries using random
activation of gene expression
JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
21227151
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
High quality sequence stop: 360.
FEATURES
Location/Qualifiers
source 1..476
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="Hrt1080"
/note="See 'Creation of Genome-wide protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is Hrt1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in Hrt1080 under normal circumstances."
BASE COUNT 120 a 99 c 107 g 149 t
ORIGIN

Alignment Scores:
Pred. No.: 1.63e-12 Length: 476
Score: 184.50 Matches: 47
Percent Similarity: 55.91% Conservative: 5
Best Local Similarity: 50.54% Mismatches: 24
Query Match: 17.64% Indels: 17
DB: 12 Gaps: 3

US-09-697-089-2_COPY_762_965 (1-204) x BG210375 (1-476)
QY 121 ThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerLeuSerSerLeuLys 140
Db 10 ACTGCAGGTGCGTCTTGGCTCCTCAGCACCCTCCGCTTCGCGGATTCCTGTTCTCTC 69
QY 141 -----HisLeuGluGluValProGlnLeuValLysLeu 151
Db 70 ATTTGCTTCTCTGAGATCTGAGATGATTCCTCTCCCTCAGCTCCAG-----TAGCTG 123
QY 152 GlyLeuLysAsnTrrpArgLeuThrAspThrGluIleArgIleLeuGlyAlaPheGly 171
Db 124 GGATTACCGGTGCATGCGCGCACT-----ATAAGTGATTTCTTGG 165
```

QY	172	LYSAsp-PROLeuLYAspPhgeInclInLeuAsnLeuAlaGLYAsnArgValSerSerAsp	191
Db	166	AAGAAACCTCTGCAAAAACCTCCAGACAGTTGATTTGGCGGGAAATCGTGTGACAGTGTAT	225
QY	192	GLYTrpLeuAlaPheMetClyValPheGLuAsnLeuLYs	204
Db	226	GGATGGCTTGGCTTGGTGGTGTATTGAGATCTTAAAG	264
RESULT	9		
LOCUS	AZ720059/c		
DEFINITION	RPci-24-88D12.TVC	RPci-24 Mus musculus genomic clone	RPci-24-88D12.
ACCESSION	AZ720059		
VERSION	AZ720059.1	GI:12461375	
KEYWORDS	GSS.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	Zhao,S., Niemman,W., Melk,J., Shatman,S., Ahnert,B., Levins,M., Tesgaie,G., Geel,K.K., Krol,M., Shavitsbeyn,A., Gebregeorgis,E., Russell,D., de Jong,P. and Fraser,C.M.		
TITLE	Mouse BAC End Sequences from Library RPci-24		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Shaying Zhao Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: szhao@tigr.org Clones are derived from the mouse BAC library RPci-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources ( <a href="http://www.choi.org/bacpac/orderingframe.htm">http://www.choi.org/bacpac/orderingframe.htm</a> ). BAC end page: <a href="http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html">http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html</a> Plate: 88 row: D column: 12 Seq primer: T7 Class: BAC ends.		
FEATURES			
SOURCE	Location/Qualifiers		
	1..728		
	/organism="Mus musculus"		
	/strain="C57BL/6J"		
	/db_xref="taxon:10090"		
	/clone="RPci-24-88D12"		
	/clone_lib="RPci-24"		
	/sex="Male"		
	/cell_type="Spleen/Brain"		
	/note="Vector: pPARBAC1. Site.1: BamHI, Site.2: BamHI, RPci-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the pPARBAC1 cloning vector at the BamHI sites using MboI partially digested male C57BL/6J DNA."		
BASE COUNT	193 a 194 c 145 g 196 t		
ORIGIN			
Alignment Scores:			
Pred. NO.:	3,15e-11	Length:	728
Score:	176.50	Matches:	41
Percent Similarity:	55.32%	Conservative:	11
Best local Similarity:	43.62%	Mismatches:	35
Query Match:	16.87%	Indels:	7
DB:	17	Gaps:	2
US-09-697-089-2_COPY_762_965 (1-204) x AZ720059 (1-728)			
QY	111	ILeAspArgMetAsnValLeuGlnLeuInLeuTrpAlaLeuMetLeuProTrpGlyCysAsp	130
Db	561	GTCGCACAGCTTGGCGCTTCTGTGGAGAGCTCACTACATGTGATCTGCTGTGGGAT	522

Qy	131	ValgInglYserIeSerIeSerIeLeuYsHsIleuGlInglValProGInleuValYs	150
Db	521	GTGCACACCAAGCCTCCCAAGCTGTGTGAAGCAGTTGGAGAGGGACCCCAAGACTTGCCAAA	462
Qy	151	LeuGlYleuYsAsnTTPaRgLeuThrsApThrgInIleuGlYlaIaPhepe	170
Db	461	CTTGATGTTGAATAACTGGAGACTCAGACGCAAGAGATTAAAGTTTAGGTAGTACACC	402
Qy	171	GIlyYsAsnPro-----IeulYsAsnPhgIn---GInleuAsnleu	183
Db	401	CAAAAGGAGCCGAGGGAGACAGGACTGACTTTAAACAAGCCTTAGTTGGGCCCTTATATGC	342
Qy	184	AlaGlYAsnAargValSerSerAspIyTrIpleuAlaPmet	197
Db	341	AGTCCTCAGAGAGCCTGACGACGCGGTCCTGCTTCCTTTC	300
RESULT 10			
AL639997			
LOCUS	AL639997		
DEFINITION	AL639997 XGC-neurula Silurana tropicalis cDNA clone TNeu003d13 5',		
ACCESSION	AL639997		
VERSION	AL639997.1		
KEYWORDS	GI:16792128		
SOURCE	EST.		
ORGANISM	western clawed frog.		
	Silurana tropicalis		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;		
	Xenopodinae; Silurana.		
REFERENCE	1 (bases 1 to 637)		
AUTHORS	Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J.		
TITLE	Sanger Xenopus tropicalis EST project 2001 (10_2001)		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Huckle E		
	Sanger Centre		
	Hinxton, Cambridgeshire, CB10 1SA, UK		
	Email: tropesanger.ac.uk		
	Sanger Xenopus tropicalis EST project 2001		
	TROPICALIS_SEQUENCE_ID: TNeu003d13.sp6		
	Sequencing primer: SP6		
	This sequence is from a Xenopus Gene Collection (XGC) library		
	constructed by Aaron M. Zorn.		
FEATURES			
source	Location/Qualifiers		
	1..637		
	/organism="Silurana tropicalis"		
	/db_xref="taxon:8364"		
	/clone="TNeu003d13"		
	/clone_lib="XGC-neurula"		
	/dev_stage="neurula"		
	/lab_host="Escherichia coli DH10B"		
	/note="Vector: pCS107; Site.1: EcoRI; Site.2: NotI; cDNA		
	was oligo dT primed from 5ug of poly A+ RNA from neurula.		
	EcoRI-NotI cut cDNA was then ligated into pCS107 with		
	EcoRI at the 5' end and NotI at the 3' end."		
BASE COUNT	226 a 93 c 132 g 185 t		
ORIGIN	1 others		
Alignment Scores:			
Pred. NO.:	6,89e-11	Length:	637
Score:	173.00	Matches:	36
Percent Similarity:	68.67%	Conservative:	21
Best Local Similarity:	43.37%	Mismatches:	26
Query Match:	16.54%	Indels:	0
DB:	9	Gaps:	0
US-09-697-089-2_COPY_762_965 (1-204) x AL639997 (1-637)			
Qy	1	LeuYsAsnleuThrYleuYleuMetAspAsnIleYsMetAsnGlInglAspAlaIle	20
Db	387	CTAGTAGGGCTTGAATAAATGTGTTTCATTAACATTAAATAGACAAAGATGATCAAAA	446
Qy	21	LysleuAlaGlInglYleuYsAsnleuYsIleYsMetCysleuPheHisleuThrsIleu	40

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Db 447 ACTGTGCTGAAGCATTTTAAGTCTGAAGAAGTTAAAGGTTATTCATTCATATC 506
Qy 41 SeraspilleglygluGlymetaspryrrileVallySersleuSerserulProcyasp 60
Db 507 TCCACATGTTGGAGATGGAGATGATATGCAAGATCAATTTCTTATGTTGCCATGG 566
Qy 61 LeugluGluGluGluGluValserCysCysleuSeralAasAlaValylleuAla 80
Db 567 CTTAAGAAGCAATTAATTAATGACTGTGTGTTGAGCTGTGAAGCTCTCAGAGCTTGCA 626
Qy 81 Gluaenleu 83
Db 627 TTCGCCTTA 635

RESULT 11
Bj037401 577 bp mRNA linear EST 07-DEC-2001
LOCUS Bj037401 NIBB Mochii normalized Xenopus neurula library Xenopus
DEFINITION laevis cDNA clone XL040g14 5', mRNA sequence.
ACCESSION Bj037401
VERSION Bj037401.1 GI:17420442
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 577)
Kitayama,A., Teresaka,C., Mochii,M., Ueno,N., Shin-I,T. and Kohara
Y.
REFERENCE Unpublished genes in X. laevis embryo
AUTHORS Unpublished (2001)
TITLE Contact: Tadasu Shin-I
JOURNAL Center For Genetic Resource Information
COMMENT National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.
FEATURES
source
location/Qualifiers
1..577
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="XL040g14"
/clone_lib="NIBB Mochii normalized Xenopus neurula
library"
/tissue_type="whole embryo"
/dev_stage="stage 15"
/Note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs
were oligo-dT primed and directionally cloned. Staging
according to Nieuwkoop and Faber. Library is substracted
and was constructed by N. Garrett. and A.M. Zorn,
(Wellcome/CRC Institute)."
BASE COUNT 176 a 107 c 114 g 179 t 1 others
ORIGIN
Alignment Scores:
Pred. No.: 3.53e-07 Length: 577
Score: 142.50 Matches: 39
Percent Similarity: 47.86% Conservative: 17
Best Local Similarity: 33.33% Mismatches: 47
Query Match: 13.62% Indels: 14
DB: 13 Gaps: 3
US-09-697-089-2_COPY_762_965 (1-204) x Bj037401 (1-577)
Qy 90 SerIleuAspLeuSerGluSerGlyLeuGluLysAspGlyAsnGluAlaLeuHis-Gl 109
Db 81 TCTTCTTGAGATATGTCGAAAT-----GTGCATGGG 113
Qy 109 uDeuIleAspArgMetAsnVal-----LeuGluGluGluLeuThrAlaLeuMetLeuProTr 127
Db 114 TTTGATTCACAGCTACCAACCTGACATCTGTGATGCAATTAAGACACTTTTCTGCTGCG 173

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Qy 127 pGlyCysAspValGlnGlySerleuSerserleuLeuYshISleuGluGluValProcl 147
Db 174 AGCAACAGATGATGATTTTTCCTGGAGGGGTTATTACTTACATTAAGCGCATTCCTAA 233
Qy 147 nLeuVallySleuGlyLeuLysAsnrrpArgleuThrpprArgIleuGluIleArgIleuGl 167
Db 234 CTTGTCAAAACCTTGCTTTTAAACAATGAAACTGACACCATGATGACATGAATACGTTAGC 293
Qy 167 yAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGluLeuAsnLeuAlaGlyAsnAr 187
Db 294 TTCTCATCTT-----AGCAGCTTTTAAAAACCTTCATATTGAGATCTTGTGATTAATGG 347
Qy 187 yValSerSerAspGlyTrpLeuAlaPheMetGlyValPheGluAsnLeu 203
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RESULT 12
AL657756 714 bp mRNA linear EST 13-DEC-2001
LOCUS AL657756
DEFINITION AL657756 XGC-neurula Silurana tropicalis cDNA clone TNeu037j15 5',
mRNA sequence.
ACCESSION AL657756
VERSION AL657756.1 GI:17670663
KEYWORDS EST.
SOURCE western clawed frog.
ORGANISM Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
Xenopodinae; Silurana.
1 (bases 1 to 714)
Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J.
REFERENCE Sanger Xenopus tropicalis EST project 2001 (10-2001)
AUTHORS Unpublished (2001)
TITLE Contact: Huckle E
JOURNAL Sanger Centre
COMMENT Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TNeu037j15.sp6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
FEATURES
source
location/Qualifiers
1..714
/organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone="TNeu037j15"
/clone_lib="XGC-neurula"
/dev_stage="neurula"
/lab_host="Escherichia coli DH10B"
/Note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
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EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end."
BASE COUNT 220 a 156 c 128 g 209 t 1 others
ORIGIN
Alignment Scores:
Pred. No.: 8.78e-07 Length: 714
Score: 140.50 Matches: 30
Percent Similarity: 52.04% Conservative: 21
Best Local Similarity: 30.61% Mismatches: 46
Query Match: 13.43% Indels: 1
DB: 9 Gaps: 1
US-09-697-089-2_COPY_762_965 (1-204) x AL657756 (1-714)
Qy 106 AlaleuHisGluLeuIleAspArgMetAsnValLeuGluGluGluLeuThrAlaLeuMetLeu 125
Db 3 TCAGTAAGAAGACTGCGGCCAACTTGACTCATCTTGATGCAATTAAGACACTTATGCTG 62
Qy 126 ProTrpGlyCysAspValGlnGlySerleuSerserleuLeuYshISleuGluGluVal 145

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[illegible]

TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409 (6821), 685-690 (2001)
MEDLINE	21085660
PMID	11217851
REFERENCE	5 (bases 1 to 1913)
AUTHORS	Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A., Arikawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayashi,N., Hill,D., Hitomoto,K., Hiraoka,T., Hori,F., Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Katsukawa,T., Kato,H., Kawaji,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kunitzuka,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,T., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Schirml,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,K., Toya,T., Yamamura,T., Yamataka,I., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M., and Hayashizaki,Y.
TITLE	Direct Submission
JOURNAL	Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-1-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp), URL: <a href="http://genome.gsc.riken.go.jp/">http://genome.gsc.riken.go.jp/</a> , Tel:81-45-503-9222, Fax:81-45-503-9216
COMMENT	Please visit our web site ( <a href="http://genome.gsc.riken.go.jp/">http://genome.gsc.riken.go.jp/</a> ) for further details. cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGGAGACGATCCAGACCTCTTTTCTTTTCTTTTATN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot - 10.0 and subtraction to Rot - 100.0. Second strand cDNA was prepared with the primer adaptor of sequence [5' GAGAGGAGATTTCTCAGTTAAATTAATTATATCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. cDNA of size comprised between 0.5 and 3 Kb was selected before cloning. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B.
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	/strain="C57BL/6J"
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	/sex="male"
	/tissue_type="testis"
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	/dev_stage="adult"
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	735..1544
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Pred. No.: 1e-05 Length: 1913
Score: 137.50 Matches: 59
Percent Similarity: 36.68% Conservatave: 25
Best Local Similarity: 25.76% Mismatches: 84
Query Match: 13.15% Indels: 61
DB: 11 Gaps: 7
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DB 870 CAGAACTTGACACACTGCTGCTGCACAAACACAGCTTGAGGACCTGAGAGAGTGCACAG 929
OY 22 LeuAlaGluGlyLeuIleuAsn-----LeuIleuMetCysLeuPheHis--- 36
DB 930 CTGTCTCAGACTGCTGAGGAATGCAGAAATGCTGCTGCAGAGGCTGATGAAATCATCTGC 989
OY 37 -----Leu 37
DB 990 AACATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1049
OY 38 ThrHisLeuSer-----AspIleGlyGluGly---MetAspTyrIleValLys 52
DB 1050 ACCCACTGAGGCTGACATGACATGACATGACATGAGGATGATGATGATGATGATGATGATG 1109
OY 53 SerLeuSerGluPheCysAspLeuGluIleuIleuValSerCysLeuSer 72
DB 1110 GCTTTAAAGGAACCTACTGTTACTTAAGAACTGAAAGAACTGAGTGCACCACTTATG 1169
OY 73 AlaAsnAlaValLysIleuAlaGlnAsnLeuHisAsnLeuValLysLeuSerIleu 92
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OY 93 AspLeuSerGluAsnTyrLeuGluIleuAspGlyAsnGluAlaLeuHisGluIleuAsp 112
DB 1230 GATCTTGTGTAACACAGCCCTGAGTGCACAAAGGATGATGATGATGATGATGATGATG 1274
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DB 1275 -----TGCAGAGGAGCTG 1286
OY 133 GlySerLeuSerSerLeuLeuHisLeuGluIleuValProGlnLeuValLysLeuGly 152
DB 1287 AAGCAAACTAGAGCTGCTGCTGAG-----AGACTTGGG 1319
OY 153 LeuLysAsnTyrArgLeuThrAspThrGluIleuArgIleuGlyAlaPhePheGlyLys 172
DB 1320 TTGGGGGGCATGTGACTTCCATTTGCTGTGATGATGATGATGATGATGATGATGATGATG 1379
OY 173 AsnProLeuLysAsnPheGlnIleuAsnLeuAlaGlyAsnArgValSerSerAspGly 192
DB 1380 AACCT-----CAGCTGAAAGAGCTTAAGAGATGATGATGATGATGATGATGATGATG 1433
OY 193 TrpLeuAlaPheMetGlyValPheGlu 201
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LOCUS BG684008 805 bp mRNA linear EST 01-MAY-2001
DEFINITION 602635613P1 NIH_MGC_48 Homo sapiens CDNA clone IMAGE:4763594 5',
mRNA sequence.
ACCESSION BG684008
VERSION BG684008.1 GI:13915405
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 805)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: ILCM1619 row: 1 column: 03
High quality sequence stop: 802.
location/Qualifiers
1. 805
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/db_xref="taxon:9606"
/clone="IMAGE:4763594"
/clone_lib="NIH_MGC_48"
/tissue_type="Primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: B-cells; Vector: pORF7; Site: 1: XhoI;
Site: 2: EcoRI; CDNA made by oligo-dT priming.
directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACAG(C). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."
BASE COUNT 147 a 273 c 249 g 136 t
ORIGIN
Alignment Scores:
Pred. No.: 5e-05 Length: 805
Score: 127.00 Matches: 41
Percent Similarity: 47.10% Conservatave: 32
Best Local Similarity: 26.45% Mismatches: 76
Query Match: 12.14% Indels: 6
DB: 12 Gaps: 4
US-09-697-089-2_COPY_762_965 (1-204) x BG684008 (1-805)
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DB 353 AAGGAGCTGGGAGCTGCGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 412
OY 60 AspLeuGluGluIleGluLeuValSerCysCysLeuSerAlaAsnAlaValLysIleu 79
DB 413 AAGATCCAGAACTGAGCTCCAGAACTGCTGCTGACGCGGCGGCTGCGGCGGCTGCTG 472
OY 80 AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspSerGluAsnTyrIleu 99
DB 473 TCCACACACATAGGACCTGCGCCAGCTGCGAGAGCTGACCTGACGAGACACACTTGG 532
OY 100 GluLysAspGlyAsnGluAlaLeuHisGlu---LeuIleAspArgMetAsnValLeuGlu 118
DB 533 GGGATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 592
OY 119 GlnLeuThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerLeuSerLeu 138

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GenCore version 5.1.3  
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OM protein - nucleic search, using frame\_plus.p2n model

Run on: January 31, 2003, 11:43:51 ; Search time 46.1802 Seconds  
(without alignments)  
1354.737 Million cell updates/sec

Title: US-09-697-089-2\_COPY\_762\_965

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 441362 segs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Database :

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	120.5	11.5	8722	4	US-09-221-017B-263
2	118	11.3	1386	2	US-08-910-731-5
3	112.5	10.8	1374	2	US-08-910-731-3
4	112.5	10.8	1374	2	US-08-910-731-1
5	111.5	10.7	1371	2	US-08-910-731-7
6	111.5	10.7	1371	2	US-08-910-731-1
7	111.5	10.7	1371	2	US-08-910-731-7
8	103	9.8	638	4	US-09-221-017B-1118
9	99.5	9.5	3979	4	US-09-180-439-1
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11	99.5	9.5	4123	4	US-09-180-439-7
12	99	9.5	2241	5	PCT-US95-10509-1

13	97	9.3	2859	4	US-09-099-041A-9	Sequence 9, Appl
14	97	9.3	2859	4	US-09-245-281-9	Sequence 9, Appl
15	97	9.3	2859	4	US-09-207-359B-9	Sequence 9, Appl
16	97	9.3	3382	4	US-09-099-041A-7	Sequence 7, Appl
17	97	9.3	3382	4	US-09-245-281-7	Sequence 7, Appl
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22	91	8.7	4758	3	US-09-191-647-1	Sequence 1, Appl
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27	90	8.6	3080	4	US-09-207-359B-25	Sequence 25, Appl
28	89.5	8.6	2296	3	US-09-188-930-228	Sequence 228, Appl
29	88.5	8.5	4141	4	US-09-245-281-42	Sequence 42, Appl
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31	88	8.4	4843	3	US-08-986-485-1	Sequence 1, Appl
32	87.5	8.4	3573	4	US-09-353-585-4	Sequence 4, Appl
33	87.5	8.4	6471	4	US-09-353-585-1	Sequence 1, Appl
34	86	8.2	3628	3	US-08-480-640A-113	Sequence 113, Appl
35	86	8.2	3628	3	US-08-295-802-113	Sequence 113, Appl
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38	86	8.2	3942	3	US-08-480-640A-189	Sequence 189, Appl
39	86	8.2	3942	4	US-08-686-968C-189	Sequence 189, Appl
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41	86	8.2	3942	4	US-08-375-992A-189	Sequence 189, Appl
42	86	8.2	5785	3	US-08-480-640A-221	Sequence 221, Appl
43	86	8.2	5785	4	US-08-686-968C-221	Sequence 221, Appl
44	86	8.2	5785	4	US-08-488-237A-221	Sequence 221, Appl
45	85.5	8.2	2582	1	US-08-514-014-3	Sequence 3, Appl

#### ALIGNMENTS

RESULT 1  
US-09-221-017B-263  
; Sequence 263, Application US/09221017B  
; Patent No. 6444799  
; GENERAL INFORMATION:  
; APPLICANT: Ross, Bruce C.  
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF  
; NUMBER OF SEQUENCES: 1120  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FASTSEQ for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/221,017B  
; FILING DATE: 23-DEC-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PP1182  
; FILING DATE: 31-DEC-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PP1546  
; FILING DATE: 30-JAN-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PP2911  
; FILING DATE: 09-APR-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/AU98/01023  
; FILING DATE: 10-DEC-1998



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: ATTORNEY/AGENT INFORMATION:
: NAME: Montoy, Gladys H
: REGISTRATION NUMBER: 32,430
: REFERENCE/DOCKET NUMBER: 27340-20021.00
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650-813-5600
: TELEFAX: 650-494-0792
:
: INFORMATION FOR SEQ ID NO: 263:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8722 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: circular
: MOLECULE TYPE: DNA (genomic)
: HYPOTHEetical: NO
: ANTI-SENSE: UNKNOWN
: ORIGINAL SOURCE:
: ORGANISM: PORPHYROMOMAS GINGIVALIS
: FEATURE:
: NAME/KEY: misc-feature
: LOCATION: 1...8722
:
US-09-221-017B-263

Alignment Scores:
Pred. No.: 0.000101 Length: 8722
Score: 120.50 Matches: 55
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DB: Gaps: 8

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Qy 21 LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPhe----- 35
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Qy 36 -----HisLeuThrHisLeuSerAspIleGlyGlyMetAspTyr 49
Db 2413 AAGCTAGAGGCTGGAAAGCTCTCAGCTGTTAGCGAGCTT-----TAT 2457
Qy 50 IleValLysSerLeuSerSerGluProCysAspLeuGluIle---GlnLeuValSer 68
Db 2458 CTTTGGATTAACCAATCAGTAAGTCTGGAACGCTCAGCTCCTTACCAACG 2517
Qy 69 CysCysLeuSerAlaAsnAlaValLysIleLeuAlaGlnAsnLeuHisAsnLeuValLys 88
Db 2518 CTTGAATCTGCGGTAAACCAATCGTAAAGCTG--GAGGGCTTGGAAAGCTTCACGCTC 2574
Qy 89 LeuSerIleLeuAspLeuSerGlnAsnTyrLeuGluLys----- 101
Db 2575 TTAGCAAGCTTGAACATCTCGGTAAACCAATCGTAAAGAGGCTTGGAAAGCTCTC 2634
Qy 102 -----AspGlyAsnGlu 105
Db 2635 ACTTCGTTAAACAAGCTTCGCTTAAGAAGTAACCAATCAGTAACCTTGAAGGCTTGGAA 2694
Qy 106 AlaLeuHisGluLeu-----IleAspArgMetAsnVal 116
Db 2695 CGTTCACAGCTCTTATGCAACGCTTGAATCGGCTAACAACCAATCGGAAGGCT 2754
Qy 117 LeuGluGlnLeuThrAlaLeuMetLeuProTrrpGlyCysAspValGlnGlySerLeuSer 136
Db 2755 CTGGAACTCTTCACGCTCTGCAACG-----CTTGAACCTCGGTTAACCAATC 2805
Qy 137 SerLeuLeuLysHisLeuGlnGluValProGlnLeuValLysLeuGlyLeuLysAsnTrp 156
Db 2806 AGTAAGCTAGAGGCTCTGGAACGCTCTCTTCGTTTAAACAAGCTTCGCTTAAAGAAGTAAC 2865

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Qy 157 ArgLeuThrAspThrGluIleArgIleLeuGlyAlaIlePheGlyLysAsnProLeuLys 176
Db 2866 CAGATCAGTAACACTAGAG-----GGCGCTGAAGCTGTACAC 2901
Qy 177 AsnPheGlnGlnLeuAsnLeuAlaGlyAsnArgValSer 189
Db 2902 TCGTAACAAACTTCTCTCTCGATTAACCAATCAGT 2940

RESULT 2
US-08-910-731-5
: Sequence 5, Application US/08910731
: Patent No. 5932440
: GENERAL INFORMATION:
: APPLICANT: CHATTERJEE, DEB K.
: APPLICANT: SHANDILYA, HARINI
: TITLE OF INVENTION: Mammalian Ribonuclease Inhibitors and Use Thereof
: NUMBER OF SEQUENCES: 16
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
: STREET: 1100 NEW YORK AVE., N.W., SUITE 600
: CITY: WASHINGTON
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20005-3934
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentln Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/910,731
: FILING DATE: (Herewith)
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/795,395
: FILING DATE: 04-FEB-1997
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/794,546
: FILING DATE: 03-FEB-1997
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 60/024,057
: FILING DATE: 16-AUG-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: ESMOND, ROBERT W.
: REGISTRATION NUMBER: 32,893
: REFERENCE/DOCKET NUMBER: 0942.3440003
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-371-2540
: TELEFAX: 202-371-2540
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1386 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: both
: TOPOLOGY: both
: MOLECULE TYPE: cDNA
:
US-08-910-731-5

Alignment Scores:
Pred. No.: 1.13e-05 Length: 1386
Score: 118.00 Matches: 41
Percent Similarity: 45.96% Conservative: 33
Best Local Similarity: 25.47% Mismatches: 81
Query Match: 11.28% Indels: 6
DB: Gaps: 4

US-09-697-089-2_COPY_762_965 (1-204) x US-08-910-731-5 (1-1386)
Qy 41 SerAspIleGlyGlu---GlyMetAspTyrIleValLysSerLeuSerGluProCys 59
Db 196 AACGAGCTGGCGGATGTGCGGCTGATTCGCTCCAGGGCTTGCAGACCCCTCTCTGC 255

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QY 60 AspLeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu 79
      ::::::::::: ||| :::::::::::
Db 256 AAGATCCAGAGCTGAGCTCCAGAACTGTGCTGACGGGGCCGGCTCCGGGCTCTG 315
QY 80 AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeu 99
      ::::::::::: ||| :::::::::::
Db 316 TCCAGCAGCACTAGCAGCACTCCGACCCCTGCAGAGAGCTGACCTGACGAGCAACTCTTG 375
QY 100 GlnLysAspGlyAsnGlnLysAlaLeuHisGlu---LeuIleAspArgMetAsnValLeuGlu 118
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 376 GGGGATGCCGGCTGACGCTGCTGCGAAGAGCTCTGAGACCCCAAGTCCCGCTGGAA 435
QY 119 GlnLeuThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlnSerLeuSerLeu 138
      ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 436 AAG-----CTGCAGCTGGAGTATGTGAGCTCTCGGCTCCAGCTCCGAGCCCTG 466
QY 139 LeuLysHisLeuGlnGluValProGlnLeuValLysLeuGlnLysAsnTyrArgLeu 158
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 487 GCTCCGCTGCTCAGGCGCAAGCCGCAAGCTTCAGAGAGCTCAGCGTGAACAACAGCATC 546
QY 159 ThrAspThrGlnIleArgIleLeuGlnAlaPhePheGlyLysAsnProLeuLysAsnPhe 178
      ::::::::::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 547 AATGAGCTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 603
QY 179 GlnGlnLeuAsnLeuAlaGlnAsnArgValSerSerAspGlyTyrLeuAlaPheMetGly 198
      ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 604 GAGCGCTCAGCTGAGAGAGCTGCGGTGTGACATCAGACAACTGCCGGAGCTGTGCGGC 663
QY 199 Val 199
      ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 664 ATT 666

RESULT 3
US-08-910-731-3
; Sequence 3, Application US/08910731
; Patent No. 5932440
; GENERAL INFORMATION:
; APPLICANT: CHATTERJEE, DEB K.
; APPLICANT: SHANDILYA, HARINI
; TITLE OF INVENTION: Mammalian Ribonuclease Inhibitors and Use thereof
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., N.W., SUITE 600
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,731
; FILING DATE: (Herewith)
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/795,395
; FILING DATE: 04-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/794,546
; FILING DATE: 03-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/024,057
; FILING DATE: 16-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: ESMOND, ROBERT W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0942.3440003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540

```

```

; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1374 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1368
; US-08-910-731-3

Alignment Scores:
Pred. No.: 5,88e-05 Length: 1374
Score: 112.50 Matches: 61
Percent Similarity: 38.708 Conservative: 28
Best Local Similarity: 26.524 Mismatches: 84
Query Match: 10.764 Indels: 57
DB: Gaps: 9

US-09-697-089-2_COPY_762_965 (1-204) x US-08-910-731-3 (1-1374)
QY 4 LeuThrLysLeuIleMetAspAsnIleLysMetAsnGlnGlnAspAlaIleLysLeuAla 23
      ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 244 ATCCAGAGAGCTGAGCTTCAGAACTGACGCTTGACGAGAGCTGCTGCTGCTGCTGCT 303
QY 24 GlnGlyLysLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis-----LeuSer 41
      ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 304 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 363
QY 42 AspIleGlyGlnGlnMetAspTyrIleValLysSerLeuSerSerGluProCysAspLeu 61
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 364 GAT-----GAGCGCTGAGAGCTGCTGCTGAGAGAGCTCCGAGACCCCACTGCTGCT 417
QY 62 GlnGlnIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAlaGln 81
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 418 GAGAGACTTCAGTGTGAGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTG 477
QY 82 AsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerLysAsnTyrLeuGlnLys 101
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 478 GTGCTCAGGCTGAACCTGACTTTAAAGAGCTGTATGAGCAAAATGACTTCCATGAG 537
QY 102 AspGlyAsnGlnLysAlaLeuHisGlu---LeuIleAspArgMetAsnValLeuGlnLeu 120
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 538 GCTGTATATCCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 597
QY 121 -----ThrAlaLeuMetLeuProTyrGlyCysAspValGlnGly 133
      ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 598 AAGCTGAGAACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 657
QY 134 SerLeuSerSerLeuLeuLysHisLeuGlnGlnValProGlnLeuValLysLeuGly--- 152
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 658 TCCAAAGCCCTGACTG-----CAAGAACTGCACTTGGGCAAGC 693
QY 152 ----- 152
Db 694 AACAGCTGGGCAACAGCAAGCATTCAGACACTGCTCAGAGACTGCTTCCCACTGC 753
QY 153 ---LeuLysAsnTyrArgLeuThrAspThrGlnIle----- 163
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 754 AGGCTGAGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 813
QY 164 ---ArgIleLeuGlnAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGlnLeuAsn 182
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 814 TGCCTGTCTCTCAGAGCC-----AAGCAGAGCTGTAAG-----GAATCAGC 855
QY 183 LeuAlaGlyAsnArgValSerSerAspGly 192
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 856 CTAGCTGCAATGAGCTGAAGATGAGGT 865

RESULT 4
US-08-795-395-3
; Sequence 3, Application US/08795395

```

```

; Patent No. 5965399
; GENERAL INFORMATION:
; APPLICANT: CHATTERJEE, DEB K.
; APPLICANT: SHANDILYA, HARINI
; TITLE OF INVENTION: Cloning and Expression of Rat Liver and
; TITLE OF INVENTION: Porcine Liver Ribonuclease Inhibitor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 NEW YORK AVE., N.W., SUITE 600
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,395
; FILING DATE: 04-FEB-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/024,057
; FILING DATE: 16-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: ESMOND, ROBERT W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0942.3440002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1374 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1368
; US-08-795-395-3

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Alignment Scores:
Pred. No.: 5.89e-05 Length: 1374
Score: 112.50 Matches: 61
Percent Similarity: 38.70% Conservative: 28
Best Local Similarity: 26.52% Mismatches: 84
Query Match: 10.76% Indels: 57
DB: 2 Gaps: 9

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US-09-697-089-2\_COPY\_762\_965 (1-204) x US-08-795-395-3 (1-1374)

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QY 4 LeuThLysLeuLLeuMetAspAsnLLeuLysMetAsnGluGluAspAlaLeuLysLeuAla 23
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 244 ATCCAGAACGCTGAGCTTCAGAACTGACCTGACGAGAGCTGGCTGGGAGCTGCGCT 303
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 24 GluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis-----LeuSer 41
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 304 GATGGCTGCGCTCTTGTCTACCTGCGCTGAGACTGACATCTCAATGACAACTCTGGGG 363
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 42 AspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerSerGluProCysAspLeu 61
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 364 GAT-----GAAGGCTGAGAGCTGCTCTGTGAAGAGCTCGGAGACCCCGAGTGCCTT 417
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 62 GluGluIleGluLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAlaGln 81
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 418 GAGAGCTTCAGTGTGGAATAGCTGTAACTGACACAGCTACCAAGCTGGAGCCCTGGGCTCA 477
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 82 AsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGluLys 101
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

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DB 478 GTGCTCAGGCTGAACCTGACTTTAAAGACTAGATTGACGACAAATGACTTCATGAG 537
QY 102 AspGlyAsnGluAlaLeuHisGlu---LeuIleAspArgMetAsnValLeuGluGlnLeu 120
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 538 GCTGTATCATCACACTGTGTGCGAGGCTGAAGAGATTGCTGTCAACTGGAGTCACTC 597
QY 121 -----ThrAlaLeuMetLeuProTyrGlyCysAspValGlnGly 133
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 598 AAACGTGAGAACTGTGTATCATATCAGCAGCACTGCAAGAGATCTGTGTGTGTGGCC 657
QY 134 SerLeuSerSerLeuLeuLysHisLeuGluValProGlnLeuValLysLeuGly--- 152
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 658 TCCAAGCCTCACTG-----CAAGAACTGACTGTGGGAGAC 693
QY 152 ----- 152
DB 694 AACAACTGGGCAACACAGGCACTTGCAAGCACTGTGCTCAGACTGCTGCTCCAGCTGC 753
QY 153 ---LeuLysAsnTyrPArgLeuThrAspThrGluLe----- 163
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 754 AGCTGAGAGCACTGTGCTGTGCGACTGTGATGTCACTGCAAGAGCTGCAAGAGACTG 813
QY 164 ---ArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGlnLeuAsn 182
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 814 TCCCGTCTCCTCAGAGCC-----AAGCAGAGCTGTAAG-----GAAGTCAAGC 855
QY 183 LeuAlaGlyAsnArgValSerSerAspGly 192
DB 856 CTAGCTGGCAATGAGCTGAAGATGAGGT 885

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RESULT 5

US-08-910-731-1

; Sequence 1, Application US/08910731

; Patent No. 5932440

; GENERAL INFORMATION:

; APPLICANT: CHATTERJEE, DEB K.

; APPLICANT: SHANDILYA, HARINI

; TITLE OF INVENTION: Mammalian Ribonuclease Inhibitors and Use Thereof

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.

; STREET: 1100 NEW YORK AVE., N.W., SUITE 600

; CITY: WASHINGTON

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005-3934

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/910,731

; FILING DATE: (Herewith)

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/795,395

; FILING DATE: 04-FEB-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/794,546

; FILING DATE: 03-FEB-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/024,057

; FILING DATE: 16-AUG-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: ESMOND, ROBERT W.

; REGISTRATION NUMBER: 32,893

; REFERENCE/DOCKET NUMBER: 0942.3440003

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-371-2600

; TELEFAX: 202-371-2540

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

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; LENGTH: 1371 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1368
US-08-910-731-1

Alignment Scores:
Pred. No.: 7.92e-05 Length: 1371
Score: 111.50 Matches: 48
Percent Similarity: 40.93% Conservative: 40
Best Local Similarity: 22.33% Mismatches: 90
Query Match: 10.66% Indels: 37
DB: Gaps: 7

US-09-697-089-2_COPY_762_965 (1-204) x US-08-910-731-1 (1-1371)
QY 9 MetAspAsnIleLeuMetAsnGluGuaSprAlaIleLeuAlaGluGluLeuLys---- 27
DB 88 CTCGAGGACTGGCGGCTCAGGAGGAGCAGCTGCAGAGACATCGCTTCCCTCCGGGCC 147
QY 28 -----AsnLeuLysLysMetCysLeuPheHisLeuThrHisLeuSerAspIleGlyIu 45
DB 148 AACCCCTCCCTGACCGAGCTGCTGC-----CGCACCAACAGAGCTGGCGCAT 195
QY 46 ---GlyMetAspTyrIleValLysSerLeuSerSerGluProCysAspIleGluIle 64
DB 196 GCGGGGTGCACCTGCTGCTGCAGAGGCTGCAGAGCCACCTGCAAGATCCAGAGCTC 255
QY 65 GlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAlaGlnAsnLeuHis 84
DB 256 ACCCTGCAGAACTGCTCCCTGACCGAGCGGCTCGGGGCTCGGCCACGACGCTGCC 315
QY 85 AsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGluLysAspGlyAsn 104
DB 316 TCCCTGCCACAGCTGGGAGCTGCATCTCAGCGACACCAACCTGGGGAGACCGCGCTG 375
QY 105 GluAlaLeuHisGlu---LeuIleAspArgMetAsnValLeuGluGlnLeuThr----- 121
DB 376 CGGCTGCTCTGTGAGGGGCTCTGCAGCCCGACGTCGACAGAGAGCTGCAGTTGGAG 435
QY 122 ---AlaLeuMetLeuProTyrPheLysAspValGlnGlySerLeuSerSerLeuLys 140
DB 436 TACTGCCGCTGACGCGCCGACGCTGCGAGCCCTGCGCTGCTGCTCAGGGCCACGCG 495
QY 141 HisLeuGluGluValPro----- 146
DB 496 GCCTTGAAGAGCTCAGCGTGACAAACGACATCGCGGAGCGCGGCCCGGGTGTCTG 555
QY 147 -----GlnLeuValLysLeuGlyLeuLysAsnTyrParg 157
DB 556 GGCAGGAGCTGCGAGAGCTGCTGCTGCAGAGCTGCAGAGCTGCAGAGCTGCAGAGCTG 615
QY 158 LeuThrAspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsn 177
DB 616 CTCAGCGCCAGCCAACTGCAGAAAGCTGTGCGGAATTTGGGCTCCAG-----GCC 669
QY 178 PheGlnGlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGly 192
DB 670 CTGAGGAGACTTGACCTGGGCGACAAAGGAGCTGGCGGAGCGCGGGC 714

RESULT 6
US-08-910-731-7
; Sequence 7, Application us/08910731
; Patent No. 5932440
; GENERAL INFORMATION:
; APPLICANT: CHATTERJEE, DEB K.
; APPLICANT: SHANDILYA, HARINI
; TITLE OF INVENTION: Mammalian Ribonuclease Inhibitors and Use Thereof
; NUMBER OF SEQUENCES: 16
```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., N.W., SUITE 600
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,731
; FILING DATE: (Herewith)
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/795,395
; FILING DATE: 04-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/794,546
; FILING DATE: 03-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/024,057
; FILING DATE: 16-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: ESMOND, ROBERT W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0942.3440003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1371 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
US-08-910-731-7

Alignment Scores:
Pred. No.: 7.92e-05 Length: 1371
Score: 111.50 Matches: 48
Percent Similarity: 40.93% Conservative: 40
Best Local Similarity: 22.33% Mismatches: 90
Query Match: 10.66% Indels: 37
DB: Gaps: 7

US-09-697-089-2_COPY_762_965 (1-204) x US-08-910-731-7 (1-1371)
QY 9 MetAspAsnIleLeuMetAsnGluGuaSprAlaIleLeuAlaGluGluLeuLys---- 27
DB 88 CTCGAGGACTGGCGGCTCAGGAGGAGCAGCTGCAGAGACATCGCTTCCCTCCGGGCC 147
QY 28 -----AsnLeuLysLysMetCysLeuPheHisLeuThrHisLeuSerAspIleGlyIu 45
DB 148 AACCCCTCCCTGACCGAGCTGCTGC-----CGCACCAACAGAGCTGGCGCAT 195
QY 46 ---GlyMetAspTyrIleValLysSerLeuSerSerGluProCysAspIleGluIle 64
DB 196 GCGGGGTGCACCTGCTGCTGCAGAGGCTGCAGAGCCACCTGCAAGATCCAGAGCTC 255
QY 65 GlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAlaGlnAsnLeuHis 84
DB 256 ACCCTGCAGAACTGCTCCCTGACCGAGCGGCTCGGGGCTCGGCCACGACGCTGCC 315
QY 85 AsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGluLysAspGlyAsn 104
DB 316 TCCCTGCCACAGCTGGGAGCTGCATCTCAGCGACACCAACCTGGGGAGACCGCGCTG 375
QY 105 GluAlaLeuHisGlu---LeuIleAspArgMetAsnValLeuGluGlnLeuThr----- 121
```

Db 376 CGGCTGCTGTGTGAGGGGCTCCTGGAGCCCGCAGTCCACCTGAGAGAGCTGATTGGAG 435  
 QY 122 ---AlaLeuMetLeuProTirpelyCysAspValGlnGlySerLeuSerSerLeuLeuYs 140  
 Db 436 TACTGCGCCGTGACGGCCGCCAGCTGCGAGCCCTGGCTGTGTCTCAGGGCCAGCGGG 495  
 QY 141 HisLeuGlnGluValPro-----GlnLeuValLysLeuGlyLeuLysAsnTirpArg 157  
 Db 496 GCCTTGAAGAGAGCTCAGCGGTGAGCAACAGCATCGGCGAGCGCGCGCGCGGTGCTG 555  
 QY 147 -----GlnLeuValLysLeuGlyLeuLysAsnTirpArg 157  
 Db 556 GCGCAGGCTGTGGCCGACTGCTGCTGCGCAGCGTGGAGCGCTGAGAGACTGCGGT 615  
 QY 158 LeuThrAspThrGlnIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsn 177  
 Db 616 CTCACGCCAGCACTGCAGAAAGACTGTGCGGAATTGGCTCCAC-----GCCCTG 669  
 QY 178 PheGlnGlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGly 192  
 Db 670 CTGGCGGAGCTGTGGCTTGGCGGAGCAACAGCTGGGTGATGTGGGC 714

## RESULT 7

US-08-795-395-1  
 ; Sequence 1, Application US/08795395  
 ; Patent No. 5965399  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CHATTERJEE, DEB K.  
 ; APPLICANT: SHANDILYA, HARINI  
 ; TITLE OF INVENTION: Cloning and Expression of Rat Liver and  
 ; TITLE OF INVENTION: Porcine Liver Ribonuclease Inhibitor  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
 ; STREET: 1100 NEW YORK AVE., N.W., SUITE 600  
 ; CITY: WASHINGTON  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20005-3934  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/795,395  
 ; FILING DATE: 04-FEB-1997  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 60/024,057  
 ; FILING DATE: 16-AUG-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: ESMOND, ROBERT W.  
 ; REGISTRATION NUMBER: 32,893  
 ; REFERENCE/DOCKET NUMBER: 0942,3440002  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 202-371-2600  
 ; TELEFAX: 202-371-2540  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1371 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: both  
 ; TOPOLOGY: both  
 ; MOLECULE TYPE: cDNA  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 1..1368  
 ; US-08-795-395-1

Alignment Scores: 7.92e-05 Length: 1371  
 Pred. No.: 111.50 Matches: 48  
 Score:

Percent Similarity: 40.93% Conservative: 40  
 Best Local Similarity: 22.33% Mismatches: 90  
 Query Match: 10.66% Indels: 37  
 Db: 2 Gaps: 7

US-09-697-089-2\_COPY\_762\_965 (1-204) x US-08-795-395-1 (1-1371)

QY 9 MetAspAsnIleLysMetAsnGlnGluAspAlaIleLysIleAlaGlnGlyLeuLys--- 27  
 Db 88 CTCGACGACTGCGGCCCTCAGGAGAGACCTGCAGACATGGTTGCTCCCTCCGGGCC 147  
 QY 28 -----AsnLeuLysLysMetCysLeuPheHisLeuThrHisLeuSerAspIleGly 45  
 Db 148 AACCCCTCCCTGACCGAGCTGTGCTC-----CGCACCAAGAGCTGGCGCAT 195  
 QY 46 ---GlyMetAspTyrIleValLysSerLeuSerSerGluProCysAspLeuGlnIle 64  
 Db 196 GCGGCGGTGACACCTGCTGCTGCGAGGCGCTGCAGAGCCCGCACCTGCAGATCCAGAAAGCTC 255  
 QY 65 GlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAlaGlnAsnLeuHis 84  
 Db 256 AGCTTCAGAACTGCTCCCTGACCGAGCGGCTGCGGGGTCTCTCCACAGACGCTGGCC 315  
 QY 85 AsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlnLysAspGly 104  
 Db 316 TCCTGCGCCACGCTCGGAGCGCTGCATCTCAGACCAACCCACTGGGAGCGCGGCTG 375  
 QY 105 GlnAlaLeuHisGlu---LeuIleAspArgMetAsnValLeuGlnGlnLeuThr----- 121  
 Db 376 CGGCTGCTGTGTGAGGGCTCCTGAGACCCCGCAGTCCACCTGGAAGCTGCAGTTGGAG 435  
 QY 122 ---AlaLeuMetLeuProTirpelyCysAspValGlnGlySerLeuSerSerLeuLeuYs 140  
 Db 436 TACTGCGCCGTGACGGCCGCCAGCTGCGAGCCCGCTGGCTGTCTCAGGGCCAGCGGG 495  
 QY 141 HisLeuGlnGluValPro-----GlnLeuValLysLeuGlyLeuLysAsnTirpArg 157  
 Db 496 GCCTTGAAGAGAGCTCAGCGGTGAGCAACAGCATCGGCGAGCGCGCGCGGTGCTG 555  
 QY 147 -----GlnLeuValLysLeuGlyLeuLysAsnTirpArg 157  
 Db 556 GCGCAGGCTGTGGCAGACTGCTGCTGCGCAGCGTGGAGCGCTGAGAGACTGCGGT 615  
 QY 158 LeuThrAspThrGlnIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsn 177  
 Db 616 CTCACGCCAGCACTGCAGAAAGACTGTGCGGAATTGGCTCCAC-----GCCCTG 669  
 QY 178 PheGlnGlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGly 192  
 Db 670 CTGAGGAGAGCTTGAAGCTGCGGAGCAACAGCGGTGGCGGAGCGCGGCG 714

RESULT 8  
 US-09-221-017B-1118/C  
 ; Sequence 1118, Application US/09221017B  
 ; Patent No. 6444799  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ROSS, BRUCE C.  
 ; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF  
 ; NUMBER OF SEQUENCES: 1120  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: MORRISON & FOERSTER  
 ; STREET: 755 PAGE MILL ROAD  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94304-1018  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM compatible  
 ; OPERATING SYSTEM: Windows  
 ; SOFTWARE: FASTSEQ for Windows Version 2.0b  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/221,017B

FILING DATE: 23-DEC-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: P11182  
FILING DATE: 31-DEC-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: P1546  
FILING DATE: 30-JAN-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: P2911  
FILING DATE: 09-APR-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/AU98/01023  
FILING DATE: 10-DEC-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: MONROY, Gladys H  
REGISTRATION NUMBER: 32,430  
REFERENCE/DOCKET NUMBER: 27340-20021.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-813-5600  
TELEFAX: 650-494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 1118:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 638 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: UNKNOWN  
ORIGINAL SOURCE:  
ORGANISM: PORPHYROMONAS GINGIVALIS  
FEATURE:  
NAME/KEY: misc.feature  
LOCATION: 1...638  
US-09-221-017B-1118

Alignment Scores:  
Pred. No.: 0.000302 Length: 638  
Score: 103.00 Matches: 43  
Percent Similarity: 46.71% Conservative: 35  
Best Local Similarity: 25.75% Mismatches: 55  
Query Match: 9.85% Indels: 34  
Gaps: 6

US-09-697-089-2\_COPY\_762\_965 (1-204) x US-09-221-017B-1118 (1-638)

OY 45 GUGUyMetAspYrILeVallySerLeuSerSerGluProCysAspLeuGluGlu 64  
DB 605 GAAAGCATGACTTGCTTATGATTTCCTGCTAATAAAGCTTGATCTATAC 546  
OY 65 Gln-----LeuValSerCysCysLeuSer 72  
DB 545 CAAATCAGTAGCTAGAGGCTGAGAACGCTCTACTTCTTAACAAACTGCTAGA 486  
OY 73 AlaAsnAlaValysILeLeuAlaGlnAsnLeuHisAsnLeuVallyLeuSerILe 92  
DB 485 AGTAACCAAACTCCGTAACCTA--GAGGCTGATAGTCTACCTCCCTACCAAACTT 429  
OY 93 AspLeuSerGluAsnTYrLeuGluILys---AspGlyAsnGluAlaLeuHisGlu 110  
DB 428 TCTCTCTCCGTAACCAATCAGTAGAGGCTCTGGAACGCTGACCTCGTTACG 369  
OY 111 -----LeaSpArgMetAsnValLeuGluGlnLeuThra 122  
DB 368 GAGCTTATCTTTGGATAACCAATCAGTAACAGAGGCTGAGACGTCACGTC 309  
OY 123 LeuMetLeuProTPGILyCysAspValGlnGlySerLeuSerSerLeuLeuHis 142  
DB 308 TTAAACGAGCTTTAT-----CTGCGGGTAACCAATCAGTAACGAGGCTG 258  
OY 143 GUGUyValProGlnLeuVallyLeuGluILysLeuAsnTYrArgLeuThraSp 162

DB 257 GAAAGCTGACTTCTGTTAACAAGCTTCGCTTAAGAAGTAACAGATCAGTA 198  
OY 163 ILearGILLeuGluYAlaPhePheGILyLysAsnProLeuLysAsnPheGln 182  
DB 197 -----GCGCTGATAGTCTCACCCTCGCTACCAAACTTCT 162  
OY 183 LeuAlaGlyAsnArgValSer 189  
DB 161 CTCCTCGATTAACCAATCAGT 141

RESULT 9  
US-09-180-439-1  
Sequence 1, Application US/09180439  
Patent No. 6225532  
GENERAL INFORMATION:  
APPLICANT: Dixon, Mark S  
APPLICANT: Hatzixanthis, Kostas  
APPLICANT: Jones, David A  
APPLICANT: Jones, Jonathan DG  
TITLE OF INVENTION: Plant pathogen resistance genes and uses thereof  
FILE REFERENCE: 620 - 53  
CURRENT APPLICATION NUMBER: US/09/180.439  
CURRENT FILING DATE: 1998-12-06  
EARLIER APPLICATION NUMBER: PCT/GB97/01249  
EARLIER FILING DATE: 1997-05-08  
EARLIER APPLICATION NUMBER: GB 9609681.3  
EARLIER FILING DATE: 1996-05-09  
EARLIER APPLICATION NUMBER: GB 9619924.5  
EARLIER FILING DATE: 1996-09-24  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 3979  
TYPE: DNA  
ORGANISM: Lycopersicon esculentum  
US-09-180-439-1

Alignment Scores:  
Pred. No.: 0.0162 Length: 3979  
Score: 99.50 Matches: 66  
Percent Similarity: 39.57% Conservative: 44  
Best Local Similarity: 23.74% Mismatches: 85  
Query Match: 9.51% Indels: 83  
Gaps: 16

US-09-697-089-2\_COPY\_762\_965 (1-204) x US-09-180-439-1 (1-3979)

OY 1 LeuYsAsnLeuThryLysLeuILeMetAspAsnILeYsMetAsnGluGluAsp 20  
DB 2013 CTGAGTCTCTTACTGAACATATTTTGGGTATTAACCTCTTAATGCTAT 2072  
OY 21 LysLeuAlaGluGlyLeuLysAsnLeuLysMetCysLeuPheHis----- 36  
DB 2073 TCATGTGGGG---AATCTTAACAACCTTGCTAGTGTCTTACAAATATCAGCTTCT 2129  
OY 37 -----LeuThHisLeuSerAsp 42  
DB 2130 GGCCTTATCTCTGCTTCAATTGGCAATATGAGAAATGCAAACTGCTGTTCT 2189  
OY 43 -----ILeGlyGluGlyMetAspTYrILeVallySerLeuSerSerGlu 57  
DB 2190 AACGATCTCATTTGGGAAATCTTTCATTTGTGTGCAATTTGACATCTGGA 2249  
OY 58 -----ProCys-----AspLeuGluGlu 63  
DB 2250 TATATGTCGAGAAACATTTTGAAGGAAAGTTCGCAATGTTTGGTAATATCAGT 2309  
OY 64 ILeGlnLeuValSerCysCysLeuSerAlaAsnAlaValys---ILeLeuAla 82  
DB 2310 CTTCATATTTGTGCG-----ATGTCATCTAATTAAGTTCAGAGGAGCTCC 2363  
OY 83 LeuHisAsnLeuVallyLeuSerILeLeuAspLeuSerGluAsnTYrLeuGlu 102

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Db 2364 ATTTCAATTTAACTACATCAAAAAATCTGATTTTGGCAGAAACAAATCTGGAGGAGCA 2423
QY 103 -----GlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeu 117
Db 2424 ATACCAATTTTGGCAATATTAGTAGCTCCAGGTTTGGATATGACAGAAAT----- 2477
QY 118 GluGlnLeuThrAlaLeuMetLeuProTyrPglYcysAspValGlnGlySerLeuSerSer 137
Db 2478 AACAACTTTCTGGG---ACTCTTCCAAACAAATTTTAGCATTTGATGTCTACATAGT 2534
QY 138 LeuLeuLysHis-----LeuGlnGluValPro----- 146
Db 2535 CTCAACTTGGCGCAATGAACCTAGACAGATGAATCCCTCGCTTTGGCAATTTGCAAA 2594
QY 147 GlnLeuValLysLeuGlnLysLeuAsnTyrParGluThrAspThr----- 161
Db 2595 AAGCTGCAAGTCTTGATTTTAGAGACATCACTCAACGACACATTTCCCATGTGGTGG 2654
QY 162 -----GluIleArgIleLeuGlnLysAlaPhePheGlyLys-----AsnProLeu 175
Db 2655 GGAATTTGGCAGAGCTGAGAGTTTAAAGTTGACATCGAATTAATTCATGACAGACTATA 2714
QY 176 Lys-----AsnPheGlnGlnLeuAsnLeuAlaGlyAsn 186
Db 2715 AGATCATCAGGGGCTGAATCATGTTCCTGATCTCCGAATCATAGATCTCTCGCAAT 2774
QY 187 ArgValSerSerAspGlyTyrPLeuAlaPheMetGlyValPheGluAsnLeuLys 204
Db 2775 GCATTCCTCGCAAGAC-----TTACCAACGAGCTATTTGAACATTTGAAA 2819

RESULT 10
US-09-180-439-2
; Sequence 2, Application US/09180439
; Patent No. 6225532
; GENERAL INFORMATION:
; APPLICANT: Dixon, Mark S
; APPLICANT: Hatzixanthis, Kostas
; APPLICANT: Jones, David A
; APPLICANT: Jonathan DG
; TITLE OF INVENTION: Plant pathogen resistance genes and uses thereof
; FILE REFERENCE: 620 - 53
; CURRENT APPLICATION NUMBER: US/09/180,439
; EARLIER FILING DATE: 1998-12-06
; EARLIER APPLICATION NUMBER: PCT/GB97/01249
; EARLIER FILING DATE: 1997-05-08
; EARLIER APPLICATION NUMBER: GB 9609681.3
; EARLIER FILING DATE: 1996-05-09
; EARLIER APPLICATION NUMBER: GB 9619924.5
; EARLIER FILING DATE: 1996-09-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 3979
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
US-09-180-439-2

Alignment Scores:
Pred. No.: 0.0162 Length: 3979
Score: 99.50 Matches: 66
Percent Similarity: 39.57% Conservative: 44
Best Local Similarity: 23.74% Mismatches: 85
Query Match: 9.51% Indels: 83
DB: 4 Gaps: 16

US-09-697-089-2_COPY_762_965 (1-204) x US-09-180-439-2 (1-3979)
QY 1 LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGlnGluAlaAspAlaIle 20
Db 2013 CTGAGTCTCTTACTGACATATTTTGGGTAATACATCTCTTAATGGCTCATTCCT 2072
QY 21 LysLeuAlaGlnGlyLeuLysAsnLeuLysLysMetCysLeuPheHis----- 36
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Db 2073 TCATTTGGGG---AATCTAAMACACTGTAGGTGATCTTACCAATATACCTTTCT 2129
QY 37 -----LeuThrHisLeuSerAsp 42
Db 2130 GGCCTATCTCTGCTTCAATTTGGCAATATGGAATCTGCAAACTCTGTTCTAGTGAT 2189
QY 43 -----IleGlyGlnGlyMetAspTyrIleValLysSerLeuSerSerGlu----- 57
Db 2190 AACGATCTCATTTGGGAAATTCCTTCATTTGTGCAATTTGACATGACTGACAGGAGTGG 2249
QY 58 -----ProCys-----AspLeuGlnGlu 63
Db 2250 TATATGTCGAGAAACAAATTTGGAAGGAAACCTCCGAATTTGGTAAATATAGTGAC 2309
QY 64 IleGlnLeuValSerCysLysSerAlaAsnAlaValLys-----IleLeuAlaGlnAsn 82
Db 2310 CTTCACATTTTGTG-----ATGTCACTTAATAGTTTCAAGAGAGAGCTCCCTTCATCT 2363
QY 83 LeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlnLysAsp 102
Db 2364 ATTTCAATTTAAACATCACTAAATACTTGAATTTTGGCAGAAACAAATCTGGAGGAGCA 2423
QY 103 -----GlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeu 117
Db 2424 ATACCAATTTTGGCAATATTAGTAGACCTCCAGGTTTGGATATGACAGAAAT----- 2477
QY 118 GluGlnLeuThrAlaLeuMetLeuProTyrPglYcysAspValGlnGlySerLeuSerSer 137
Db 2478 AACAACTTTCTGGG---ACTCTTCCAAACAAATTTTAGCATTTGATGTCTACATAGT 2534
QY 138 LeuLeuLysHis-----LeuGlnGluValPro----- 146
Db 2535 CTCAACTTGGCGCAATGAACCTAGACAGATGAATCCCTCGCTTTGGCAATTTGCAAA 2594
QY 147 GlnLeuValLysLeuGlnLysLeuAsnTyrParGluThrAspThr----- 161
Db 2595 AAGCTGCAAGTCTTGATTTTAGAGACATCACTCAACGACACATTTCCCATGTGGTGG 2654
QY 162 -----GluIleArgIleLeuGlnLysAlaPhePheGlyLys-----AsnProLeu 175
Db 2655 GGAATTTGGCAGAGCTGAGAGTTTAAAGTTGACATCGAATTAATTCATGACAGACTATA 2714
QY 176 Lys-----AsnPheGlnGlnLeuAsnLeuAlaGlyAsn 186
Db 2715 AGATCATCAGGGGCTGAATCATGTTCCTGATCTCCGAATCATAGATCTCTCGCAAT 2774
QY 187 ArgValSerSerAspGlyTyrPLeuAlaPheMetGlyValPheGluAsnLeuLys 204
Db 2775 GCATTCCTCGCAAGAC-----TTACCAACGAGCTATTTGAACATTTGAAA 2819

RESULT 11
US-09-180-439-7
; Sequence 7, Application US/09180439
; Patent No. 6225532
; GENERAL INFORMATION:
; APPLICANT: Dixon, Mark S
; APPLICANT: Hatzixanthis, Kostas
; APPLICANT: Jones, David A
; APPLICANT: Jonathan DG
; TITLE OF INVENTION: Plant pathogen resistance genes and uses thereof
; FILE REFERENCE: 620 - 53
; CURRENT APPLICATION NUMBER: US/09/180,439
; EARLIER FILING DATE: 1998-12-06
; EARLIER APPLICATION NUMBER: PCT/GB97/01249
; EARLIER FILING DATE: 1997-05-08
; EARLIER APPLICATION NUMBER: GB 9609681.3
; EARLIER FILING DATE: 1996-05-09
; EARLIER APPLICATION NUMBER: GB 9619924.5
; EARLIER FILING DATE: 1996-09-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
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:	LENGTH:4123	
:	TYPE: DNA	
:	ORGANISM: Lycopersicon esculentum	
:	US-09-180-439-7	
Alignment Scores:		
Pred. No.:	0.0172	Length: 4123
Score:	99.50	Matches: 66
Percent Similarity:	39.57%	Conservative: 44
Best Local Similarity:	23.74%	Mismatches: 85
Query Match:	9.51%	Indels: 83
DB:	4	Gaps: 16
US-09-697-089-2_COPY_762_965 (1-204) x US-09-180-439-7 (1-4123)		
QY	1	LeuLysAsnLeuThrLysLeuLeuIleMetAspAsnIleLysMetAsnGluGlnAspAlaIle 20
Db	2157	CTGAGTCTCTCTTACTGACATATTTTGGGTATTAATCTCTTAATGGCTATTCCTCT 2216
QY	21	LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHis----- 36
Db	2217	TCATTTGGGG--AATCTMAACAACCTGTCTAGGGTATCTTTACAAATAACAGCTTCT 2273
QY	37	-----LeuThrHisLeuSerSerp 42
Db	2274	GGCTATATTCCTCTTCATTTGGCAATATGAGAAATTCGCAAACTCTGTCTCTCAGTAT 2333
QY	43	-----IleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerpGlu----- 57
Db	2334	AAGCATCTCATTTGGGAAATCTCTTCATTTGTGTGCAATTTGACATTCACATCGGAAGCTTG 2393
QY	58	-----ProCys-----AspLeuGluGlu 63
Db	2394	TATATTCGAGAAACAATTTGAAGCGAAAGTTCGCAATGTTCGGTAATATACAGTAC 2453
QY	64	IleGluLeuValSerCysLeuSerIleAsnAlaValLys---IleLeuAlaGlnAsn 82
Db	2454	CTTCACATTTTGTGCG-----ATGTCATCTAATATGATTCAGAGAGACCTCCCTTCATCT 2507
QY	83	LeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGluLysAsp 102
Db	2508	ATTTCACATTTTAACATCACACAAAAAATCTGATTTTGGAGAAACAATCTGGAGGAGCA 2567
QY	103	-----GlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeu 117
Db	2568	ATACCACAATTTTGGCAATATTAATGATACCTCCAGGTTTTGGATATGAGAAAT----- 2621
QY	118	GluGlnLeuThrAlaLeuMetLeuProTTPGlyCysAspValGlnGlySerLeuSerSer 137
Db	2622	AACCAAACTTTTCTGGG--ACTCTTCCACAACAATTTTACGATTGATGTCTACCTGATAGT 2678
QY	138	LeuLeuLysHis-----LeuGluGluValPro----- 146
Db	2679	CTCAACTGTGATGGCAATGACATGACAGATGAAATTCCTCGGCTCTTGGCAATTTGCAGAA 2738
QY	147	GlnLeuValLysLeuGlyLeuLysAsnTTPArgLeuThrAspThr----- 161
Db	2739	AAGCTCAAGTCTCTGATTTAGGAGACATCAACTCAAGACACATTTCCCATGTGGTGG 2798
QY	162	-----GluLeuArgIleLeuGlyAlaIlePheGlyLys-----AsnProLeu 175
Db	2799	GGAACTTTGGCAGAGCTGAGAGATTTTAAGTTTGACATCGAATAAATTCATGAGACCTATA 2858
QY	176	Lys-----AsnPheGlnGlnLeuAsnLeuAlaGlyAsn 186
Db	2859	AGATCATCAGAGGCTGAATATCATGTTTCTGTGATCTCCGATCTCATGATCTCTCTCGCAAT 2918
QY	187	ArgValSerSerAspGlyTTPLeuAlaPheMetGlyValPheGluAsnLeuLys 204
Db	2919	GCATCTCCGCAACAC-----TTACCAAGAGATCTATTTGAAACATTTTGAAA 2963

[illegible]



```
OY 85 AsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGluLysAspGlyAsn 104
|||||
Db 451 AATTAAACAACTGACGACGACGATGATTTCAACTAAT----- 489
OY 105 GluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeuThrAlaLeuMet 124
490 -----AAGGTGCAGATATATGCTGTTGGCTTAAC----- 525
OY 125 LeuProTyrGlyCysAspValGlnGlySerLeuSerSerLeuLeuHisLeuGluGln 144
526 -----AATTAGAAAGTCTTATCGCTACTACCAACCA 558
OY 145 ValProGlnLeuValLysLeuGly-----LeuLysAsnTyrParGlyLeuThrAsp 160
559 ATAAGTATATTAACCTGACCTGCGATTTTAACAAATTTGACGAGATATCTTAATAGGT 618
OY 161 ThrGluIleArgIleLeuGlnGlyAlaIlePheGlyLysAsnProLeuLysAsnPheGlnGln 180
619 AACCGTTAAAGATATAGCGACATTTGGCGAGT-----TTAACAAACCTTACAGAT 669
OY 181 LeuAsnLeuAlaGlyLysArgValSerSer 190
Db 670 TTAGATTAGCAAAATTAACCAATTAATGAT 699

RESULT 13
US-09-099-041A-9
: Sequence 9, Application US/09099041A
: Patent No. 6340576
: GENERAL INFORMATION:
: APPLICANT: Berlin, John
: TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
: FILE REFERENCE: 07334-076001
: CURRENT APPLICATION NUMBER: US/09/099,041A
: PRIOR FILING DATE: 1998-06-17
: PRIOR APPLICATION NUMBER: 09/019,942
: NUMBER OF SEQ ID NOS: 37
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 9
: LENGTH: 2859
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-099-041A-9

Alignment Scores:
Pred. No.: 0.0203 Length: 2859
Score: 97.00 Matches: 42
Percent Similarity: 35.00% Conservative: 21
Best Local Similarity: 23.33% Mismatches: 65
Query Match: 9.27% Indels: 52
DB: 4 Gaps: 5

US-09-697-089-2_COPY_762_965 (1-204) x US-09-099-041A-9 (1-2859)
OY 65 GlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAlaGlnAsn----- 82
|||||
Db 2005 CAGCTGGGGCGACGAGGATGTCGCGCAACTACCTCAAGCTGACTGACGACGCGCTGC 2064
OY 83 -----LeuHisAsnLeuValLysLeuSerIleLeu 92
2065 TCGGCGGACGACGAGCGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2124
OY 93 AspLeuSerGluAsnTyrLeuGlnLysArgLysAsnGluAlaLeuHisGluLeuLeuAsp 112
2125 GACCTAGCAACAAACAAATCTCAAGCACTAGCGGCGGAGCTGCACGCGCTGCTGACG 2184
OY 113 ArgMetAsnValLeu-----GluGlnLeuThrAlaLeuMetLeuProTyrGly 128
2185 CGCCTCAGCTGTTCTCAGACTGACGCTAAACGAGATCACT----- 2223
OY 129 CysAspValGlnGlySerLeuSerSerLeuLeuLysHisLeuGluGluValProGlnLeu 148
```

```
Db 2224 -----GACGCTGGGGTAAGGTGCTAAGCGAAGAGCTGACCAATATACAAATTTGTG 2274
OY 149 ValLysLeuGlyLysLeuLysAsnTyrParGlyLeuThrAspThrGlnIleArgIleLeuGlyAla 168
2275 ACCTATTGGGTTTATTAACAAACACGATCACCGATGTCGGAGCGGACGCTGACGCAAA 2334
OY 169 Phe-----PheGlyLysAsnProLeu----- 175
Db 2335 ATCTGTGATGATGCAAGGCGCTCAGCATCTTAATCTGGGAAAAACAAATATACAGT 2394
OY 176 -----LysAsnPheGlnGlnLeuAsn 182
Db 2395 GAAGGAGGAAATATCTGCGCTGCTGGAAGAACACCAATCAATCTGAGGTTGGG 2454
OY 183 LeuAlaGlyAsnArgValSerSerAspGlyTyrLeuAlaIlePheMetGlyValPheGlnAsn 202
Db 2455 ATGTGGCGAATCAAGTTGGGATGAGAGCAAAAGGCTTTCGACAGAGCTCTGCGGAAAC 2514

RESULT 14
US-09-245-281-9
: Sequence 9, Application US/09245281
: Patent No. 6369196
: GENERAL INFORMATION:
: APPLICANT: Berlin, John
: TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
: FILE REFERENCE: 07334/118001
: CURRENT APPLICATION NUMBER: US/09/245,281
: PRIOR FILING DATE: 1999-02-05
: EARLIER APPLICATION NUMBER: US 09/207,359
: EARLIER FILING DATE: 1998-12-08
: EARLIER APPLICATION NUMBER: US 09/099,041
: EARLIER FILING DATE: 1998-06-17
: EARLIER APPLICATION NUMBER: US 09/019,942
: NUMBER OF SEQ ID NOS: 44
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 9
: LENGTH: 2859
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-245-281-9

Alignment Scores:
Pred. No.: 0.0203 Length: 2859
Score: 97.00 Matches: 42
Percent Similarity: 35.00% Conservative: 21
Best Local Similarity: 23.33% Mismatches: 65
Query Match: 9.27% Indels: 52
DB: 4 Gaps: 5

US-09-697-089-2_COPY_762_965 (1-204) x US-09-245-281-9 (1-2859)
OY 65 GlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAlaGlnAsn----- 82
|||||
Db 2005 CAGCTGGGGCGACGAGGATGTCGCGCAACTACCTCAAGCTGACTGACGACGCGCTGC 2064
OY 83 -----LeuHisAsnLeuValLysLeuSerIleLeu 92
2065 TCGGCGGACGACGAGCGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2124
OY 93 AspLeuSerGluAsnTyrLeuGlnLysArgLysAsnGluAlaLeuHisGluLeuLeuAsp 112
2125 GACCTAGCAACAAACAAATCTCAAGCACTAGCGGCGGAGCTGCACGCGCTGCTGACG 2184
OY 113 ArgMetAsnValLeu-----GluGlnLeuThrAlaLeuMetLeuProTyrGly 128
2185 CGCCTCAGCTGTTCTCAGACTGACGCTAAACGAGATCACT----- 2223
OY 129 CysAspValGlnGlySerLeuSerSerLeuLeuLysHisLeuGluGluValProGlnLeu 148
Db 2224 -----GACGCTGGGGTAAGGTGCTAAGCGAAGAGCTGACCAATATACAAATTTGTG 2274
```

Oy	149	VaLysLeuIleuLysAsnTrpArgLeuThrAspThrGluIleArgIleLeuLysAla	168
Dd	2275	ACCAATTGGGTATTACAACAACCAGATCCGATGTGGAGCCAGTACTCACCAA	2334
Oy	169	Phe-----PheGLYLyAsnProLeu-----	175
		:	
Dd	2335	ATCTCGATGAATGCAAAAGCCTCAGCAGATCTTTAAACTGGAAAAAACAAATATACAGT	2394
		:::	
Oy	176	-----LYAsnPhcGIInGLEuAsn	182
		::  :::	
Dd	2395	GAAAGAGAAGATATCTCGCCCTGCCTGTGAAGAACAGCAATCATCATCTGAGCGTTGG	2454
		:::::	
Oy	183	LcuLaIGLYAsnArgValSerSerASpGYLTTPleuAlaPheMeGLYalPheLIuSn	202
		:::	
Dd	2455	ATGTGGGGCATCAAGTTGGGGATGAAGAGCAAAAAGCCTTGCGAAGAGCTTCGCGAAC	2514
		:::	

```

RESULT 15
US-09-207-359B-9
; Sequence 9, Application US/09207359B
; Patent No. 6469140
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARP-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-112001
; CURRENT APPLICATION NUMBER: US/09/207,359B
; CURRENT FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2859
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-207-359B-9

```

Alignment Scores:	
Pred. No.:	0.0203
Score:	2859
Percent Similarity:	97.00
Best Local Similarity:	35.00%
Best Local Similarity:	23.33%
Query Match:	9.27%
DB:	4
Length:	2859
Matches:	42
Conservative:	21
Mismatches:	65
Indels:	52
Gaps:	5

US-09-697-089-2\_COPY\_762\_965 (1-204) X US-09-207-359B-9 (1-2859)

Oy	65	glnleuvalsercyscysleuSERalaasnalaVallysileleuAlaGlnasp-----	82
		: : : : :       : : : : :	
Db	2005	CAGCTGGCGGCGACAGGGGCACTGGCGCAACTCACTAACTGACTACTGCAAGCGCTGC	2064
Oy	83	-----LeuHisAsnleuVallysleuSERleu	92
Db	2065	TTCGGCCACATGCAAGCGCCCTCTCTCTTCGTCGTCGATCACTTCCCAAGCGGTGGCCCTA	2124
		: : : : :       : : : : :	
Oy	93	AspleuSERgluasnTYrleuGluLysaspSgIyasnGluAlaLeuHisGluLeuIleasp	112
Db	2125	GACCTACACAACAACATCTCAACAGCACTAGGGGTGGGAGCTGCAGCGCTTCACG	2184
Oy	113	ArgMetAsnValleu-----GluGlnleuThrAlaLeuMetleuProTropIly	128
		: : : : :       : : : : :	
Db	2185	CGCCTCACTGTCGACAGACTCAGCTGAACCAACAGATCAGT-----	2223
Oy	129	CysaspValGlnGlySerleuSERleuLeuLysHisleuGluGluValProGlnleu	148
		: : : : :     : : : : :     : : : : :	
Db	2224	-----GACGGTGGGGTAAAGGTGCTCAAGCGAAGACTGACCAAAATATCAAAATATGTG	2274
Oy	149	VallysleuGlnleuLysasnTYrpatGlyleuThrAspThrGluIleArgIleleuGluAla	168
Db	2275	ACCTATTATTGGATTATACCAACAACAGATCCAGCATGTGGAGCCAGATGCCTACCAA	2334

Qy	169	Phe-----	PhcglYlyAsnProLeu-----	175
Db	2335	ATCCGTGATGAATGCAAAAGGCTCCACGCATCTTTAAACTGGGAAAAACAAATAACAACT	2394	
Qy	176	-----	LyAsnPhcglInlInLeuAsn	182
Db	2335	GAAAGAGGAAGTATCTTCGCCCTGGCTGTCAAGAACAGCAAAATCAATCTCTGAGGTTGGG	2454	
Qy	183	LeuAlaGlyAsnArgValSerSerAspGlyTTrpLeuAlaPheMetGlyValPheGluAsn	202	
Db	2455	ATTCGGGCAATCAAGTTGGGGATGAAGAGACAAAAGCCTTCGCAGAGGCTCTGGCGAAC	2514	

Search completed: January 31, 2003, 15:16:46  
Job time : 51.1802 secs

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LENGTH: 618  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)...(618)  
US-09-864-921-181

## Alignment Scores:

Pred. No.:	3,76e-126	Length:	618
Score:	1046.00	Matches:	204
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-697-089-2\_COPY\_762\_965 (1-204) x US-09-864-921-181 (1-618)

QY 1 LeuYsAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAlaIle 20  
|||||  
Db 7 TTGAAGAAGCTTACAAAGCTCATATGATGATTAAGATGAAGATGAAGATGCTATA 66  
QY 21 LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeu 40  
|||||  
Db 67 AAAGTAGCTGAAGGCTGAAAAACCTGAAGAGATGTTTATTTTCATTGACCCACTTG 126  
QY 41 SerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAsp 60  
|||||  
Db 127 TCTGACATTTGAGAGAGGAATGATGATTAAGCTCTGTCAGTGAAGCCCTGTGAC 186  
QY 61 LeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAla 80  
|||||  
Db 187 CTTGAAGAATTCATTAAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 246  
QY 81 GlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu 100  
|||||  
Db 247 CAGATATCTTCACATTTTGTGTCACAACTGACATCTCTGATTTATTCAGAAAAATACCTGAAA 306  
QY 101 LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeu 120  
|||||  
Db 307 AAAGATGGAATGAAGGCTCTTCATGAAGCTGATCGACAGAGATGAAGCTGCTGAACAGCTG 366  
QY 121 ThrAlaLeuMetLeuProTprGlyCysAspValGlnGlySerLeuSerSerLeuLeuLys 140  
|||||  
Db 367 ACCGACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 426  
QY 141 HisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTprArgLeuThrAsp 160  
|||||  
Db 427 CATTTGGAGAGGTCCTCCCAACTGCTCAAGCTTGAGTTGAAAAAACTGGAGACTCACAGAT 486  
QY 161 ThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGln 180  
|||||  
Db 487 ACAGAGATTAGAAATTTTGTGTCATTTTGTGAAGAAGCCCTGAAAAAATCTCCAGAG 546  
QY 181 LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTprLeuAlaPheMetGlyValPhe 200  
|||||  
Db 547 TTGATTTTGGGGGAAAAATCGTGTGAGCAGTATGATGATGCTTGCCTCATGGGTATATT 606  
QY 201 GluAsnLeuLys 204  
|||||  
Db 607 GAGAAATCTTAAG 618

## RESULT 2

US-09-864-921-98  
Sequence 98, Application US/09864921  
Patent No. US20020176853A1

## GENERAL INFORMATION:

APPLICANT: Reed, John C.  
APPLICANT: Pilo, Frederick F.  
APPLICANT: Godzik, Adam  
APPLICANT: Stehlik, Christian  
APPLICANT: Damiano, Jason S.  
APPLICANT: Lee, Sug-Hyun

APPLICANT: Oliveira, Vasco A.  
APPLICANT: Hayashi, Hideki  
APPLICANT: Pawlowski, Krzysztof  
TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing  
TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods of Use  
FILE REFERENCE: P-LJ 4752  
CURRENT APPLICATION NUMBER: US/09/864, 921  
PRIOR FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 09/579,240  
PRIOR FILING DATE: 2000-05-24  
PRIOR APPLICATION NUMBER: US 09/686,347  
PRIOR FILING DATE: 2000-10-10  
PRIOR APPLICATION NUMBER: US 60/275,980  
PRIOR FILING DATE: 2001-03-14  
NUMBER OF SEQ ID NOS: 195  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 98

LENGTH: 1395

TYPE: DNA

ORGANISM: Homo sapien

FEATURE:  
NAME/KEY: CDS  
LOCATION: (277)...(1353)  
US-09-864-921-98

## Alignment Scores:

Pred. No.:	1.33e-125	Length:	1395
Score:	1046.00	Matches:	204
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-697-089-2\_COPY\_762\_965 (1-204) x US-09-864-921-98 (1-1395)

QY 1 LeuYsAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAlaIle 20  
|||||  
Db 565 TTGAAGAAGCTTACAAAGCTCATATGATGATTAAGATGAAGATGAAGATGCTATA 624  
QY 21 LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu 40  
|||||  
Db 625 AAAGTAGCTGAAGGCTGAAAAACCTGAAGAGATGTTTATTTTCATTGACCCACTTG 684  
QY 41 SerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAsp 60  
|||||  
Db 685 TCTGACATTTGAGAGAGGAATGATGATTAAGCTCAAGCTCTGTCAGTGAAGCCCTGTGAC 744  
QY 61 LeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAla 80  
|||||  
Db 745 CTTGAAGAATTCATTAAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 804  
QY 81 GlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu 100  
|||||  
Db 805 CAGATATCTTCACATTTTGTGTCACAACTGACATCTCTGATTTATTCAGAAAAATACCTGAAA 864  
QY 101 LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeu 120  
|||||  
Db 865 AAAGATGGAATGAAGGCTCTTCATGAAGCTGATCGACAGAGATGAAGCTGCTGAACAGCTG 924  
QY 121 ThrAlaLeuMetLeuProTprGlyCysAspValGlnGlySerLeuSerSerLeuLeuLys 140  
|||||  
Db 925 ACCGACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 984  
QY 141 HisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTprArgLeuThrAsp 160  
|||||  
Db 985 CATTTGGAGAGGTCCTCCCAACTGCTCAAGCTTGAGTTGAAAAAATCTGGAGACTCACAGAT 1044  
QY 161 ThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGln 180  
|||||  
Db 1045 ACAGAGATTAGAAATTTTGTGTCATTTTGTGAAGAAGCCCTGAAAAAATCTCCAGAG 1104  
QY 181 LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTprLeuAlaPheMetGlyValPhe 200  
|||||

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Db 1105 TTGAATTTGGCGGAAATCGTGTGAGACGTGATGATGGCTTGCTTCATGGGTGATT 1164
QY 201 GIuAsnLeuLys 204
Db 1165 GAGAAATCTTAAG 1176

RESULT 3
US-09-841-739-3
; Sequence 3, Application US/09841739
; Patent No. US20020034784A1
; GENERAL INFORMATION:
; APPLICANT: Berlin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-329001
; CURRENT APPLICATION NUMBER: US/09/841,739
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3072
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-841-739-3

Alignment Scores:
Pred. No.: 4,51e-125 Length: 3072
Score: 1046.00 Matches: 204
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-697-089-2_COPY_762_965 (1-204) x US-09-841-739-3 (1-3072)
QY 1 LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluLysAlaIle 20
Db 2284 TTGAAGAACCTTACAAAGCTCTAATGATTAACATTAAGATGAAGAGATGCTATA 2343
QY 21 LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu 40
Db 2344 AAACTAGCTGAAGGCCCTGAAAAAAGCTGAAGAGATGCTGTTATTCATTGACCCACTTG 2403
QY 41 SerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAsp 60
Db 2404 TCTGACATTGGAGAGGAGATGATTAACATGACAGTCTCTCAAGTGAACCCCTGTGAC 2463
QY 61 LeuGluGluIleGluLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAla 80
Db 2464 CTTGAAGAAATTCATTTAGTCTCCTGCTGCTTGCTGCAAAATGACGTAAGATCCTAGCT 2523
QY 81 GluAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu 100
Db 2524 CAGAATCTTCCACATTTGGTCAAACTGAGCATTTGATTATTCAGAAAATTAACCTGGAA 2583
QY 101 LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluInLeu 120
Db 2584 AAAGATGGAATGAAGCTCTTCATGACTGACAGAGATGAAGTGTGTAAGAACAGCTC 2643
QY 121 ThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerLeuSerSerLeuLys 140
Db 2644 ACCGACATGATGCTCCCTGGGGCTGTGACGTGCAAGGACAGCCTGAGACGCTGTTGAAA 2703
QY 141 HisLeuGluGluValProGluLeuValLysLeuGlyLeuLysAsnTyrArgLeuThrAsp 160
Db 2704 CATTGGAGGAGGTCCCACTCAAGCTTGAGGTTGAAAATGCGAGACTCAAGAT 2763
QY 161 ThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln 180
Db 2764 ACAGAGATTAGAAATTTAGGTGCAATTTTGGAAAGAACCTCTGAAAACCTCCAGCAG 2823
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QY 181 LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrPheAlaPheMetGlyValPhe 200
Db 2824 TTGAATTTGGCGGAAATCGTGTGAGACGTGATGATGGCTTGCTTCATGGGTGATT 2883
QY 201 GIuAsnLeuLys 204
Db 2884 GAGAAATCTTAAG 2895

RESULT 4
US-09-841-739-1
; Sequence 1, Application US/09841739
; Patent No. US20020034784A1
; GENERAL INFORMATION:
; APPLICANT: Berlin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES TH
; FILE REFERENCE: 07334-329001
; CURRENT APPLICATION NUMBER: US/09/841,739
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3133
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (36)...(3107)
US-09-841-739-1

Alignment Scores:
Pred. No.: 4,65e-125 Length: 3133
Score: 1046.00 Matches: 204
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-697-089-2_COPY_762_965 (1-204) x US-09-841-739-1 (1-3133)
QY 1 LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluLysAlaIle 20
Db 2319 TTGAAGAACCTTACAAAGCTCTAATGATTAACATTAAGATGAAGAGATGCTATA 2378
QY 21 LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu 40
Db 2379 AAACTAGCTGAAGGCCCTGAAAAAAGCTGAAGAGATGCTGTTATTCATTGACCCACTTG 2438
QY 41 SerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAsp 60
Db 2439 TCTGACATTGGAGAGGAGATGATTAACATGACAGTCTCTCAAGTGAACCCCTGTGAC 2498
QY 61 LeuGluGluIleGluLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAla 80
Db 2499 CTTGAAGAAATTCATTTAGTCTCCTGCTGCTTGCTGCAAAATGACGTAAGATCCTAGCT 2558
QY 81 GluAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu 100
Db 2559 CAGAATCTTCCACATTTGGTCAAACTGAGCATTTGATTATTCAGAAAATTAACCTGGAA 2618
QY 101 LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluInLeu 120
Db 2619 AAAGATGGAATGAAGCTCTTCATGACTGACAGAGATGAAGTGTGTAAGAACAGCTC 2678
QY 121 ThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerLeuSerSerLeuLys 140
Db 2679 ACCGACATGATGCTCCCTGGGGCTGTGACGTGCAAGGACAGCCTGAGACGCTGTTGAAA 2738
QY 141 HisLeuGluGluValProGluLeuValLysLeuGlyLeuLysAsnTyrArgLeuThrAsp 160
```

```
|||||
Db 2739 CATTGGAGGAGGTCCCAACTGCTCAAGCTGGGTTGAAAACCTGAGACTCAGAT 2798
Qy 161 ThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln 180
Db 2799 ACAGAGATTAGATTGTTAGTGCAATTTTGGAAAGAACCCCTGAAAACCTCCAGAG 2858
Qy 181 LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrPleuAlaPheMetGlyValPhe 200
Db 2859 TTGAATTTGGCGGGAATCGTGTGAGCAGTATGATGGCTTGCCCTCATGGGTATTT 2918
Qy 201 GluAsnLeuLys 204
Db 2919 GAGAACTTTAAG 2930

RESULT 5
US-09-864-921-96
: Sequence 96, Application US/09864921
: Patent No. US20020176853A1
: GENERAL INFORMATION:
: APPLICANT: Reed, John C.
: APPLICANT: Plo, Frederick F.
: APPLICANT: Godzik, Adam
: APPLICANT: Stehlik, Christian
: APPLICANT: Damiano, Jason S.
: APPLICANT: Lee, Sug-Hyun
: APPLICANT: Oliveira, Vasco A.
: APPLICANT: Hayashi, Hideki
: APPLICANT: Pawlowski, Krzysztof
: TITLE OF INVENTION: No. US20020176853A1el Card Domain Containing
: TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods of Use
: FILE REFERENCE: P-LJ 4752
: CURRENT APPLICATION NUMBER: US/09/864, 921
: PRIOR FILING DATE: 2001-05-23
: PRIOR APPLICATION NUMBER: US 09/579, 240
: PRIOR FILING DATE: 2000-05-24
: PRIOR APPLICATION NUMBER: US 09/686, 347
: PRIOR FILING DATE: 2000-10-10
: PRIOR APPLICATION NUMBER: US 60/275, 980
: PRIOR FILING DATE: 2001-03-14
: NUMBER OF SEQ ID NOS: 195
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 96
: LENGTH: 3396
: TYPE: DNA
: ORGANISM: Homo sapien
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (277)...(3348)
: US-09-864-921-96

Alignment Scores:
Pred. No.: 5,27e-125 Length: 3396
Score: 1046.00 Matches: 204
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 9

US-09-697-089-2_copy_762_965 (1-204) x US-09-864-921-96 (1-3396)

Qy 1 LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluLysAlaIle 20
Db 2560 TTGAAGAACCCTTAACAACCTCATATGATGAATAAAGATGAATGAAGAAGATGCTATA 2619
Qy 21 LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu 40
Db 2620 AAACCTAGCTGAAGGCCCTGAAAACCTGAAGAAGATGTGTATTTCATTGACCCACTTG 2679
Qy 41 SerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAsp 60
Db 2680 TCTGACATTGGAGAGGGAATGATTAACATAGTCAAGTCTGTCTCAAGTGAACCCCTGTAC 2739
```

```
Qy 61 LeuGluGluIleGlnLeuValSerCysLeuSerAlaAsnAlaValLysIleLeuAla 80
Db 2740 CTTGAAGAAATTCATATTGATCTCCGTGCTGTCTCCAAATGACAGTGAATTCCTAGCT 2799
Qy 81 GluAsnLeuHisAsnLeuValLysLeuSerIleLeuAsnLeuSerGluAsnTyrLeuGlu 100
Db 2800 CAGAATCTTCACAAATTTGTCAAACTGACATTTCTTGATTTATCGAAAATTTACCTGAA 2859
Qy 101 LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeu 120
Db 2860 AAAGATGAATGAAAGCTCTTCATGAATGATCGACAGAGATGAAGCTGTGAACAGCTC 2919
Qy 121 ThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerLeuSerSerLeuLys 140
Db 2920 ACCGCACATGATGCTGCCCTGGGGGCTGTGACCTGCAAGGACACCTGAGAGCTGTGAA 2979
Qy 141 HisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrArgLeuThrAsp 160
Db 2980 CATTGGAGGAGGTCCCAACTGCTCAAGCTTGGGTTGAAAACCTGAGACTCAGAT 3039
Qy 161 ThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln 180
Db 3040 ACAGAGATTAGATTGTTAGTGCAATTTTGGAAAGAACCCCTGAAAACCTCCAGAG 3099
Qy 181 LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrPleuAlaPheMetGlyValPhe 200
Db 3100 TTGAATTTGGCGGGAATCGTGTGAGCAGTATGATGGCTTGCCCTCATGGGTATTT 3159
Qy 201 GluAsnLeuLys 204
Db 3160 GAGAACTTTAAG 3171

RESULT 6
US-09-841-739-6
: Sequence 6, Application US/09841739
: Patent No. US20020034784A1
: GENERAL INFORMATION:
: APPLICANT: Berlin, John
: TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES TH
: FILE REFERENCE: 07334-328001
: CURRENT APPLICATION NUMBER: US/09/841, 739
: CURRENT FILING DATE: 2001-08-29
: PRIOR APPLICATION NUMBER: US 09/697, 089
: PRIOR FILING DATE: 2000-10-26
: PRIOR APPLICATION NUMBER: US 60/161, 822
: PRIOR FILING DATE: 1999-10-27
: NUMBER OF SEQ ID NOS: 16
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 6
: LENGTH: 3612
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-841-739-6

Alignment Scores:
Pred. No.: 5,79e-125 Length: 3612
Score: 1046.00 Matches: 204
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 10
DB: 10

US-09-697-089-2_copy_762_965 (1-204) x US-09-841-739-6 (1-3612)

Qy 1 LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluLysAlaIle 20
Db 2755 TTGAAGAACCCTTAACAACCTCATATGATGAATAAAGATGAATGAAGAAGATGCTATA 2814
Qy 21 LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu 40
Db 2815 AAACCTAGCTGAAGGCCCTGAAAACCTGAAGAAGATGTGTATTTCATTGACCCACTTG 2874
Qy 41 SerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAsp 60
```

```
|||||
Db 2875 TGTGACATTGGAGAGGAGGATGATTACATAGTCAATCTCTGTGCAAGTGACACCTGTGAC 2934
QY 61 LeuGlugluIleGlnLeuValSerCysLeuSerAlaAsnAlaValLysIleLeuAla 80
Db 2935 CTTGAAGAAATTCATTAAGTCTCTGTGCTGTCTGCAAAATGACAGTAAATCCTAGCT 2994
QY 81 GlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGlnAsnTrpTrpLeuGlu 100
Db 2995 CAGAAATCTTCACAAATTTGGTCAAACTGACACATCTTGATTTTTCAGAAAAATTAACCTGGAA 3054
QY 101 LysAspGlyAsnGluAlaLeuHisGlnLeuIleAspArgMetAsnValLeuGlnGlnLeu 120
Db 3055 AAAGATGGAATAAGAACTCTTATGACATCGACAGATGACAGTACCTGTAGAACGCTC 3114
QY 121 ThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeuLys 140
Db 3115 ACCGACATGATGCTGCCCTGGGGCTGTGTGACGTGCAAGCAGCAGCTGAGCAGCTGTGAAA 3174
QY 141 HisLeuGlnGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThrAsp 160
Db 3175 CATTTGGAGAGAGTCCCAACACTGTCAGACTGGGTTGAAAAAACTGGAGACTCACAGAT 3234
QY 161 ThrGluIleArgIleLeuGlnAlaPhePheGlyLysAsnProLeuLysAsnPhenGln 180
Db 3235 ACAGAGATTAGAAATTTTAGTGTCATTTTGGAAAAAACCCCTGTGAAAACTTCCAGCAG 3294
QY 181 LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGlyValPhe 200
Db 3295 TTGAATTTGGCGGGAATCGTGTGACAGTGTGATGGCTTGCCCTTCATGGGTGTATTT 3354
QY 201 GluAsnLeuLys 204
Db 3355 GAGAAATCTTAAG 3366
```

## RESULT 7

US-09-841-739-4  
; Sequence 4, Application US/09841739  
; Patent No. US20020034784A1

## GENERAL INFORMATION:

; APPLICANT: Berlin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE  
; FILE REFERENCE: 07334-329001  
; CURRENT APPLICATION NUMBER: US/09/841,739  
; CURRENT FILING DATE: 2001-08-29  
; PRIOR APPLICATION NUMBER: US 09/697,089  
; PRIOR FILING DATE: 2000-10-26  
; PRIOR APPLICATION NUMBER: US 60/161,822  
; PRIOR FILING DATE: 1999-10-27  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 3615  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(3612)  
US-09-841-739-4

## Alignment Scores:

Pred. No.: 5.8e-125 Length: 3615  
Score: 1046.00 Matches: 204  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 10 Gaps: 0

US-09-697-089-2\_COPY\_762\_965 (1-204) x US-09-841-739-4 (1-3615)

QY 1 LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGlnGluLysAlaLe 20  
Db 2755 TTGAAGAACCTTAACAAGCTCTATATGATATACATTAAGATGAATGAGAAGATGCTATA 2814

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QY 21 LysLeuAlaGlnGluLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu 40
Db 2815 AAACGTGCTGAAGCCCTGAAAAACCTGAAGAACATGTGTTATTTATTTGACCCACTTG 2874
QY 41 SerAspIleGlyGlnGlyMetAspTrpIleValLysSerLeuSerSerGlnUpProCysAsp 60
Db 2875 TGTGACATTGGAGAGGAAATGATTCATATGTAAGTCTCTGCAAGTGACACCTGTGAC 2934
QY 61 LeuGlnGluIleGlnLeuValSerCysLeuSerAlaAsnAlaValLysIleLeuAla 80
Db 2935 CTTGAAGAAATTCATTAAGTCTCTGCTGCTGTCGCAAAATGACATGAAATCCTAGCT 2994
QY 81 GlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGlnAsnTrpTrpLeuGlu 100
Db 2995 CAGAAATCTTCACAAATTTGGTCAAACTGACACATCTTGATTTTACAAAAATTAACCTGGAA 3054
QY 101 LysAspGlyAsnGluAlaLeuHisGlnLeuIleAspArgMetAsnValLeuGlnGlnLeu 120
Db 3055 AAAGATGGAATAAGAACTCTTATGACATCGACAGATGACAGTACCTGTAGAACGCTC 3114
QY 121 ThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeuLys 140
Db 3115 ACCGACATGATGCTGCCCTGGGGCTGTGTGACGTGCAAGCAGCAGCTGAGCAGCTGTGAAA 3174
QY 141 HisLeuGlnGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThrAsp 160
Db 3175 CATTTGGAGAGAGTCCCAACACTGTCAGACTGGGTTGAAAAAACTGGAGACTCACAGAT 3234
QY 161 ThrGluIleArgIleLeuGlnAlaPhePheGlyLysAsnProLeuLysAsnPhenGln 180
Db 3235 ACAGAGATTAGAAATTTTAGTGTCATTTTGGAAAAAACCCCTGTGAAAACTTCCAGCAG 3294
QY 181 LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGlyValPhe 200
Db 3295 TTGAATTTGGCGGGAATCGTGTGACAGTGTGATGGCTTGCCCTTCATGGGTGTATTT 3354
QY 201 GluAsnLeuLys 204
Db 3355 GAGAAATCTTAAG 3366
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## RESULT 8

US-09-841-739-12/c  
; Sequence 12, Application US/09841739  
; Patent No. US20020034784A1

## GENERAL INFORMATION:

; APPLICANT: Berlin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES TH  
; FILE REFERENCE: 07334-329001  
; CURRENT APPLICATION NUMBER: US/09/841,739  
; CURRENT FILING DATE: 2001-08-29  
; PRIOR APPLICATION NUMBER: US 09/697,089  
; PRIOR FILING DATE: 2000-10-26  
; PRIOR APPLICATION NUMBER: US 60/161,822  
; PRIOR FILING DATE: 1999-10-27  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 3615  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-841-739-12

## Alignment Scores:

Pred. No.: 5.8e-125 Length: 3615  
Score: 1046.00 Matches: 204  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 10 Gaps: 0

US-09-697-089-2\_COPY\_762\_965 (1-204) x US-09-841-739-12 (1-3615)



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Qy 1 LeuLysAsnLeuThLysLeuLleMetAspAsnLleLysMetAsnGluLysAlaIle 20
    |||||||
Db 861 TTGGAAGACCTTACAAACCTCATATGATTAACATAAAGATGAATGAAGAGATCTATA 802
Qy 21 LysLeuAlaGluGlyLeuLysAsnLeuLysMetCysLeuPheHisLeuThrHisLeu 40
    |||||||
Db 801 AAACAGCTGAAGGCGCTCAAAAACTGAAGAAGATGTTTATTTTCATTGTGACCACTTG 742
Qy 41 SerAspLleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAsp 60
    |||||||
Db 741 TCTGACATTTGGAGAGGATGATGATACATAGTCAAGTCTCTCTCAAGTCAACCTGTGAC 682
Qy 61 LeuGluGluLleGluLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAla 80
    |||||||
Db 681 CTTGAAGAAATTCATTAATGATCTCTGCTGCTGCTGCAAAATGACAGTGAATTCCTAGCT 622
Qy 81 GluAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu 100
    |||||||
Db 621 CAGAATCTTCACAAATTTGGTCAAACTGAGCATTCTTGATTTATCAGAAAAATTACCTGGA 562
Qy 101 LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGluLeu 120
    |||||||
Db 561 AAAGATGGAATGAAGCTCTTCATCATAGTACGACAGATGAACGTGCTTAAGAAGCTTC 502
Qy 121 ThrAlaLeuMetLeuProTropLysCysAspValGlnGlySerLeuSerSerLeuLeuLys 140
    |||||||
Db 501 ACCGCACTGATGCTGCTGCTGGGGCTGTGACGTGCAAGGAGCGCTGAGCCTGTGTA 442
Qy 141 HisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrArgLeuThrAsp 160
    |||||||
Db 441 CATTGGAGGAGCTCCCACTCCTCAAGCTTGAGTGAACCTGGGTTGAAAACTGGAGCTCAGAGAT 382
Qy 161 ThrGluIleArgIleLeuGlyValaPhePheGlyLysAsnProLeuLysAsnPheGlnGlu 180
    |||||||
Db 381 ACAGGATTAAGATTTTGGATGTCATTTTGGAAAAAACCCCTCTGAAAAAACTTCCAGCAG 322
Qy 181 LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrPheAlaPheMetGlyValaPhe 200
    |||||||
Db 321 TTGAATTTGGCGGAAATCGTCTGACAGATGATGATGCTGCTGCTGATGCGGTATTT 262
Qy 201 GluAsnLeuLys 204
    |||||||
Db 261 GAGAAATCTTAAG 250

RESULT 9
US-09-864-761-4236
; Sequence 4236, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmica-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664

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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 4236
; LENGTH: 421
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011232.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
US-09-864-761-4236

Alignment Scores:
Pred. No.: 2,79e-17 Length: 421
Score: 202.00 Matches: 38
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 19.31% Indels: 0
DB: 10 Gaps: 0

US-09-697-089-2_copy_762_965 (1-204) x US-09-864-761-4236 (1-421)
Qy 167 GlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGluLeuAsnLeuAlaGlyAsn 186
    |||||||
Db 181 GGTGATTTTGGAAAGAACCTCTGAAAACTTCCAGCACTGAATTTGGCGGGAAT 240
Qy 187 ArgValSerSerAspGlyTyrPheAlaPheMetGlyValaPheGluAsnLeuLys 204
    |||||||
Db 241 CCGTGAGAGATGATGATGATGCTTCCCTTCATGAGGTATTTGAAGATCTTAAG 294

RESULT 10
US-09-986-224-20
; Sequence 20, Application US/09986224
; Patent No. US20020150920A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Wang, Weiye
; APPLICANT: Blatcher, Maria
; TITLE OF INVENTION: NOVEL MOLECULES OF THE NBS/LRR PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-333001
; CURRENT APPLICATION NUMBER: US/09/986,224
; CURRENT FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 09/848,035

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Qy 171 GlyLysAsnProLeuLysAsnPhelGlnLeuAsnLeuAlaGlyAsnArgValSerSer 190
Db 2788 AGCAGCAGCT-----AAGAGCGCTGTCATATCTGAACCTTTCAGCAATGATGTGATCT 2841
Qy 191 AspGly 192
Db 2842 GATGCT 2847

RESULT 12
US-09-938-842A-1194
; Sequence 1194, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPL300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1194
; LENGTH: 1581
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1194

Alignment Scores:
Pred. No.: 8.69e-06 Length: 1581
Score: 120.00 Matches: 58
Percent Similarity: 40.08% Conservative: 41
Best Local Similarity: 23.48% Mismatches: 82
Query Match: 11.47% Indels: 66
DB: 9 Gaps: 11

US-09-697-089-2_COPY_762_965 (1-204) x US-09-938-842A-1194 (1-1581)
Qy 3 AsnLeuThrLysLeuIleMetAspAsnIleLysMetAlaGlnLysAlaIleLysLeu 22
Db 628 AATTTCAGCAGCAGGCTGATGATCAGCTCAATGGCTTCGATTCCTAGCGCAAGTTA 687
Qy 23 AlaGlnGlyLeuLys--AsnLeuLysLysMetCysLeuPheHisLeu----- 37
Db 688 TCGAGTCTTTCAGGCTGATCTCTGAGAATGTATCATGCTACTACCGGCAACCATTA 747
Qy 38 -----ThrHisLeuSerAspIleGlyGlu----- 45
Db 748 GGAGGGCTATTATCTTTGACGAGCGCTGATTGCAATGCAATAGAAATGGTCAGCTCCCT 807
Qy 46 -----GlyMetAspTyrIleValLysSerLeuSer 55
Db 808 GAGCTTATAGAGATTTCTTAACCTGTCACACCTGAATCTTAGTGGAAACCAATTATCA 867
Qy 56 SerGlnProCysAspLeuGlnu---IleGlnLeuValSerCysCysLeuSerAlaAsn 74
Db 868 TCTCTTCATGCTGCTATTATTAATAGATGATGATCATCTTGGAGAACTGATTGGCTCTAAC 927
Qy 75 AlaValLysIleLeuAlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeu 94
Db 928 AGCCTCTCTATTCCTCCCTGAATCTATGTGTTCTCTCGTACGACCTAAGAGAGCTCGATGT 987
Qy 95 SerGlnAsnTyrLeuGlnLys----- 101
Db 988 GAACCAATTAACATCGAAGAGATTCACATAGTATCTGTGCTGTTCTTCATGGAGAA 1047
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Qy 102 -----AspGlyAsn-----GlnAlaLeuHisGlnLeuIleAspArgMetAlaVal 116
Db 1048 CTCCTGTCAGATTTACACAGACTTAACACTCTTCCAGAGAGCTGTGGAGATTTATCTACC 1107
Qy 117 LeuGlnGlnLeuThrAla-----LeuMetLeuProTyrGlyCysAspVal 131
Db 1108 TTAGAGATTTCTGACTGCTCGTTAATAATCAATGCGAGCTACCCACAAATGCTCTCC 1167
Qy 132 GlnGlySerLeuSerSerLeu-----LeuLysHisLeuGlnGlnLysValProGln--- 147
Db 1168 ATGCTTAACCTCAAGAGACTGATGCTGATTCAACGAGCTTGAAGTCACTCCAGAGAGCT 1227
Qy 148 -----LeuValLysLeuGlyLeuLysAsnTyrPargLeuThrAspThr 161
Db 1228 TTATGTTATGCCAAACACCTTGTTAAGCTTAAACATCGCGAAC-----AATTTCGC 1278
Qy 162 GluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPhelGlnLeu 181
Db 1279 AACCTTAAGTCACTCCCGGATTTATAGCAAC-----CTTGAGAACCTAAGAGAGCTT 1332
Qy 182 AsnLeuAlaGlyAsnArgVal 188
Db 1333 GATATGAGCAATTAACAGATC 1353

RESULT 13
US-09-905-291A-27
; Sequence 27, Application US/09905291A
; Patent No. US20020160374A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Askenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Flivarov, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertschen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paonli, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,291A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
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PRIOR FILING DATE: 1998-09-10	PRIOR APPLICATION NUMBER: 60/099811
PRIOR FILING DATE: 1998-09-10	PRIOR APPLICATION NUMBER: 60/099812
PRIOR FILING DATE: 1998-09-10	PRIOR APPLICATION NUMBER: 60/099813
PRIOR FILING DATE: 1998-09-10	PRIOR APPLICATION NUMBER: 60/100858
PRIOR FILING DATE: 1998-09-17	PRIOR APPLICATION NUMBER: 60/101922
PRIOR FILING DATE: 1998-09-24	PRIOR APPLICATION NUMBER: 60/106032
PRIOR FILING DATE: 1998-10-28	PRIOR APPLICATION NUMBER: 60/109304
PRIOR FILING DATE: 1998-11-20	PRIOR APPLICATION NUMBER: 60/125778
PRIOR FILING DATE: 1999-03-23	PRIOR APPLICATION NUMBER: 60/139695
PRIOR FILING DATE: 1999-06-15	PRIOR APPLICATION NUMBER: 60/145070
PRIOR FILING DATE: 1999-07-20	PRIOR APPLICATION NUMBER: 60/145698
PRIOR FILING DATE: 1999-07-26	PRIOR APPLICATION NUMBER: 60/149366
PRIOR FILING DATE: 1999-08-17	PRIOR APPLICATION NUMBER: 60/164945
PRIOR FILING DATE: 1999-12-07	PRIOR APPLICATION NUMBER: 60/1918874
PRIOR FILING DATE: 1997-08-26	PRIOR APPLICATION NUMBER: 60/933821
PRIOR FILING DATE: 1997-09-19	PRIOR APPLICATION NUMBER: 60/933821
PRIOR FILING DATE: 1997-10-29	PRIOR APPLICATION NUMBER: 60/960507
PRIOR FILING DATE: 1997-10-29	PRIOR APPLICATION NUMBER: 60/114844
PRIOR FILING DATE: 1998-07-14	PRIOR APPLICATION NUMBER: 60/136801
PRIOR FILING DATE: 1998-08-19	PRIOR APPLICATION NUMBER: 60/136804
PRIOR FILING DATE: 1998-08-19	PRIOR APPLICATION NUMBER: 60/136828
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; PRIOR APPLICATION NUMBER: PCT/US99/05028
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: PCT/US99/20111
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547

Alignment Scores:
Pred. No.:      4.95e-05          Length:      2479
Score:         116.50           Matches:     46
Percent Similarity: 44.59%       Conservative: 20
Best Local Similarity: 31.08%     Mismatches:  59
Query Match:    11.14%           Indels:      7
DB:             9               Gaps:        23

US-09-697-089-2_COPY_762_965 (1-204) x US-10-0666-500-114 (1-2479)

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||| :|||| :|||||:||||: |||:: |||::
Db      870 CTCACGACTTGGAGCGCTATTATGTGCAGCGAACCTCCTGCACAACAAG----- 920

QY      20 IleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetGlySLeuPheHISleuThrHis 39
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      921 ---GGTAATCCGCGAGGCG-----ACCTTCACCACTCTCACCAAG 956

40 LeuSerAspIIleGlyGluGlyMetAspTyrlIleValLysSerLeuSerSerGluProCys 59

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Db      957 CTCACGAA-----TTTCAATTGTACTAATTCCTGTCCACCCTCCTCC    1006
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QY      79 LEUALIADLNSHLSNSHLNSHLNSVALYLSLESERILELNASPLNSERCULNSHYR 98
Db      1065 CTTTGACACACCTTTCGAATATGTGGCTTAAGCTGGAAGCGCTGGATATATCCAACAACCAA 11226
QY      99 LEUCLUYASPSPLYASNGLUALALEUHLISGLULEILASPARGMETASNVALLEUGLU 118
Db      1125 CTCCGGCATG-----CTGACTCAAGGGGTTTTGGATNAATCTCCACAACTGAG 11727
QY      119 GLNLTHRLALEUKETLEUPRTTPGLYCYSASPVALINGLYSERLEUSERSERLEU 138
Db      1173 CAGCTCACCTCTCGAATAACCTTGTTGGTTTGTGACTGC-----AGTATTAATGGTTC 12264
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RESULT 15
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; Sequence 27, Application US/09902853
; Publication No. US20020192659A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Grimaldi, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Peoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OR INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
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; PRIOR APPLICATION NUMBER: US 60/143, 048
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; PRIOR FILING DATE: 1999-07-26
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; PRIOR FILING DATE: 1999-07-28
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; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547

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: PRIOR APPLICATION NUMBER: PCT/US99/23089
: PRIOR FILING DATE: 1999-10-05
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: PRIOR FILING DATE: 1999-11-29
: PRIOR APPLICATION NUMBER: PCT/US99/28313
: PRIOR FILING DATE: 1999-11-30
: PRIOR APPLICATION NUMBER: PCT/US99/28564
: PRIOR FILING DATE: 1999-12-02
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: PRIOR FILING DATE: 1999-12-02
: PRIOR APPLICATION NUMBER: PCT/US99/30095
: PRIOR FILING DATE: 1999-12-16
: PRIOR APPLICATION NUMBER: PCT/US99/30911
: PRIOR FILING DATE: 1999-12-20
: PRIOR APPLICATION NUMBER: PCT/US99/30999
: PRIOR FILING DATE: 1999-12-20
: PRIOR APPLICATION NUMBER: PCT/US00/00219
: PRIOR FILING DATE: 2000-01-05
: NUMBER OF SEQ ID NOS: 423
: SEQ ID NO 27
: LENGTH: 2479
: TYPE: DNA
: ORGANISM: Homo Sapien
US-09-902-853-27

Alignment Scores:
Pred. No.: 4.95e-05 Length: 2479
Score: 116.50 Matches: 46
Percent Similarity: 44.59% Conservative: 20
Best Local Similarity: 31.08% Mismatches: 59
Query Match: 11.14% Indels: 23
DB: 9 Gaps: 7

US-09-697-089-2_COPY.762_965 (1-204) x US-09-902-853-27 (1-2479)

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DB 921 ---GGTATCGCCGAGGGC-----ACCTTCAGCCATCTCACCAAG 956

QY 40 LeuSerAspIleGlyGluIuGlyMetAspTYrIleValLysSerLeuSerSerGluProCys 59
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DB 957 CTCGAAGAA-----TTTCAATGTGACGTAATTCGCTGTGCCACCGCTCTGCC 1004

QY 60 AspLeuGluIuIleGluLeuValSerCysCysLeuSerAlaAsnAlaValys---Ile 78
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DB 1005 GATCTCCCGAGGTACGATCTGATCAGGCTCTATTTCAGAGCAACAGATMAACCCACATY 1064

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QY 119 GlnLeuThrAlaLeuMetLeuProTPbGlyCysAspValaGlnGlySerLeuSerSerLeu 138
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QY 139 LeuYsHisLeuGluIuValPro 146
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Search completed: January 31, 2003, 18:05:20
Job time : 61.4923 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

# OM protein - nucleic search, using frame\_plus.p2n model

Run on: January 31, 2003, 13:16:47 ; Search time 2594.61 Seconds  
(without alignments)  
1976.816 Million cell updates/sec

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Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 49582208

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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3	1046	100.0	1959	US-09-864-921-98	Sequence 98, Appl
4	1046	100.0	2350	PCT-US00-35017A-416	Sequence 416, Appl
5	1046	100.0	3072	PCT-US00-29643-3	Sequence 3, Appl1
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7 1046 100.0 3072 32 US-09-841-739-3 Sequence 3, Appl1
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32 905 86.5 6012 22 US-09-557-676-911 Sequence 911, App
33 905 86.5 6012 22 US-09-557-676-917 Sequence 917, App
34 905 86.5 6012 38 US-10-042-938-917 Sequence 917, App
35 905 86.5 6012 38 US-10-042-938-917 Sequence 917, App
36 737 70.5 642 18 US-09-404-284-4030 Sequence 4030, App
37 737 70.5 642 19 US-09-524-038-4030 Sequence 4030, App
38 737 70.5 642 38 US-10-011-154-4030 Sequence 4030, App
39 645 61.7 407 17 US-09-359-067-46762 Sequence 46762, A
40 645 61.7 4275 76 US-60-324-185-22577 Sequence 22577, A
41 626 59.8 2735 40 US-10-106-698-1263 Sequence 1263, Ap
42 626 59.8 2735 1 PCT-US01-14826-498 Sequence 498, App
43 622 59.5 791 18 US-09-489-036-31154 Sequence 31154, A
44 622 59.5 791 22 US-09-577-408-3075 Sequence 3075, Ap
45 622 59.5 791 22 US-09-577-408-3075 Sequence 3075, Ap
```

## ALIGNMENTS

```
RESULT 1
US-09-864-921-181
: Sequence 181, Application US/096864921
: GENERAL INFORMATION:
: APPLICANT: Reed, John C.
: APPLICANT: Pio, Frederick F.
: APPLICANT: Godzik, Adam
: APPLICANT: Stehlik, Christian
: APPLICANT: Damiano, Jason S.
: APPLICANT: Lee, Sung-Hyung
: APPLICANT: Oliveira, Vasco A.
: APPLICANT: Hayashi, Hideki
: APPLICANT: Pawlowski, Krzysztof
: TITLE OF INVENTION: Novel Card Domain Containing
: FILE REFERENCE: P-LJ 4752
: CURRENT APPLICATION NUMBER: US/09/864,921
: CURRENT FILING DATE: 2001-05-23
: PRIOR APPLICATION NUMBER: US 09/579,240
: PRIOR FILING DATE: 2000-05-24
: PRIOR APPLICATION NUMBER: US 09/686,347
: PRIOR FILING DATE: 2000-10-10
: PRIOR APPLICATION NUMBER: US 60/275,980
: PRIOR FILING DATE: 2001-03-14
: NUMBER OF SEQ ID NOS: 195
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 181
: LENGTH: 618
: TYPE: DNA
: ORGANISM: Homo sapiens
```

```
FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)...(618)
: US-09-864-921-181
Alignment Scores:
Pred. No.: 2,11e-98 Length: 618
Score: 1046.00 Matches: 204
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-09-697-089-2_COPY_762_965 (1-204) x US-09-864-921-181 (1-618)
QY 1 LeuysanleuTrprrysleuIlleMetAspnsnIlleYsMetAsnGluGluAspAlaIle 20
: TTTGAAGAACCTTACCAAACTCATATGATATACATTAAGATGAATGAAGAAAGATGCTATA 66
Db 7
QY 21 LysleuAlaGluGluLeuYAsnleuYsLysMetCysleuPheHisleuThrHisleu 40
: AAACCTAGCTGAAGGCGCTGAAAACCTGAGAAGATGCTTATTTCAATTTGACCCACTTG 126
Db 67
QY 41 SerAspIleGlyGluGlyMetAspTyrIleValYsSerLeuSerLeuSerGluProCysasp 60
: TCTGACATTTGAGAGGAGGATGATTAATGATCAAGTCTCTGTAAGTGAACCTGTGAC 186
Db 127
QY 61 LeuGluGluIleGluLeuValSerCysCysLeuSerAlaAsnAlaValYsIleLeuAla 80
: CTTGAGAGAAATTCATTAATTTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 246
Db 187
QY 81 GluAsnleuHisAsnleuValYsleuSerIleLeuAspLeuSerGluAsnTyrLeuGlu 100
: CAGAAATCTTCAAAATTTGCTCAAACTGACATCTTGAATTTATGAGAAATTAACCTGGA 306
Db 247
QY 101 LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlu 120
: AAAAGTGAATGAAGGCTCTTCAATGATGACAGACAGAGAAAGCTGTGAGAACAGCTC 366
Db 307
QY 121 ThrAlaLeuMetLeuProTrrpGlyCysAspValGlnGlySerLeuSerSerLeuLeuYs 140
: ACCGCACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 426
Db 367
QY 141 HisLeuGluGluValProGluLeuValYsleuGlyLeuYsAsnTrrpArgLeuThrAsp 160
: CATTGGAGAGGAGTCCCACTGCAAGCTTGGAATAAATGAGAGCTCACAGAT 486
Db 427
QY 161 ThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuYsAsnPheGluGln 180
: ACAGAGATTGAATTTTAGTGATTTTGTGAAAGAACTCTGAAATACTCCAGCAG 546
Db 487
QY 181 LeuAsnleuAlaGlyAsnArgValSerSerAspGlyTrrpLeuAlaPheMetGlyValPhe 200
: TTGAATTTGGCGGGAATTCGTGACGATGATGATGATGATGATGATGATGATGATGATG 606
Db 547
QY 201 GluAsnleuYs 204
: GAGAAATCTTAAG 618
Db 607
RESULT 2
US-09-686-347-98
: Sequence 98, Application US/09686347
: GENERAL INFORMATION:
: APPLICANT: Reed, John C.
: APPLICANT: Pio, Frederick F.
: APPLICANT: Godzik, Adam
: APPLICANT: Oliveira, Vasco A.
: APPLICANT: Lee, Sung-Hyung
: APPLICANT: Stehlik, Christian
: TITLE OF INVENTION: Novel Card-Domain Containing
: FILE REFERENCE: P-LJ 4271
: CURRENT APPLICATION NUMBER: US/09/686,347
```

;; CURRENT FILING DATE: 2000-10-10  
;; PRIOR APPLICATION NUMBER: US 09/579,240  
;; PRIOR FILING DATE: 2000-05-24  
;; NUMBER OF SEQ ID NOS: 109  
;; SOFTWARE: FASTSEQ for Windows Version 4.0  
;; SEQ ID NO 98  
;; LENGTH: 1395  
;; TYPE: DNA  
;; ORGANISM: Homo sapien  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: (277)...(1353)  
US-09-686-347-98

## Alignment Scores:

Pred. NO.:	5.89e-98	Length:	1395
Score:	1046.00	Matches:	204
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	27	Gaps:	0

US-09-697-089-2\_copy\_762\_965 (1-204) x US-09-686-347-98 (1-1395)

Oy 1 LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAlaIle 20  
|||||  
Db 565 TTGAAGAACCCTTACAAAGCTCATATGATACATTAAGATGATGAAGAGATCTATA 624  
Oy 21 LysLeuAlaGluGlyLeuLysAsnLeuLysMetCysLeuPheHisLeuThrHisLeu 40  
|||||  
Db 625 AAACAGCTGAAGGCTGAAAAACCTGAAGAAGATGTTTATTTTCATTGACCCACTTG 684  
Oy 41 SerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAsp 60  
|||||  
Db 665 TCTGCATTGGAGAGGAGGATGATTACATGATCAAGTCTCTCTCAAGTGAACCTGTTGAC 744  
Oy 61 LeuGluGluIleGlnLeuValSerCysLeuSerSerAlaAsnAlaValLysIleLeuAla 80  
|||||  
Db 745 CTGGAAGAAATTCATTAGTCTCCCTGCTGCTGCTGCAAAATGCAAGTAAATCTAGCT 804  
Oy 81 GlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerSerGluAsnTyrLeuGln 100  
|||||  
Db 805 CAGATCTTCAACAATTTGGTCAAACTGAGACATTTTGATTATTCAGAAATTAACCTGGA 864  
Oy 101 LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeu 120  
|||||  
Db 865 AAAGATTGGAATAAGAGCTTTCATGAACTGACAGAGATGAACGCTCTAGAACAGCTTC 924  
Oy 121 ThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerLeuSerSerLeuLys 140  
|||||  
Db 925 ACCGCACTGATGCTGCCCTGGGGCTGTGACGTGCAAGGAGCCTGAGCAGCCTGTTGAA 984  
Oy 141 HisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrArgLeuThrAsp 160  
|||||  
Db 985 CATTGGAGAGAGGTCCCACTCAAGCTGCTCAAGCTTGGAATAAATGAGAGTCAAGAT 1044  
Oy 161 ThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGln 180  
|||||  
Db 1045 ACAGAGATTAGAAATTTAGTGTCATTTTGGAAAGAACCCCTGAAAAACTTCAGCAG 1104  
Oy 181 LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrPheAlaPheMetGlyValPhe 200  
|||||  
Db 1105 TTGAATTTGGCGGGAATCGTGTGAGCAGTGAATGATGGCTTGCTCATGGGTATTT 1164  
Oy 201 GlnAsnLeuLys 204  
|||||  
Db 1165 GAGATCTTAAAG 1176

RESULT 3  
US-09-864-921-98  
; Sequence 98, Application us/09864921  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John C.

;; APPLICANT: Plo, Frederick F.  
;; APPLICANT: Godzik, Adam  
;; APPLICANT: Stehlik, Christian  
;; APPLICANT: Damiano, Jason S.  
;; APPLICANT: Lee, Sug-Hyung  
;; APPLICANT: Oliveira, Vasco A.  
;; APPLICANT: Hayashi, Hideki  
;; APPLICANT: Pawlowski, Krzysztof  
;; TITLE OF INVENTION: Novel Card Domain Containing  
;; TITLE OF INVENTION: Polypeptides, Encoding Nucleic Acids, and Methods of Use  
;; FILE REFERENCE: P-IJ 4752  
;; CURRENT APPLICATION NUMBER: US/09/864,921  
;; PRIOR FILING DATE: 2001-05-23  
;; PRIOR APPLICATION NUMBER: US 09/579,240  
;; PRIOR FILING DATE: 2000-05-24  
;; PRIOR APPLICATION NUMBER: US 09/686,347  
;; PRIOR FILING DATE: 2000-10-10  
;; PRIOR APPLICATION NUMBER: US 60/275,980  
;; PRIOR FILING DATE: 2001-03-14  
;; NUMBER OF SEQ ID NOS: 195  
;; SOFTWARE: FASTSEQ for Windows Version 4.0  
;; SEQ ID NO 98  
;; LENGTH: 1395  
;; TYPE: DNA  
;; ORGANISM: Homo sapien  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: (277)...(1353)  
US-09-864-921-98

## Alignment Scores:

Pred. No.:	5.89e-98	Length:	1395
Score:	1046.00	Matches:	204
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	33	Gaps:	0

US-09-697-089-2\_copy\_762\_965 (1-204) x US-09-864-921-98 (1-1395)

Oy 1 LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAlaIle 20  
|||||  
Db 565 TTGAAGAACCCTTACAAAGCTCATATGATACATTAAGATGATGAAGAGATCTATA 624  
Oy 21 LysLeuAlaGluGlyLeuLysAsnLeuLysMetCysLeuPheHisLeuThrHisLeu 40  
|||||  
Db 625 AAACAGCTGAAGGCTGAAAAACCTGAAGAAGATGTTTATTTTCATTGACCCACTTG 684  
Oy 41 SerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAsp 60  
|||||  
Db 665 TCTGCATTGGAGAGGAGGATGATTACATGATCAAGTCTCTGCAAAATGCAAGTAAATCTAGCT 744  
Oy 61 LeuGluGluIleGlnLeuValSerCysLeuSerSerAlaAsnAlaValLysIleLeuAla 80  
|||||  
Db 745 CTGGAAGAAATTCATTAGTCTCCCTGCTGCTGCTGCAAAATGCAAGTAAATCTAGCT 804  
Oy 81 GlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerSerGluAsnTyrLeuGln 100  
|||||  
Db 805 CAGATCTTCAACAATTTGGTCAAACTGAGACATTTTGATTATTCAGAAATTAACCTGGA 864  
Oy 101 LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeu 120  
|||||  
Db 865 AAAGATTGGAATAAGAGCTTTCATGAACTGACAGAGATGAACGCTCTAGAACAGCTTC 924  
Oy 121 ThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerLeuSerSerLeuLys 140  
|||||  
Db 925 ACCGCACTGATGCTGCCCTGGGGCTGTGACGTGCAAGGAGCCTGAGCAGCCTGTTGAA 984  
Oy 141 HisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrArgLeuThrAsp 160  
|||||  
Db 985 CATTGGAGAGAGGTCCCACTCAAGCTTGGGTTGAAATAAATGAGAGTCAAGAT 1044  
Oy 161 ThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGln 180

```
|||||
Db 1045 ACAAGATTAGAAATTTTGGTCATTTTGGAAAGAACCCCTCGAAACCTCCACAG 1104
Qy 181 Leuasnleu1agiLysAsnArgValSerSeraspGlyTrpLeuAlaPheMetGlyValPhe 200
Db 1105 TTGAATTTGGCGGGAAATCGTGTGAGCAGTGTGATGCTTGCCCTCATGGGTATTT 1164
Qy 201 GluasnleuLys 204
Db 1165 GAGAAATCTTAAG 1176
```

```
RESULT 4
PCT-US00-35017A-416
; Sequence 416, Application PC/TUS0035017A
; GENERAL INFORMATION:
; APPLICANT: Hysseq Inc
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: PCT/US00/35017A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 416
; LENGTH: 2950
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US00-35017A-416
```

```
Alignment Scores:
Pred. No.: 1,51e-97 Length: 2950
Score: 1046.00 Matches: 204
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
```

US-09-697-089-2\_COPY\_762\_965 (1-204) x PCT-US00-35017A-416 (1-2950)

```
Qy 1 LeuLysasnleuThrLysleu1leuMetaspasn1leuLysMetasnGluGluaspAla1le 20
Db 1139 TTGAAGAACCTTACAAAGCTATATGATGATGAATGAAGAAAGAAAGATGCTATA 1198
Qy 21 Lysleu1agiLuglyLeuLysAsnleuLysLysMetCysLeuPheHisleuThrHisleu 40
Db 1199 AAACCTAGCTGAAGGCTGAAAAACCTGAAGAAGATGCTTATTTATTTGATTCACCCACTTG 1258
Qy 41 Serasp1leuGlyGluGlyMetaspTyrlleValLysSerLeuSerSerGluProCysasp 60
Db 1259 TCTGACATTTGAGAGGGAGATGATTACATGCTCAAGCTCTGTCMAAGTGAACCCCTGTAC 1318
Qy 61 LeuGluGlu1leuGlnleuValSerCysCysLeuSerAlaAsnAlaValLys1leuAla 80
Db 1319 CTGGAAGAAATTCATATGATGCTGCTGCTGTGCTGCAAAATGCAAGTAAATCTTACT 1378
Qy 81 GlnasnleuHisasnleuValLysLeuSer1leuAsnleuSerGluAsnTyrlleuGlu 100
Db 1379 CAGAAATCTTCACAATTTTGGTCAAACTGAGCATTTCTTGTATTCAGAAATATTAACCTGAA 1438
Qy 101 LysaspGlyAsnGluAlaLeuHisGluLeu1leuAspArgMetAsnValleuGluGlnleu 120
Db 1439 AAAAGTGAATTAAGAGCTCTTCATGAACTGATCGACAGAGAAAGCTGCTAGACAGCTC 1498
Qy 121 ThrAlaLeuMetLeuProTrpGlyCysaspValGlnGlySerLeuSerSerLeuLeuLys 140
Db 1499 ACCGCACATGATGCTGCCCTGGGGCTGTGTACGTGGAAGGCAACCTGAGAGCCTGTGAAA 1558
Qy 141 HisleuGluGluVal1ProGlnleuValLysleuGlyLeuLysAsnTrpArgLeuThrAsp 160
Db 1559 CATTTGGAGAGGTCCCAACACTGCTCAAGCTTGGGTTGAAAAAACTGAGACTCAGAGAT 1618
```

```
Qy 161 ThrGlu1leuArg1leuLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln 180
Db 1619 ACAGAGATTAGAAATTTTGGTCATTTTGGAAAGAACCCCTCGAAACCTCCACAG 1678
Qy 181 Leuasnleu1agiLysAsnArgValSerSeraspGlyTrpLeuAlaPheMetGlyValPhe 200
Db 1679 TTGAATTTGGCGGGAAATCGTGTGAGCAGTGTGATGCTTGCCCTCATGGGTATTT 1738
Qy 201 GluasnleuLys 204
Db 1739 GAGAAATCTTAAG 1750
```

```
RESULT 5
PCT-US00-29643-3
; Sequence 3, Application PC/TUS0029643
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-136M01
; CURRENT APPLICATION NUMBER: PCT/US00/29643
; CURRENT FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3072
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US00-29643-3
```

```
Alignment Scores:
Pred. No.: 1,59e-97 Length: 3072
Score: 1046.00 Matches: 204
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
```

US-09-697-089-2\_COPY\_762\_965 (1-204) x PCT-US00-29643-3 (1-3072)

```
Qy 1 LeuLysasnleuThrLysleu1leuMetaspasn1leuLysMetasnGluGluaspAla1le 20
Db 2284 TTGAAGAACCTTACAAAGCTATATGATGATGAATGAAGAAAGAAAGATGCTATA 2343
Qy 21 Lysleu1agiLuglyLeuLysAsnleuLysLysMetCysLeuPheHisleuThrHisleu 40
Db 2344 AAACCTAGCTGAAGGCTGAAAAACCTGAAGAAGATGCTTATTTATTTGATTCACCCACTTG 2403
Qy 41 Serasp1leuGlyGluGlyMetaspTyrlleValLysSerLeuSerSerGluProCysasp 60
Db 2404 TCTGACATTTGAGAGGGAGATGATTACATGCTCAAGTCTGTCAAGTGAACCCCTGTGAC 2463
Qy 61 LeuGluGlu1leuGlnleuValSerCysCysLeuSerAlaAsnAlaValLys1leuAla 80
Db 2464 CTGGAAGAAATTCATATGATGCTGCTGCTGTGCTGCAAAATGCAAGTAAATCTTACT 2523
Qy 81 GlnasnleuHisasnleuValLysLeuSer1leuAsnleuSerGluAsnTyrlleuGlu 100
Db 2524 CAGAAATCTTCACAATTTTGGTCAAACTGAGCATTTCTTGTATTCAGAAATATTAACCTGAA 2583
Qy 101 LysaspGlyAsnGluAlaLeuHisGluLeu1leuAspArgMetAsnValleuGluGlnleu 120
Db 2584 AAAAGTGAATTAAGAGCTCTTCATGAACTGATCGACAGAGAAAGCTGCTAGACAGCTC 2643
Qy 121 ThrAlaLeuMetLeuProTrpGlyCysaspValGlnGlySerLeuSerSerLeuLeuLys 140
Db 2644 ACCGCACATGATGCTGCCCTGGGGCTGTGTACGTGGAAGGCAACCTGAGAGCCTGTGAAA 2703
Qy 141 HisleuGluGluVal1ProGlnleuValLysleuGlyLeuLysAsnTrpArgLeuThrAsp 160
Db 2704 CATTTGGAGAGGTCCCAACACTGCTCAAGCTTGGGTTGAAAAAACTGAGACTCAGAGAT 2763
```

Qy	161	ThrcilulearglleleuqlalaphnepheglylsasnpLeuLysAsnphcIncln	180
Db	2764	ACAGAGATTGAAATTTTAGTGCATTTTGGAAAGAACCCCTGTAAAAAATTCACAG	2823
Qy	181	LeuAsnLeuNlaaIlysAsnArgValSerSerAspGlyTTPLeuAlaIaphetclYalphe	200
Db	2824	TTGCAATTTGGCGGGAATCTGTGACACAGTGAATGATGAGCTTGCCCTCATGGGTGTATT	2883
Qy	201	GlusAsnLeuLys	204
Db	2884	GAGAAATCTTTAAG	2895

## RESULT 6

```

US-09-697-089-3
: Sequence 3, Application US/09697089
:
: GENERAL INFORMATION:
:
: APPLICANT: Bertlin, John
:
: APPLICANT: Robison, Keith E.
:
: TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
:
: TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
:
: FILE REFERENCE: 07334-136601
:
: CURRENT APPLICATION NUMBER: US/09/697,089
:
: CURRENT FILING DATE: 2000-10-26
:
: PRIOR APPLICATION NUMBER: US 60/161,822
:
: PRIOR FILING DATE: 1999-10-27
:
: NUMBER OF SEQ ID NOS: 12
:
: SOFTWARE: FastSeq for Windows Version 4.0
:
: SEQ ID NO 3
:
: LENGTH: 3072
:
: TYPE: DNA
:
: ORGANISM: Homo sapiens
:
: US-09-697-089-3

```

### Alignment Scores:

Pred. No.:	1.59e-97	3072
Score:	1046.00	204
Percent Similarity:	100.00%	0
Best local Similarity:	100.00%	0
Query Match:	100.00%	0
DB:	27	0
Gaps:		0

US-09-697-089-2\_COPY\_762\_965 (1-204) x US-09-697-089-3 (1-3072)

OY	1	Leuysasneuthrlystleuilemetaspasnillelysmetasngluinspalalle	20
Db	2284	TTGGAGAACCTTTCACAAAGCTCAATAAGATTAACATMAAGATGAAGAAAGATCTCTATA	2343
OY	21	LysleuailagluilyleuylsasneuleuylsYsmetCysleuPhehisleuthrhisleu	40
Db	2344	AAACTAGCTAAGAGCTGAAAAAACCTCGAAGAAAGATGTGTTTATTTTCATTGTGACCCACTTG	2403
OY	41	SeraspilleglygluylmetaspyrillevalYsserleuSerSergluProcysasp	60
Db	2404	TCTACACTTTGGAGAGGAATGATTCACATAGCAAGATCTCTCAAGTCAAGAACCTGTGAC	2463
OY	61	leugluiluilegineuvalserCysylserSerglisaasalaivalylsleuila	80
Db	2464	CTTGAAACAAATTAATTAAGTCTCTCTCTCTCTGTCGCAATGACAGTGAATAATCTTACT	2523
OY	81	GlnasneuhisasnleuvallylsleuSerileleuaspleuSergluasntryleu	100
Db	2524	CAGAACTTCCAAATTTGGTCAAACTGACACTTCTTGATTATTCAGAAATTAACCTGGA	2583
OY	101	LysaspelyasnclualaleuhsigluLeulleasparMetasnaValleuglu	120
Db	2584	AAAGATGCAATGAACCTCTTCATGAAACGATCGAAGGATGAACGTGTATGAACAGCTC	2643
OY	121	ThrallaleuMetleuProTpyglyCysaspValGlnlySerleuSerSerleu	140
Db	2644	ACCGCACTGATGCTGCCCTGGGGCTTGTGACGTGCAGCAAGCAAGCTTATGCAAGCTGTGGAA	2703
OY	141	HisleuigluValProgluineuvalYlsleuglyleuYasnTTParjleuthrasp	160

D <sub>b</sub>	2704	CATTGGAGGAGGTCCACAACTGCACAAGCTTGCGTTGAATAACTGGAGCACTCACAAT	2763
Q <sub>y</sub>	161	ThrcTulleArGLIELeuGLyAlAPhePheGLYsAsnProLeuLysAsnPheGLInI	180
D <sub>b</sub>	2764	ACAAGAATTTCGAATTTTAGGTGCATTTTTTGGAAAACCCCTGTAATAAACTCCACAG	2823
Q <sub>y</sub>	181	LeuAsnLeuAIGLYsArGVAlSerSerASPGLYrIPLeuAlAPheMetGIyALPhe	200
D <sub>b</sub>	2824	TTCGAATTTGGCGGGAATCGTGTGACACAGATGATGCGCTTCATGGGTATATT	2883
Q <sub>y</sub>	201	GIuAsnLeuLys	204
D <sub>b</sub>	2884	GAGAAATCTTAAG	2895

## RESULT 7

```

US-09-841-739-3
: Sequence 3, Application US/09841739
: GENERAL INFORMATION:
: APPLICANT: Berlin, John
: TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES TH
: FILE REFERENCE: 07334-329001
: CURRENT APPLICATION NUMBER: US/09/841,739
: CURRENT FILING DATE: 2001-08-29
: PRIOR APPLICATION NUMBER: US 09/697,089
: PRIOR FILING DATE: 2000-10-26
: PRIOR APPLICATION NUMBER: US 60/161,822
: PRIOR FILING DATE: 1999-10-27
: NUMBER OF SEQ ID NOS: 16
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 3
: LENGTH: 3072
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-841-739-3

```

**Alignment Scores:**

Pred. No.:	1.59e-97	Length:	3072
Score:	1046.00	Matches:	204
Percent Similarity:	100.00%	Conservative:	0
Best local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	32	Gaps:	0

US-09-697-089-2\_COPY\_762\_965 (1-204) X US-09-841-739-3 (1-3072)

QY	1	L	leuysasneuh	hr	ly	lysleuile	met	asp	asn	lle	lys	met	asn	glu	lna	pal	lle	20
Db	2284	TTG	AAG	ACCTT	ACAAAG	CCATAA	AGGATTAAC	ATAAAGATTAAGAA	GAAGAAGAT	GTATATA							2343	
QY	21	L	lysleu	la	glu	ly	leu	lys	asn	leu	lys	met	cys	leu	phe	his	leu	40
Db	2344	AAACT	ACTAGT	AAGG	CCCTG	AAAAAAC	CTGAAGAGAT	GTGTTTATTT	CAATTG	ACCCACTG							2403	
QY	41	S	er	asp	lle	glu	ly	met	asp	yr	lle	val	lys	ser	leu	ser	ser	60
Db	2404	TCT	GACATTTG	AAGGGA	AGATGATTCAT	AATGCA	AGTCAAGTCTCTG	CAAGTCAAC	CCCTGT	GAC							2463	
QY	61	L	eu	lu	lu	lle	glu	leu	val	ser	cys	cys	leu	ser	ala	asn	ala	80
Db	2464	CTTG	TAACAAATTC	AAATTAG	CTCTCTCTCTCTCTCTCTCTG	CAAAAGCA	AGTAAATTCCT	ACTACT									2523	
QY	81	G	ln	asn	leu	his	asn	leu	val	lys	leu	ser	lle	leu	asp	leu	ser	100
Db	2524	CAG	ATTTTAC	CAATTTTGG	CCAAACTG	AGCATTTCTTG	ATTTCAG	AAAAATTA	CTTG	GGAA							2583	
QY	101	L	ys	asp	le	ys	asn	glu	ala	leu	his	glu	leu	ile	asn	par	met	120
Db	2584	AAA	GATGGA	ATGAA	TGACGCTTCTTCAT	GACATG	ATGCAG	ATGACAGATGA	AGCTGCTGA	ACAGCTC							2643	
QY	121	T	hr	ala	eu	met	leu	pro	trp	gly	cys	asp	val	gln	gly	ser	leu	140
Db	2644	ACC	GCATGT	ATGCTG	CCCTG	GGGCTGTG	ACGTG	CAAGG	CAGGCTT	AGAGGCTGT	GTG	GAA					2703	

QY	141	HisLeuGIuGIuValProGluLeuValLysLeuGIyLeuLysAsnTrpArgLeuThrAsp	160
Db	2704	CATTGGAGGAGGCTCCACACACTGTCAGACTTGGGTTGAAAACGGGAGCTCACAGAT	2763
QY	161	ThrcGluIleArgIleLeuGIyAlaPhePheGIyLysAsnProLeuLysAsnPheGlnGln	180
Db	2764	ACAGAGATTGGAATTTAGGTGCATTTTGGAAAAGAACCCCTGTGAAAACCTTCACAGAG	2823
QY	181	LeuAsnLeuAlaGlyAsnArgValSerSerAspGIyTrpLeuAlaPheMetClyAlaPhe	200
Db	2824	TTGGAATTTGGGGGAAATCTGTGAGCAGATGATGATGGCTTGCCTTCATGGGTATTAT	2883
QY	201	GluAsnLeuLys	204
Db	2884	GAGAACTCTTAAG	2895
RESULT 8			
US-10-156-733-1			
: Sequence 1, Application US/10156733			
: GENERAL INFORMATION:			
: APPLICANT: Alnemrl, Emed S.			
: TITLE OF INVENTION: IPAP, AN ICE-PROTEASE ACTIVATING			
: FILE REFERENCE: FACTOR			
: CURRENT APPLICATION NUMBER: US/10/156,733			
: CURRENT FILING DATE: 2002-05-24			
: NUMBER OF SEQ. ID NOS: 14			
: SOFTWARE: FastSeq for Windows Version 4.0			
: SEQ. ID NO 1			
: LENGTH: 3075			
: TYPE: DNA			
: ORGANISM: Homo sapiens			
: FEATURE:			
: NAME/KEY: CDS			
: LOCATION: (1)...(3075)			
US-10-156-733-1			
Alignment Scores:			
Pred. No.: 1,59e-97			
Score: 1046,00			
Percent Similarity: 100,00%			
Best Local Similarity: 100,00%			
Query Match: 100,00%			
DB: 41			
US-09-697-089-2_COPY_762_965 (1-204) x US-10-156-733-1 (1-3075)			
QY	1	LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluLysPAlaIle	20
Db	2284	TTTGAGAGAACTTACCAAAAGCCCAATTAATGATTAACATTAAGATTAAGAAGAAAGATCTCTATA	2343
QY	21	LysLeuAlaGluGlyLeuLysAsnLeuLysMetCysLeuPheHisLeuThrHisLeu	40
Db	2344	AAATCTAGCTGAAGGCCCTGAAAAACCTGAAGAGAGATGTGTTTATTTTCATTTGACCCACTTG	2403
QY	41	SerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGlnProCysAsp	60
Db	2404	TCTGACATTTGGAGAGGGAATGATTTACATAGTCAAGTCTCTGTCAAGGAAACCCGTGTAC	2463
QY	61	LeuGluGluIleGlnLeuValSerCysGlySerSerAlaAsnAlaValLysIleLeuAla	80
Db	2464	CTTTGAAGAAATTCAAATTAAAGTCTCTCTCTCTGTCTGCAAAAGCAGGTGAAATCTTACT	2523
QY	81	GlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGlnAsnTrpTyrLeuGln	100
Db	2524	CAGAACTTTCACAAATTTGGTCAAACTGAGCATTTCTTGATTATTCAGAAAATTAATCTGAA	2583
QY	101	LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeu	120
Db	2584	AAAGATGGAATGAAGCTCTTCATGAACATGATGACGAGATGAAGATGAAGCTGTGAACAAGCTC	2643
QY	121	ThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeuLys	140

Db	2644	ACGGCATGATGCTGGCCCTGGGGCTGTGACGTGTCAAGCAGCGCTGAGCGCTGTGGAA	2703
QY	141	HisLeuGIuGIuValProGInLeuValLysLeuGIyLeuLysAsnTTrpArgLeuThraSp	160
Db	2704	CATTGGAGAGGCGCCACACACTGCTCAAGCTGTGGGTTAAAACTGAGACTCACAGAT	2763
QY	161	ThrGluLeuArgTLeuGIuValAlphePheGlyLysAsnProLeuLysAsnPhedInGIn	180
Db	2764	ACAGAGATTGGAATTTAGGTGGATTTTTTGGAAAGAACCTCTGAAAACTTCCAGCAG	2823
QY	181	LeuAsnLeuAlaGIyLysAsnArgValSerSerAspGIyTrpLeuAlAlpheMetGIyAlPhe	200
Db	2824	TTGAATTTGGCGGGAATCTGTGACAGATGATGATGCTTGCCATTATGGGTATATT	2883
QY	201	GIuAsnLeuLys 204	
Db	2884	GAGAACTCTTAAG 2895	
RESULT 9			
PCT-US00-29643-1			
: Sequence 1, Application PCT/TUS0029643			
: GENERAL INFORMATION:			
: APPLICANT: Millennium Pharmaceuticals, Inc.			
: TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED			
: TITLE OF INVENTION: PROTEIN FAMILY AND USGS THEREOF			
: FILE REFERENCE: 07334-136M01			
: CURRENT APPLICATION NUMBER: PCT/US00/29643			
: PRIOR FILING DATE: 2000-10-26			
: PRIOR APPLICATION NUMBER: US 60/161,822			
: PRIOR FILING DATE: 1999-10-27			
: NUMBER OF SEQ. ID NOS: 11			
: SOFTWARE: FastSeq for Windows Version 4.0			
: SEQ ID NO 1			
: LENGTH: 3133			
: TYPE: DNA			
: ORGANISM: Homo sapiens			
: FEATURE:			
: NAME/KEY: CDS			
: LOCATION: (36)...(3107)			
PCT-US00-29643-1			
Alignment Scores:			
Pred. No.: 1 63e-97 Length: 3133			
Score: 1046.00 Matches: 204			
Percent Similarity: 100.00% Conservative: 0			
Best Local Similarity: 100.00% Mismatches: 0			
Query Match: 100.00% Indels: 0			
DB: 1 Gaps: 0			
US-09-697-089-2_COPY_762_965 (1-204) x PCT-US00-29643-1 (1-3133)			
QY	1	LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGIuGIuAspAlaIle	20
Db	2319	TTGAGAGAACTTACAAAGCTCAATATGATTAACATTAAGATGAAGAAGATGCTATA	2378
QY	21	LysLeuAlaGIuGIyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu	40
Db	2379	AAATACTCTGAAGGCGTGAAGAAACCTGGAAGAAGATGTGTTATTCATTGACCCACTTG	2438
QY	41	SerAspIleGIyGIuGIyMetAspTrpTyrIleValLysSerLeuSerGIuProCysAsp	60
Db	2439	TCTGTACATTGGAGGGGAATGATTTCAATAGTCAAGTCTCTGTCAAGTCAACCTGTGAC	2498
QY	61	LeuGIuGIuIleGInLeuValSerCysCysLeuSerAlaAsnAlValLysIleLeuAla	80
Db	2499	CTTGAAGAAATTCATATTAGTCTCTGCTGCTGTGTCTGCAAAATGCAGTGAANAATCTACCT	2558
QY	81	GIuAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGIuAsnTyrLeuGIu	100
Db	2559	CAGAAATCTTCACAATTGGTGGCAAACTGAGAGATCTTGATTATTCAGAAAAATTAAGTGGAA	2618
QY	101	LysAspGIyAsnGIuAlaLeuHisGIuLeuIleAspArgMetAsnValLeuGIuGIuLeu	120

|||||  
Db 2619 AAGATGGAATGAAAGCTTCATGACACTGATCGACAGATGAAGCTGCTAGAACAGCTC 2678  
Oy 121 ThrAlaLeuMetLeuProTfPglYcysAspValGlnGlySerLeuSerSerLeuLeuLys 140  
Db 2679 ACCGACTGAAATGAAAGCTTCATGACACTGATCGACAGATGAAGCTGCTAGAACAGCTC 2738  
Oy 141 HisLeuGlnGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThrAsp 160  
Db 2739 CATTTGGAGGAGGTCCACAACTGCTCAAGCTTGGGTTGAAAACCTGGAGACTCACAGAT 2798  
Oy 161 ThrGluIleArgIleLeuGlnValAlaPhePheGlyLysAsnProLeuLysAsnPhelGln 180  
Db 2799 ACAGAGATTAGAAATTTTGGTGCATTTTGGAAAGAACCTCTGAAAACTCCAGCAG 2858  
Oy 181 LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGlyValPhe 200  
Db 2859 TTGAATTTGGCGGAAATCGTGTGAGCAGTGTGATGCTGCTTCATGGGTGTATTT 2918  
Oy 201 GluAsnLeuLys 204  
Db 2919 GAGAACTTTAAG 2930

## RESULT 10

US-09-697-089-1  
; Sequence 1, Application US/09697089  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; APPLICANT: Robison, Keith E.  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED  
; FILE REFERENCE: 07334-136001  
; CURRENT APPLICATION NUMBER: US/09/697, 089  
; CURRENT FILING DATE: 2000-10-26  
; PRIOR APPLICATION NUMBER: US 60/161,822  
; PRIOR FILING DATE: 1999-10-27  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 3133  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (36)...(3107)  
US-09-697-089-1

## Alignment Scores:

Pred. No.:	1,63e-97	Length:	3133
Score:	1046.00	Matches:	204
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	27	Gaps:	0

US-09-697-089-2\_COPY\_762\_965 (1-204) x US-09-697-089-1 (1-3133)

Oy 1 LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGlnGluAspAlaIle 20  
Db 2319 TTGAAGAAGCTTACAAAGCTCATATATGATTAACATTAAGATGAAGAGATGCTATATA 2378  
Oy 21 LysLeuAlaGlnGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu 40  
Db 2379 AAACCTAGCTGAAGGCCCTGAAAAAAGCTGAAGAAGATGTGTTTATTTTCATTTTGACCCACTTG 2438  
Oy 41 SerAspIleGlyGlnGlyMetAspTrpIleValLysSerLeuSerSerGluProCysAsp 60  
Db 2439 TCTGCATTTGGAGAGGAAATGATGATTACATAGTCAAGTCTCTGTCAAGTGAACCCCTGTGAC 2498  
Oy 61 LeuGlnGluIleGlnLeuValSerCysLeuSerAlaAsnAlaValLysIleLeuAla 80  
Db 2499 CTTGAAGAAATTCATATAGTCTCTGCTGCTGCTGCAAAATGACGTAAGTAAATCTTACTACT 2558

Oy 81 GluAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTrpLeuGlu 100  
Db 2559 CAGAACTTTCACAAATTTGGTCAAACTGACATTTTGATTTATTCGAAAAATTAAGCTGAAA 2618  
Oy 101 LysAspGlyAsnGlnValAlaLeuHisGlnLeuIleAspArgMetAsnValLeuGlnLeu 120  
Db 2619 AAGATGGAATGAAAGCTTCATGACACTGATCGACAGATGAAGTGTGTAGAACAGCTC 2678  
Oy 121 ThrAlaLeuMetLeuProTfPglYcysAspValGlnGlySerLeuSerSerLeuLeuLys 140  
Db 2679 ACCGACTGAAATGAAAGCTTCATGACACTGATCGACAGATGAAGCTGCTAGAACAGCTC 2738  
Oy 141 HisLeuGlnGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThrAsp 160  
Db 2739 CATTTGGAGGAGGTCCACAACTGCTCAAGCTTGGGTTGAAAACCTGGAGACTCACAGAT 2798  
Oy 161 ThrGluIleArgIleLeuGlnValAlaPhePheGlyLysAsnProLeuLysAsnPhelGln 180  
Db 2799 ACAGAGATTAGAAATTTTGGTGCATTTTGGAAAGAACCTCTGAAAACTCCAGCAG 2858  
Oy 181 LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGlyValPhe 200  
Db 2859 TTGAATTTGGCGGAAATCGTGTGAGCAGTGTGATGCTGCTTCATGGGTGTATTT 2918  
Oy 201 GluAsnLeuLys 204  
Db 2919 GAGAACTTTAAG 2930

## RESULT 11

US-09-841-739-1  
; Sequence 1, Application US/09841739  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES TH  
; FILE REFERENCE: 07334-329001  
; CURRENT APPLICATION NUMBER: US/09/841, 739  
; CURRENT FILING DATE: 2001-08-29  
; PRIOR APPLICATION NUMBER: US 09/697, 089  
; PRIOR FILING DATE: 2000-10-26  
; PRIOR APPLICATION NUMBER: US 60/161,822  
; PRIOR FILING DATE: 1999-10-27  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 3133  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (36)...(3107)  
US-09-841-739-1

## Alignment Scores:

Pred. No.:	1,63e-97	Length:	3133
Score:	1046.00	Matches:	204
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	32	Gaps:	0

US-09-697-089-2\_COPY\_762\_965 (1-204) x US-09-841-739-1 (1-3133)

Oy 1 LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGlnGluAspAlaIle 20  
Db 2319 TTGAAGAAGCTTACAAAGCTCATATATGATTAACATTAAGATGAAGAGATGCTATATA 2378  
Oy 21 LysLeuAlaGlnGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu 40  
Db 2379 AAACCTAGCTGAAGGCCCTGAAAAAAGCTGAAGAAGATGTGTTTATTTTCATTTTGACCCACTTG 2438  
Oy 41 SerAspIleGlyGlnGlyMetAspTrpIleValLysSerLeuSerSerGluProCysAsp 60  
Db 2439 TCTGCATTTGGAGAGGAAATGATGATTACATAGTCAAGTCTCTGTCAAGTGAACCCCTGTGAC 2498

Oy	61	LeuIleuIuIleGInleuValSerCysCysLeuSerAlaAsnAlaValysIleLeuIla	80
Db	2499	CTTAAGAAANTCATTTAGTCTCTGCTGCTTCTGCAAAATGACGTGAAATCTTACT	2558
Oy	81	GlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGlnAsnTrpLeuIu	100
Db	2559	CAGATCTTCACAAATTTGGTCAAACTGAGCATCTTGATTATTCAGAAATTAATCTGCA	2618
Oy	101	LysAspGlyAsnGluValAlaLeuHisGluLeuIleAspArgMetAsnValLeuIuIuLeu	120
Db	2619	AAAGTTGGAAATGACGCTCTTCATGCACTGATGCACAGATGACGCTGTAGACAGCTC	2678
Oy	121	ThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeuLys	140
Db	2679	ACCCCATCGATGCTGCCCTGGGGCTGTGACGTGCACGACGAGCTGACGCTGTGGAA	2738
Oy	141	HisLeuGlnGluValProGlnLeuLeuValLysLeuGlyLeuLeuLysAsnTrpArgLeuThr	160
Db	2739	CATTGGAGGGAGGCTCCACACACTGTCACGCTTGGGTTGATAAAACCTGGAGACTCCACA	2798
Oy	161	ThrGluLeuArgIleLeuGlnGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGln	180
Db	2799	ACAGAGATTGGAATTTAGTGCATTTTTTGGAAAAACCCCTGTGAAAAACTTCCAGCAG	2858
Oy	181	LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGlyValPhe	200
Db	2859	TTTGATTGGGGGGCAAACTCTGTGACACAGTGAATGATGCTTGCCTCATGGGTATATT	2918
Oy	201	GlnAsnLeuLys 204	
Db	2919	GAGAACTCTTAAG 2930	

```

RESULT 12
US-09-471-275-7095
Sequence 7095, Application US/09471275
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: Novel Contigs Obtained
TITLE OF INVENTION: From Various Libraries
FILE REFERENCE: 782
CURRENT APPLICATION NUMBER: US/09/471,275
CURRENT FILING DATE: 1999-12-23
EARLIER APPLICATION NUMBER: US 09/235,076
EARLIER FILING DATE: 1999-01-20
EARLIER APPLICATION NUMBER: US 09/234,611
EARLIER FILING DATE: 1999-01-22
EARLIER APPLICATION NUMBER: US 09/240,371
EARLIER FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: US 09/277,227
EARLIER FILING DATE: 1999-03-25
EARLIER APPLICATION NUMBER: US 09/271,490
EARLIER FILING DATE: 1999-03-18
EARLIER APPLICATION NUMBER: US 09/293,972
EARLIER FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: US 09/274,861
EARLIER FILING DATE: 1999-03-23
EARLIER APPLICATION NUMBER: US 60/125,453
EARLIER FILING DATE: 1999-03-19
EARLIER APPLICATION NUMBER: US 60/126,605
EARLIER FILING DATE: 1999-03-26
EARLIER APPLICATION NUMBER: US 09/306,350
EARLIER FILING DATE: 1999-05-07
EARLIER APPLICATION NUMBER: US 09/399,720
EARLIER FILING DATE: 1999-09-21
EARLIER APPLICATION NUMBER: US 09/404,284
EARLIER FILING DATE: 1999-09-21
EARLIER APPLICATION NUMBER:
EARLIER FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 10451
SOFTWARE: pt_ct_genes Version 1.0
SEQ ID NO 7095
LENGTH: 3152

```

```

? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (20)..(1903)
? OTHER INFORMATION: similar to g15933010 in the genepept database release 114
? OTHER INFORMATION: Run with FASTX 3.3c00, default parameters
US-09-471-275-7095

```

Alignment Scores:	
Pred. No.:	1.64e-97
Score:	1046.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
Ds:	18
Length:	315
Matches:	204
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-697-089-2\_COPY\_762\_965 (1-204) X US-09-471-275-7095 (1-3152)

Oy	1	Leuysasneutrrtlysleuilemetasasnilleymetasniglunspalalle	20
Db	1139	TTGAGAACCTTCACAAAGCTCATATGGATACATATAATGATGATGAGAGATCTCTA	11398
Oy	21	LysleuAlaagllyleuLysAsnleuLysMetCysleuPhehisleuthrisleu	40
Db	1199	AAACTAGCTGAGCCCGAAAAACCTGAGAGAGATGTGTTATTCATTATGACCCACTTG	1258
Oy	41	SeraspilleglygluylmetaspyrillevalysSerleuSerSerGIuProCysp	60
Db	1259	TCTGACATTTGGAGGGGAATGATTCATAGTCACACTCTCTGCAAGTGAAACCCGTGTAC	1318
Oy	61	LeugluguilleginleuValSerCysCysleuSerAlaAsnAlValyslleuAla	80
Db	1319	CTTAGAGAAATTCATTATGATGCTCTGCTGCTGTCTGTGCAAAATGCAAGTAATCTTACT	1378
Oy	81	GlinsnleuHisAsnleuValLysleuSerIleleuAspLeuSerGIuAsnTyrleuGlu	100
Db	1379	CAGATCTTCACATTTTGGTCAAACTGAGACTTCTTGATTTTCAGAAAAATTAACCTGGA	1438
Oy	101	LysaspelysngualaleuHisgluleuIleaspArgMetAsnValleuglunleu	120
Db	1439	AAAGATGGAATGAAAGCTCTTCATGAAACGATGACAGATGAACGTGCTAGAACACCTC	1498
Oy	121	ThrAlaleuMetleuProTrrpGIyCysAspValGlnGlySerleuSerSerleuLeuys	140
Db	1499	ACCACATGAGTGCCTGGCTTGGCTGTGAGCTGCAAGGAGCCTGAGCGCCTGTGTGAA	1558
Oy	141	HisleugluguValProginleuValLysleuGlyLeuLysAsnTrrpArgleuthrasp	160
Db	1559	CATTGGAGGAGGTCCCAACACTGTCAGACTTGGGTAAAAAATCTGAGACTCAAAAT	1618
Oy	161	ThrcuIleArgIleleuGlyAlaPhePheGlyLysAsnProleuLysAsnPheGlnGlu	180
Db	1619	ACAAGAGTTAGAAATTTAGTGCATTTTTTGGAAAAAACCTCTGAAAAAATCTCCAGAG	1678
Oy	181	LeuAsnleuAlaGlyAsnArgValSerSerAspGIyTrrleuAlaPheMetGlyAlaPhe	200
Db	1679	TTGATTTGGCGGGAAATCTGTGACACAGATGATGATGCTTGCCCTCATGGGTGTATTT	1738
Oy	201	GlusnleuLys 204	
Db	1739	GAGATCTTAAG 1750	
RESULT 13			
PCT-US01-07143-23			
; Sequence 23, Application PC/TUS0107143			
; GENERAL INFORMATION:			
; APPLICANT: SMITHKLINE BEECHAM CORPORATION			
; APPLICANT: SMITHKLINE BEECHAM P.1.C.			
; TITLE OF INVENTION: NOVEL COMPOUNDS			
; FILE REFERENCE: GP50016			
; CURRENT APPLICATION NUMBER: PCT/US01/07143			
; CURRENT FILING DATE: 2001-03-08			



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; PRIOR APPLICATION NUMBER: 60/187,107
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/236,874
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/188,916
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/237,846
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 3213
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-07143-23

Alignment Scores:
Pred. No.: 1,686-97      Length: 3213
Score: 1046.00          Matches: 204
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
DB: 1                      Gaps: 0

US-09-697-089-2_COPY_762_965 (1-204) x PCT-US01-07143-23 (1-3213)
QY 1 LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAlaIle 20
DB 2422 TTGAAGAACCTTACAAAGCTCAATGATACATTAAGATGAATGAAGATGCTATA 2481
QY 21 LysIleuAlaGluGluLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu 40
DB 2482 AACACTAGCTGAAGGCGCTGAAAAACCTGAAGAGATGTGTTATTCATTGACCCACTG 2541
QY 41 SerAspIleGluGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAsp 60
DB 2542 TCTGACATTGGAGAGGATGATGATACATGCAAGTCTCTCAAGTGAACCTGTGAC 2601
QY 61 LeuGluGluIleGlnLeuValSerCysLeuSerAlaAsnAlaValLysIleLeuAla 80
DB 2602 CTTGAAGAAATTCATATGATCTCTGCTGCTGCTGCAAAATGAGTGAATCCTAGCT 2661
QY 81 GlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu 100
DB 2662 CAGATCTTCACAAATTTGGTCAACTGACCATTTGATTATTCGAAAAATTAACCTGGA 2721
QY 101 LysAspGluAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGluLeu 120
DB 2722 AAAGATGGAATGAAGCTCTTCATGACATGACAGATGACAGTGTCTAGAACAGCTC 2781
QY 121 ThrAlaLeuMetLeuProTropGlyCysAspValGlnGlySerLeuSerSerLeuLeuLys 140
DB 2782 ACCGCACTGATGCTGCTCCCTGGGGCTGTGACGTGCAAGGAGCGCTGAGCGCTGTGAAA 2841
QY 141 HisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrArgLeuThrAsp 160
DB 2842 CATTGGAGAGAGTCCCACTCACTGCTGAGCTTGGGTTGAAAACTGGAGACTCACAGAT 2901
QY 161 ThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGln 180
DB 2902 ACAGAGATTAGAAATTTAGTGCATTTTGGAAAAACCTCTGAAAAAATTCCAGCAG 2961
QY 181 LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrPheAlaPheMetLysValPhe 200
DB 2962 TTGAATTTGGCGGGAATTCGTGTGACAGTGTGATGATGAGCTTGCTTCATGGGTGATTT 3021
QY 201 GlnAsnLeuLys 204
DB 3022 GAGAAATCTTAAG 3033

RESULT 14
US-10-221-097-23
; Sequence 23, Application US/10221097
```

```
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdoch, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall F.
; APPLICANT: Xiang, Zhaoying
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50016
; CURRENT APPLICATION NUMBER: US/10/221,097
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: PCT/US01/07143
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/187,107
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/236,874
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/188,916
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/237,846
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 3213
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-221-097-23

Alignment Scores:
Pred. No.: 1,686-97      Length: 3213
Score: 1046.00          Matches: 204
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
DB: 42                      Gaps: 0

US-09-697-089-2_COPY_762_965 (1-204) x US-10-221-097-23 (1-3213)
QY 1 LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAlaIle 20
DB 2422 TTGAAGAACCTTACAAAGCTCAATGATGATACATTAAGATGAATGAAGATGCTATA 2481
QY 21 LysIleuAlaGluGluLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu 40
DB 2482 AACACTAGCTGAAGGCGCTGAAAAACCTGAAGAGATGTGTTATTCATTGACCCACTG 2541
QY 41 SerAspIleGluGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAsp 60
DB 2542 TCTGACATTGGAGAGGATGATGATACATGCAAGTCTCTCAAGTGAACCTGTGAC 2601
QY 61 LeuGluGluIleGlnLeuValSerCysLeuSerAlaAsnAlaValLysIleLeuAla 80
DB 2602 CTTGAAGAAATTCATATGATCTCTGCTGCTGCTGCAAAATGAGTGAATCCTAGCT 2661
QY 81 GlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu 100
DB 2662 CAGATCTTCACAAATTTGGTCAACTGACCATTTGATTATTCGAAAAATTAACCTGGA 2721
QY 101 LysAspGluAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGluLeu 120
DB 2722 AAAGATGGAATGAAGCTCTTCATGACATGACAGATGACAGTGTCTAGAACAGCTC 2781
QY 121 ThrAlaLeuMetLeuProTropGlyCysAspValGlnGlySerLeuSerSerLeuLeuLys 140
DB 2782 ACCGCACTGATGCTGCTCCCTGGGGCTGTGACGTGCAAGGAGCGCTGAGCGCTGTGAAA 2841
QY 141 HisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrArgLeuThrAsp 160
DB 2842 CATTGGAGAGAGTCCCACTCACTGCTGAGCTTGGGTTGAAAACTGGAGACTCACAGAT 2901
QY 161 ThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGln 180
DB 2902 ACAGAGATTAGAAATTTAGTGCATTTTGGAAAAACCTCTGAAAAAATTCCAGCAG 2961
```



Oy	181	LeuhsnleuualaglYasnaArgValSerSeraSPGLyTPrleuAlaphmetelYalPhe	200
Dd	2962	TTGAATTTGGCGGGAATACTGTGTAGCAGTGAGATGAGCTTCCTCATGGGCTATT	3021
Oy	201	GlusnleuLys 204 	
Dd	3022	GAGAATCTTAG 3033	
RESULT 15			
US-10-156-733-14			
; Sequence 14, Application US/10156733			
; GENERAL INFORMATION:			
; APPLICANT : Alnemir, Emad S.			
; TITLE OF INVENTION: IPAF AN ICE -PROTEASE ACTIVATING			
; TITLE OF INVENTION: FACTOR			
; FILE REFERENCE: 4B0140.477			
; CURRENT APPLICATION NUMBER: US/10/156,733			
; CURRENT FILING DATE: 2002-05-24			
; NUMBER OF SEQ ID NOS: 14			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 14			
; LENGTH: 3219			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-156-733-14			
Alignment Scores:			
Pred. No.: 1,69e-97 Length: 3219			
Score: 1046.00 Matches: 204			
Percent Similarity: 100.00% Conservative: 0			
Best Local Similarity: 100.00% Mismatches: 0			
Query Match: 100.00% Indels: 0			
DB: 41 Gaps: 0			
US-09-697-089-2_COPY_762_965 (1-204) x US-10-156-733-14 (1-3219)			
Oy	1	LeuYsaSnleuThrLyLSleuIImetAsPaSnIlleYsMeFaSnglunPalatle	20
Dd	2428	TTGAGAAACCTTACAAGCTCATATGATTAACATTAAGATGAATGAAGAGATCTATA	2487
Oy	21	LysLeuAInagluLYleuLYSaSnleuLYsMetCYsLeuPhenHisLeuthrHisLeu	40
Dd	2488	AAACTAGCTGAAGCCCTGAAAACCCTGAAGAAGATGTGTTATTCATTATGGACCACTTG	2547
Oy	41	SeraspIleglyugLYmetAsPryIlleValLYserLeuSerSercIuProCyasp	60
Dd	2548	TCTGACATTTGGAGGGGAAGATGTACATAGTCAACTCTGTCAAAGTGAACCCGTGAC	2607
Oy	61	LeuGlunGIleGlnLeuValSerCYsCYsLeuSerAlaSnAlaValYsIlleLeuAla	80
Dd	2608	CTTGAGAAATTCATTATTAAGTCTCTGCTGCTTGTCTGCAGAAATGCAOTGAAATCTACT	2667
Oy	81	GlnAsnLeuHisAsnLeuValLYsLeuSerIlleLeuAsPlenSercIuAsnTYrLeuGlu	100
Dd	2668	CAGATCTTCCACATTTTGGTCCAACCTGACGATCTTGATTTTTCAGAAAAATTACTGGAA	2727
Oy	101	LYSaSpGIYaSnglUAlaleuHISgluleuIIeaSPArMeFaSnValleunglunleu	120
Dd	2728	AAGATGGAAATGAAGCTCTTCATGAACCTGATGACAGATGAGATGACGTGTAGAACGCTC	2787
Oy	121	ThraLaeuMetleuProTPrgLYcyaSPVaIGlngLYserLeuSerSerLeuLeuLYs	140
Dd	2788	ACCGACGATGAGCTGCCCTGGGGCTGTGAGCTGCAAGCAGCCTAGCAGCCTGTGGAA	2847
Oy	141	HISleuGluGluVALProGlnLeuValLYsLeuGlyLeuLYsAsnTrpArgLeuThrASP	160
Dd	2848	CATTGGAGGAGGCTCCCAACAACCTGCTCAAGCTTGCTGTAAGAAACCTGAGACTCACAGAT	2907
Oy	161	ThrcIuileArgIleleuGlyAlaIlePheGlyLYsaSPProLeuLYsaSnPheGlnIu	180
Dd	2908	ACAAGATTTGAATTTTAAGTGCATTTTTTGGAAAGAACCCCTGTGAAAACTTCAGAG	2967

GenCore version 5.1.3  
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OM protein - nucleic search, using frame\_plus.p2n model

Run on: January 31, 2003, 13:24:32 ; Search time 191.895 Seconds  
(without alignments)  
1295.994 Million cell updates/sec

Title: US-09-697-089-2\_COPY\_762\_965

Perfect score: 1046  
Sequence: 1 LKNLTKLIMDKMNEEDAI.....GNRVSSDDGLAFMGVFENLK 204

Scoring table:

BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 2500250 seqs, 609544256 residues

Total number of hits satisfying chosen parameters: 5000500

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame\_plus.model -DEV=xlh  
-Q=/cgn2\_1/USPTO\_spool/US09697089/runat\_29012003\_092755\_19775/app\_query.fasta.1.981  
-DB=Pending\_Patents\_NA\_New -OFMT=fastap -SUFFIX=p2n.inpn -MINMATCH=0.1  
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsu62  
-TRANS=human0.cdi -LIST=45 -DOCALL=200 -THR SCORE=pcr -THR\_MAX=100  
-THR\_MIN=0 -ALLEN=15 -MODE=LOCAL -OUTFMT=ptc -NOR=ext -HEAPSIZE=500 -MILEN=0  
-MAXLEN=2000000000 -USER=US09697089\_@CGN\_1.1.91\_etunat\_29012003\_092755\_19775  
-NCPD=6 -ICPD=3 -NO\_XLPHY -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCAPOP=6  
-FCAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Pending\_Patents\_NA\_New.\*  
1: /cgn2\_6/ptodata/2/pna/PCF\_NEW\_COMB.seq.\*  
2: /cgn2\_6/ptodata/2/pna/US06\_NEW\_COMB.seq.\*  
3: /cgn2\_6/ptodata/2/pna/US07\_NEW\_COMB.seq.\*  
4: /cgn2\_6/ptodata/2/pna/US08\_NEW\_COMB.seq.\*  
5: /cgn2\_6/ptodata/2/pna/US09\_NEW\_COMB.seq.\*  
6: /cgn2\_6/ptodata/2/pna/US10\_NEW\_COMB.seq.\*  
7: /cgn2\_6/ptodata/2/pna/US60\_NEW\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1046	100.0	3075	1	PCF-US02-21946A-1
2	1046	100.0	3219	1	PCF-US02-21946A-14
3	1046	100.0	3545	6	US-10-276-781-111
4	202	19.3	421	6	US-10-203-138A-4307
5	126	12.0	2142	6	US-10-161-493-5
6	120.5	11.5	8722	6	US-10-194-163-263
7	118	11.3	916	5	US-09-724-676-19376
8	118	11.3	916	5	US-09-724-676A-19376
9	118	11.3	945	5	US-09-724-676-19370
10	118	11.3	945	5	US-09-724-676A-19370
11	118	11.3	1012	5	US-09-724-676-19364

12	118	11.3	1012	5	US-09-724-676A-19364	Sequence 19364, A
13	118	11.3	1103	5	US-09-724-676-19382	Sequence 19382, A
14	118	11.3	1103	5	US-09-724-676A-19382	Sequence 19382, A
15	118	11.3	1132	5	US-09-724-676-19395	Sequence 19395, A
16	118	11.3	1132	5	US-09-724-676A-19395	Sequence 19395, A
17	118	11.3	1170	5	US-09-724-676-19390	Sequence 19390, A
18	118	11.3	1170	5	US-09-724-676A-19390	Sequence 19390, A
19	118	11.3	1176	5	US-09-724-676-19375	Sequence 19375, A
20	118	11.3	1176	5	US-09-724-676A-19375	Sequence 19375, A
21	118	11.3	1199	5	US-09-724-676-19359	Sequence 19359, A
22	118	11.3	1199	5	US-09-724-676A-19359	Sequence 19359, A
23	118	11.3	1205	5	US-09-724-676-19369	Sequence 19369, A
24	118	11.3	1205	5	US-09-724-676A-19369	Sequence 19369, A
25	118	11.3	1272	5	US-09-724-676-19363	Sequence 19363, A
26	118	11.3	1272	5	US-09-724-676A-19363	Sequence 19363, A
27	118	11.3	1363	5	US-09-724-676-19380	Sequence 19380, A
28	118	11.3	1363	5	US-09-724-676A-19380	Sequence 19380, A
29	118	11.3	1392	5	US-09-724-676-19394	Sequence 19394, A
30	118	11.3	1392	5	US-09-724-676A-19394	Sequence 19394, A
31	118	11.3	1430	5	US-09-724-676-19389	Sequence 19389, A
32	118	11.3	1430	5	US-09-724-676A-19389	Sequence 19389, A
33	118	11.3	1459	5	US-09-724-676-19358	Sequence 19358, A
34	118	11.3	1459	5	US-09-724-676A-19358	Sequence 19358, A
35	118	11.3	1489	5	US-09-724-676-19373	Sequence 19373, A
36	118	11.3	1489	5	US-09-724-676A-19373	Sequence 19373, A
37	118	11.3	1518	5	US-09-724-676-19367	Sequence 19367, A
38	118	11.3	1518	5	US-09-724-676A-19367	Sequence 19367, A
39	118	11.3	1585	5	US-09-724-676-19361	Sequence 19361, A
40	118	11.3	1585	5	US-09-724-676A-19361	Sequence 19361, A
41	118	11.3	1645	5	US-09-724-676-19374	Sequence 19374, A
42	118	11.3	1645	5	US-09-724-676A-19374	Sequence 19374, A
43	118	11.3	1674	5	US-09-724-676-19368	Sequence 19368, A
44	118	11.3	1674	5	US-09-724-676A-19368	Sequence 19368, A
45	118	11.3	1676	5	US-09-724-676-19378	Sequence 19378, A

#### ALIGNMENTS

RESULT 1  
PCF-US02-21946A-1  
; Sequence 1, Application PC/TUS0221946A  
; GENERAL INFORMATION:  
; APPLICANT: Alnemri, Emad S.  
; TITLE OF INVENTION: IPAF, AN ICE-PROTEASE ACTIVATING  
; FILE REFERENCE: 480140.477PC  
; CURRENT APPLICATION NUMBER: PCF-US02/21946A  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 3075  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(3075)  
PCF-US02-21946A-1

#### Alignment Scores:

Pred. No.: 9.43e-109  
Score: 1046.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
DB: 1  
Length: 3075  
Matches: 204  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Gaps: 0

US-09-697-089-2\_COPY\_762\_965 (1-204) x PCF-US02-21946A-1 (1-3075)

0Y 1 LeuLYASnleuThrylsleuilemetaspasnielysMeAsnclnclunspIarle 20  
DB 2284 TTGAGAACCTTCAACAGCTCAATGATTAACATTAAGATCAATGAGAACGATCTATA 2343

QY 21 LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu 40  
|||||  
Db 2344 AACACTAGCTGAAGGCGCTGAAAAACCTGAGAGAGATGTGTTTATTTTCATTGACCCACTTG 2403  
QY 41 SerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAsp 60  
|||||  
Db 2404 TCTGACATTTGGAGAGGAGGATGATTCATAGTCAGTCTCTGTCAGTGAACCTGTCAG 2463  
QY 61 LeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAla 80  
|||||  
Db 2464 CTGGAAGAAATTCATTAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2523  
QY 81 GlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu 100  
|||||  
Db 2524 CAGAATCTTCACAAATTTGGTCAAACTGACGACATTTGATTATTCAGAAAATTAACCTGGA 2583  
QY 101 LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeu 120  
|||||  
Db 2584 AAGAGTGGAAATGAAGCTCTTCATGAACTGACAGATGAACCTGCTAGAACAGCTC 2643  
QY 121 ThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeuLys 140  
|||||  
Db 2644 ACCGCACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2703  
QY 141 HisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrParGluThrAsp 160  
|||||  
Db 2704 CATTTGGAGAGAGTCCCAACACTGTCAGCTGGGTTGAAAACGAGACTGCACAGAT 2763  
QY 161 ThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPhcGlnGln 180  
|||||  
Db 2764 ACAGAGATTAGAAATTTAGTGCATTTTGGAAAGAACCCCTGTAACAACTTCCAGCAG 2823  
QY 181 LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrPheAlaPheMetGlyValPhe 200  
|||||  
Db 2824 TTGAATTTGGCGGGAATGCTGTGAGCAGTATGATGATGCTGCTGCTGCTGCTGCTGCT 2883  
QY 201 GluAsnLeuLys 204  
|||||  
Db 2884 GAGAACTCTTAAG 2895

## RESULT 2

PCT-US02-21946A-14  
; Sequence 14, Application PC/TUS0221946A  
; GENERAL INFORMATION:  
; APPLICANT: Thomas Jefferson University  
; APPLICANT: Alnemri, Emdad S.  
; TITLE OF INVENTION: IPAF, AN ICE-PROTEASE ACTIVATING  
; TITLE OF INVENTION: FACTOR  
; FILE REFERENCE: 480140.4/77PC  
; CURRENT APPLICATION NUMBER: PCT/US02/21946A  
; CURRENT FILING DATE: 2002-05-24  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 3219  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US02-21946A-14

## Alignment Scores:

Pred. No.: 1e-108 Length: 3219  
Score: 1046.00 Matches: 204  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 1 Gaps: 0

US-09-697-089-2\_COPY\_762\_965 (1-204) x PCT-US02-21946A-14 (1-3219)

QY 1 LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAlaIle 20  
|||||  
Db 2428 TTGAAGAACCTTACAAAGCTCAATATGATTAACATTAAGATGAATGAAGAGATGCTATA 2487

QY 21 LysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeu 40  
|||||  
Db 2488 AACACTAGCTGAAGGCGCTGAAAAACCTGAGAGAGATGTGTTTATTTTCATTGACCCACTTG 2547  
QY 41 SerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysAsp 60  
|||||  
Db 2548 TCTGACATTTGGAGAGGAGGATGATTCATAGTCAGTCTCTGTCAGTGAACCTGTCAG 2607  
QY 61 LeuGluGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAla 80  
|||||  
Db 2608 CTGGAAGAAATTCATTAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2667  
QY 81 GlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu 100  
|||||  
Db 2668 CAGAATCTTCACAAATTTGGTCAAACTGACGACATTTGATTATTCAGAAAATTAACCTGGA 2727  
QY 101 LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeu 120  
|||||  
Db 2728 AAGAGTGGAAATGAAGCTCTTCATGAACTGACAGATGAACGCTGCTAGAACAGCTC 2787  
QY 121 ThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeuLys 140  
|||||  
Db 2788 ACCGCACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2847  
QY 141 HisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrParGluThrAsp 160  
|||||  
Db 2848 CATTTGGAGAGAGTCCCAACACTGTCAGCTGGGTTGAAAACGAGACTGCACAGAT 2907  
QY 161 ThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPhcGlnGln 180  
|||||  
Db 2908 ACAGAGATTAGAAATTTAGTGCATTTTGGAAAGAACCCCTGTAACAACTTCCAGCAG 2967  
QY 181 LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrPheAlaPheMetGlyValPhe 200  
|||||  
Db 2968 TTGAATTTGGCGGGAATGCTGTGAGCAGTATGATGATGCTGCTGCTGCTGCTGCTGCT 3027  
QY 201 GluAsnLeuLys 204  
|||||  
Db 3028 GAGAACTCTTAAG 3039

## RESULT 3

US-10-276-781-111  
; Sequence 111, Application US/10276781  
; GENERAL INFORMATION:  
; APPLICANT: Hyseed, Inc.  
; APPLICANT: Tang et al.  
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides  
; FILE REFERENCE: 21272-018 (785 contig)  
; CURRENT APPLICATION NUMBER: US/10/276,781  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 09/491,404  
; NUMBER OF SEQ ID NOS: 2018  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 111  
; LENGTH: 3545  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-276-781-111

## Alignment Scores:

Pred. No.: 1.14e-108 Length: 3545  
Score: 1046.00 Matches: 204  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-09-697-089-2\_COPY\_762\_965 (1-204) x US-10-276-781-111 (1-3545)

QY 1 LeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAlaIle 20  
|||||  
|||||

```
Db 2515 TTGAAGAACCTTACAAAGCTCATTAATGATTAACATTAAGATGAAGAGACAGATCTATA 2574
Oy 21 LysleuAlaGluGlyLeuLysAsnLeuLysMetCysLeuPheHisLeuThrHisLeu 40
Db 2575 AAACATGAGCGAAGGCGCTGAAAAAAGCTGAGAGAGATGTGTTATTCATTGACCACTTG 2634
Oy 41 SerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGluProCysasp 60
Db 2635 TCTGACATTTGGAGAGAGATGATTAACATAGTCAAGTCTCTCTCAAGTGAACCTGTGAC 2694
Oy 61 LeuGluGluIleGluLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeuAla 80
Db 2695 CTTGGAAGAAATCAATTAAGTCTCTGCTGCTGCTGCAAAATGACAGTGAATCTTACGT 2754
Oy 81 GluAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGlu 100
Db 2755 CAGAAATCTTACAAATTTGGTCAAACTGAGACATCTTGAATTTATCAGAAAAATTAACCTGGAA 2814
Oy 101 LysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeu 120
Db 2815 AAAGATGGAATGAAGACCTTCTATGACTGACAGAGATGAACGTCTAGAACACGCTC 2874
Oy 121 ThrAlaLeuMetLeuProTyrGlyCysAspValGlnGlySerLeuSerSerLeuLeuLys 140
Db 2875 ACCGACATGATGCTGCGCTGGGGCTGTGACGTGCAAGGACGCTGAGAGCCTGTGAAA 2934
Oy 141 HisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTyrArgLeuThrAsp 160
Db 2935 CATTTGGAGAGAGTCCACACACTGCTCAAGCTTGGGTGAAAAAACTGGAGACTCACAGAT 2994
Oy 161 ThrGluIleArgIleLeuGluValaPhePheGlyLysAsnProLeuLysAsnPhelGlnGln 180
Db 2995 ACAGAGATTAGAAATTTTATGATGATTTTGGAAAAAGAACCTCTGAAAAAACTCCAGCAG 3054
Oy 181 LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTyrLeuAlaPheMetGlyValaPhe 200
Db 3055 TTGAATTTGGCGGGAATTCGTGTGAGCAGTGTATGATGATGCTGCTCATGGGTATATT 3114
Oy 201 GluAsnLeuLys 204
Db 3115 GAGAAATCTTAAG 3126

RESULT 4
US-10-203-138A-4307
: Sequence 4307, Application US/10203138A
: GENERAL INFORMATION:
: APPLICANT: Molecular Dynamics, Inc.
: APPLICANT: Penn, Sharon G.
: APPLICANT: Rank, David R.
: APPLICANT: Hanzel, David K.
: APPLICANT: Chen, Wensheng
: TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
: TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN BT 474
: FILE REFERENCE: PB 0004 WO 8
: CURRENT APPLICATION NUMBER: US/10/203,138A
: CURRENT FILING DATE: 2002-08-02
: PRIOR APPLICATION NUMBER: US 60/180,312
: PRIOR FILING DATE: 04 February 2000 (04.02.00)
: PRIOR APPLICATION NUMBER: US 60/207,456
: PRIOR FILING DATE: 26 May 2000 (26.05.00)
: PRIOR APPLICATION NUMBER: US 09/632,366
: PRIOR FILING DATE: 03 August 2000 (03.08.00)
: PRIOR APPLICATION NUMBER: GB 24263,6
: PRIOR FILING DATE: 03 October 2000 (03.10.00)
: PRIOR APPLICATION NUMBER: US 60/236,359
: PRIOR FILING DATE: 27 September 2000 (27.09.00)
: PRIOR APPLICATION NUMBER: US 60/234,687
: PRIOR FILING DATE: 21 September 2000 (21.09.00)
: PRIOR APPLICATION NUMBER: US 09/608,408
: PRIOR FILING DATE: 30 June 2000 (30.06.00)
: NUMBER OF SEQ ID NOS: 15438
: SOFTWARE: Molecular Dynamics Sequence Listing Engine
: SEQ ID NO 4307
```

```
: LENGTH: 421
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: MAP TO AC011232.3
: OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.5
US-10-203-138A-4307

Alignment Scores:
Pred. No.: 8,11e-14 Length: 421
Score: 202.00 Matches: 38
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 19.31% Indels: 0
DB: 6 Gaps: 0

US-09-697-089-2_copy_762_965 (1-204) x US-10-203-138A-4307 (1-421)
Oy 167 GlyAlaPhePheGlyLysAsnProLeuLysAsnPhelGlnLeuAsnLeuAlaGlyAsn 186
Db 191 GGTGCAATTTTGGAAAAAGACCTCTGAAAAAATTCACAGCATGTAATTTGGCGGGAAT 240
Oy 187 ArgValSerSerAspGlyTyrLeuAlaPheMetGlyValPheGluAsnLeuLys 204
Db 241 CCGTGACACATGATGATGATGCTTCCCTTCATGGGTATATTGAGAAATCTTAAG 294

RESULT 5
US-10-161-493-5
: Sequence 5, Application US/10161493
: GENERAL INFORMATION:
: APPLICANT: Anderson, David W
: APPLICANT: Zernhusen, Bryan D
: APPLICANT: Li, Li
: APPLICANT: Zhong, Mel
: APPLICANT: Casman, Stacie J
: APPLICANT: Gerlach, Valerie
: APPLICANT: Shinkets, Richard A
: APPLICANT: Gorman, Linda
: APPLICANT: Pena, Carol EA
: APPLICANT: Kekuda, Ramesh
: APPLICANT: Paturajan, Meera
: APPLICANT: Spytek, Kimberly A
: APPLICANT: Rastelli, Luca
: APPLICANT: MacDougall, John R
: APPLICANT: Taupier Jr., Raymond J
: APPLICANT: Guo, Xiaojia Sasha
: APPLICANT: Miller, Charles E
: APPLICANT: Shenoy, Suresh G
: APPLICANT: Hjal, Tord
: APPLICANT: Voss, Edward Z
: APPLICANT: Boldog, Ferenc L
: APPLICANT: Malyankar, Uriel M
: APPLICANT: Padigaru, Muralidhara
: APPLICANT: Ji, Weizhen
: APPLICANT: Smithson, Glenda
: APPLICANT: Edinger, Shlomit R
: APPLICANT: Miller, Isabelle
: APPLICANT: Ellerman, Karen
: TITLE OF INVENTION: Novel Antibodies that Bind to Antigenic Polypeptides, Nucleic
: TITLE OF INVENTION: Acids Encoding the Antigens, and Methods of Use
: FILE REFERENCE: 21402-377A
: CURRENT APPLICATION NUMBER: US/10/161,493
: CURRENT FILING DATE: 2002-06-03
: PRIOR APPLICATION NUMBER: 60/295,607
: PRIOR FILING DATE: 2001-06-04
: PRIOR APPLICATION NUMBER: 60/337,524
: PRIOR FILING DATE: 2001-11-16
: PRIOR APPLICATION NUMBER: 60/296,404
: PRIOR FILING DATE: 2001-06-06
: PRIOR APPLICATION NUMBER: 60/296,418
: PRIOR FILING DATE: 2001-06-06
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PRIOR APPLICATION NUMBER: 60/296,575  
PRIOR FILING DATE: 2001-06-07  
PRIOR APPLICATION NUMBER: 60/359,151  
PRIOR FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: 60/297,414  
PRIOR FILING DATE: 2001-06-11  
PRIOR APPLICATION NUMBER: 60/297,573  
PRIOR FILING DATE: 2001-06-12  
PRIOR APPLICATION NUMBER: 60/341,143  
PRIOR FILING DATE: 2001-12-14  
PRIOR APPLICATION NUMBER: 60/297,567  
PRIOR FILING DATE: 2001-06-12  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 299  
SEQ ID NO: 5  
LENGTH: 2142  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (34)..(2077)  
US-10-161-493-5

Alignment Scores:  
Pred. No.: 0.000323 Length: 2142  
Score: 126.00 Matches: 59  
Percent Similarity: 40.97% Conservative: 34  
Best Local Similarity: 25.99% Mismatches: 86  
Query Match: 12.05% Indels: 48  
DB: Gaps: 9

US-09-697-089-2\_COPY\_762\_965 (1-204) x US-10-161-493-5 (1-2142)

QY 6 Lysleuilemetaspasnillelymetasnlu----- 16  
DB 1363 AAGTTGAGTGTTCAGCCGATTTCAAACAACACTGGAGAAATGCAACTTGTGGCAGCC 1422  
QY 17 -----gluaspaiailelyleuaglulyleuysasnleuylsylemetcysleu 34  
DB 1423 AGCTGTGAGCAGCTAGCCTTGTCTCCACACAGATCCAAACAGACGATGATGCTG 1482  
QY 35 PhehtisleuthrhisleuSeraspilleglyglulylemetasptryllevallyserleu 54  
DB 1483 ---GGATTTAATCGGCTCCAGAT---GATGGCAATAAGCTATGTGTGGCGCCCTG 1533  
QY 55 SersegiuprocysaspLeuGlulilegInleuValserCysLeuSerAlasn 74  
DB 1534 ACTCAGCCCAAGTGTGCTTAGAGAGACTGAGCTCTGTTTGCACACTGGCAGACCC 1593  
QY 75 AlavallysileleuAlaglnasnleuHisasnleuVallyLeuSerileleuaspLeu 94  
DB 1594 GCTTGCAAGCACTTGCTGATGCTCTCTCGAGAAACAGACAGCCTGACACCTGATCTG 1653  
QY 95 SerGlusantyrleuGlulysaspGlyasnGlnalaleuHisGlnleuileaspArgmet 114  
DB 1654 AGCAAGAAGACCGCTGAGAGAGAGAGAGTCAAGTTCTGTGTGGCGCCCA 1713  
QY 115 AsnVallleuGlulileuThrAlaleuMetleuProtpgLyCysAspValGln----- 132  
DB 1714 GAT-----GGTAACCTTCAGAGCCTGAGTTGTCA---GGTTGTTCTTTACAGAGAG 1764  
QY 133 -----glySerleuSerleuLeuylshisLeuGlulualProGlnleu----- 148  
DB 1765 GCGTGTGAGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1824  
QY 149 -----Vallys----- 150  
DB 1825 GGAGAAATGATCTTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1884  
QY 151 -----LeuGlyleuLysasnTrpArgleuThrAspThrGlnleuArgyle 165  
DB 1885 CGTGCAATTGACACACCTTGCTGGCGAATGCAATCTGACAACTGCTGCTGCCAGCAT 1944

QY 166 LeuGlyAlaPhehegilylsasnProleuylsasnPheGlnInleuasnleuAlagly 185  
DB 1945 CTCCT 1998  
QY 186 AsnArgylaserSeraspGly 192  
DB 1999 AATGAATGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2019

## RESULT 6

US-10-194-163-263  
Sequence 263, Application US/10194163

GENERAL INFORMATION:

APPLICANT: Ross, Bruce Carter

TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS POLYNUCLEOTIDES

NUMBER OF SEQUENCES: 1120

CORRESPONDENCE ADDRESSES:

ADDRESSEE: MORRISON & FOERSTER

STREET: 755 PAGE MILL ROAD

CITY: PALO ALTO

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows

SOFTWARE: FastSeq for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/194,163

FILING DATE: 04-Nov-2002

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Basu, Shantanu

REGISTRATION NUMBER: 43,318

REFERENCE/DOCKET NUMBER: 529282000101

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-813-5995

TELEFAX: 650-494-0792

TELEX: 706141

INFORMATION FOR SEQ ID NO: 263

SEQUENCE CHARACTERISTICS:

LENGTH: 8722 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: UNKNOWN

ORIGINAL SOURCE:

ORGANISM: PORPHYROMONAS GINGIVALIS

FEATURE:

NAME/KEY: misc.feature

LOCATION: 1...8722

SEQUENCE DESCRIPTION: SEQ ID NO: 263

US-10-194-163-263

Alignment Scores:  
Pred. No.: 0.00899 Length: 8722  
Score: 120.50 Matches: 55  
Percent Similarity: 42.92% Conservative: 45  
Best Local Similarity: 23.61% Mismatches: 72  
Query Match: 11.52% Indels: 61  
DB: Gaps: 8

US-09-697-089-2\_COPY\_762\_965 (1-204) x US-10-194-163-263 (1-8722)

QY 1 Leuysasnleuthrhisleuilemetaspasnillelymetasnluaglulaspalaile 20  
DB 2293 CTGGAAGCTCTCAGCTTGTCTTAACAAGCTTCGTCTAAGAGTACCAAGATCAGTAACTA 2352  
QY 21 LysleuAlagluGlyleuLysasnleuLysMetCysleupe----- 35

```
Dh 2353 GAGGGCTGTAGTCTCACCCTCGTAAACAATTCTCTCTCCGATTAACAATCACT 2412
Qy 36 -----HisLeuThrHisLeuSerAspIleGlyGlnGlyMetAspTyr 49
Dh 2413 AAGCTAGAGGCTGTGGAACGCTCTCCTCGTTAGCGGAGCTT-----TAT 2457
Qy 50 ILeValysSerLeuSerGlnProCysAspLeuGlnIle---GlnLeuValSer 68
Dh 2458 CTTTGGTATACCAATATCAGTAACGTAGAGGCTGTGGAACGCTCAGCTCTTACCAACG 2517
Qy 69 CysCysLeuSerAlaAsnAlaValLysIleLeuAlaGlnAsnLeuHisAsnLeuValLys 88
Dh 2518 CTTGACATGATACCAATATCCGTAAGCTG---GAGGGCTGTGGAACGCTCTCAGCTCC 2574
Qy 89 LeuSerIleLeuAspLeuSerGlnAsnTyrIleuGlnLys----- 101
Dh 2575 TTACCAACGCTTGAATATCGGGTAAACCAATCCGTAAGCTAGAGGCTGTGGAACGCTCTC 2634
Qy 102 -----AspGlyAsnGln 105
Dh 2635 ACTTCGTTAACAAAGCTTCTCTTAAGAATACCAATCACTAAGCTAGAGGCTGTGGA 2694
Qy 106 AlaLeuHisGlnLeu-----IleAspArgMetAsnVal 116
Dh 2695 CGTCTCAGCTCTTACCAACGCTTGAACCTATCGGGTAAACCAATCCGTAAGCTGAGGGT 2754
Qy 117 LeuGlnGlnLeuThrAlaLeuMetLeuProTrrpGlyCysAspValGlnGlySerLeuSer 136
Dh 2755 CTGGAACGCTCTCAGCTCTCTTACCAACG-----CTTGAACGCTCGGTAAACCAATC 2805
Qy 137 SerLeuLeuLysHisLeuGlnIleValProGlnLeuValLysGlnLysAsnTrrp 156
Dh 2806 AGTAAGCTAGAGGCTGTGGAACGCTCTCTCTCGTTAACAAAGCTTCTCTTAAGAATAC 2865
Qy 157 ArgLeuThrAspThrGlnIleArgIleLeuGlnAlaPhePheGlyLysAsnProLeuLys 176
Dh 2866 CAGATCAGCTAAACTAGAG-----GGCTGTGGAACGCTCTCACC 2901
Qy 177 AsnPheGlnGlnLeuAsnLeuAlaGlyAsnArgValSer 189
Dh 2902 TCGCTAACAAACCTTCTCTCTCGATTAACAATCACT 2940

RESULT 7
US-09-724-676-19376
; Sequence 19376, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19376
; LENGTH: 916
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-19376

Alignment Scores:
Pred. No.: 0.000843 Length: 916
Score: 118.00 Matches: 41
Percent Similarity: 45.96% Conserves: 33
Best Local Similarity: 25.47% Mismatches: 81
Query Match: 11.28% Indels: 6
Gaps: 4

US-09-697-089-2_COPY_762_965 (1-204) x US-09-724-676-19376 (1-916)
Qy 41 SerAspIleGlyGlu---GlyMetAspTyrIleValLysSerLeuSerGlnProCys 59
Dh 353 AACGAGCTGGCGATGTCGCGTGCATTCGCTCCAGGGCGTGCAGACCCCTCTCTGC 412
```

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Qy 60 AspleuGlnGlnIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu 79
Dh 413 AAGATCCGAAAGCTGAGCTCCAGAACCTGCTCGAGCGGGGCGCGTGGGGGCTCTG 472
Qy 80 AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGlnAsnTyrLeu 99
Dh 473 TCCAGCACACTAACCCACCCTGCCACCTGCAGAGCTGACCTTCAGGACCACTCTTG 532
Qy 100 GlnLysAspGlyAsnGlnAlaLeuHisGlu---LeuIleAspArgMetAsnValLeuGln 118
Dh 533 GGGGATGGGCGCTGCAGACTCTGTGCGAAGACTCTCGAACCCCACTGCCGCTGGAA 592
Qy 119 GlnLeuThrAlaLeuMetLeuProTrrpGlyCysAspValGlnGlySerLeuSerLeu 138
Dh 593 AAG-----CTGCACCTGAGATTCGACCTCTGCGCTGCCAGCTGGAGCCCTG 643
Qy 139 LeuLysHisLeuGlnGlnIleValProGlnLeuValLysLeuGlnLysAsnTrrpArgLeu 158
Dh 644 GCCTCCGCTCAGAGGCGCCAGCCGAGCTTCAAGAGCTCAGCGTTAGCAACAGACATC 703
Qy 159 ThrAspThrGlnIleArgIleLeuGlnAlaPhePheGlyLysAsnProLeuLysAsnPhe 178
Dh 704 AATGAGCTGGCGCTCGTGTCTGTGCGCAGGCTGGAAGACTCCCTCCAG---CTG 760
Qy 179 GlnGlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrrpLeuAlaPheMetGly 198
Dh 761 GAGCGCTCAAGCTGTGAGAGCTGGCGGTGTGACATCAGCAACTGCCGGAGCTGTGGCG 820
Qy 199 Val 199
Dh 821 ATT 823

RESULT 8
US-09-724-676A-19376
; Sequence 19376, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19376
; LENGTH: 916
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-19376

Alignment Scores:
Pred. No.: 0.000843 Length: 916
Score: 118.00 Matches: 41
Percent Similarity: 45.96% Conserves: 33
Best Local Similarity: 25.47% Mismatches: 81
Query Match: 11.28% Indels: 6
Gaps: 4

US-09-697-089-2_COPY_762_965 (1-204) x US-09-724-676A-19376 (1-916)
Qy 41 SerAspIleGlyGlu---GlyMetAspTyrIleValLysSerLeuSerGlnProCys 59
Dh 353 AACGAGCTGGCGATGTCGCGTGCATTCGCTCCAGGGCGTGCAGACCCCTCTCTGC 412
Qy 60 AspleuGlnGlnIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu 79
Dh 413 AAGATCCGAAAGCTGAGCTCCAGAACCTGCTCCAGAGGCGCGCTGCGGGGCTCTG 472
Qy 80 AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSerGlnAsnTyrLeu 99
Dh 473 TCCAGCACACTAACCCACCCTGCCACCTGCAGAGCTGACCTTCAGGACCACTCTTG 532
Qy 100 GlnLysAspGlyAsnGlnAlaLeuHisGlu---LeuIleAspArgMetAsnValLeuGln 118
Dh 533 GGGGATGGGCGCTGCAGACTCTGTGCGAAGACTCTCGAACCCCACTGCCGCTGGAA 592
Qy 119 GlnLeuThrAlaLeuMetLeuProTrrpGlyCysAspValGlnGlySerLeuSerLeu 138
Dh 593 AAG-----CTGCACCTGAGATTCGACCTCTGCGCTGCCAGCTGGAGCCCTG 643
Qy 139 LeuLysHisLeuGlnGlnIleValProGlnLeuValLysLeuGlnLysAsnTrrpArgLeu 158
Dh 644 GCCTCCGCTCAGAGGCGCCAGCCGAGCTTCAAGAGCTCAGCGTTAGCAACAGACATC 703
Qy 159 ThrAspThrGlnIleArgIleLeuGlnAlaPhePheGlyLysAsnProLeuLysAsnPhe 178
Dh 704 AATGAGCTGGCGCTCGTGTCTGTGCGCAGGCTGGAAGACTCCCTCCAG---CTG 760
Qy 179 GlnGlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrrpLeuAlaPheMetGly 198
Dh 761 GAGCGCTCAAGCTGTGAGAGCTGGCGGTGTGACATCAGCAACTGCCGGAGCTGTGGCG 820
Qy 199 Val 199
Dh 821 ATT 823
```

Dh 533 GGGATCGGGGCTGCAGCTGCTCGCAGAGACTCTGCAGCCCGCCAGTCCCTGGA 592  
Qy 119 Glnleuthralaleumelleuprotprglycysaspyalglnglyserleuserleu 138  
Dh 593 AAG-----CTGCAGCTGGAGTATTGGACGCTCTCGGTGGCAGCTGGAGCCCTG 643  
Qy 139 LeulyshtleugluvalProglneulvallylsleuglyleuLysasnTTPargleu 158  
Dh 644 GCGTCCTGCTCAGGCGCAAGCCGACTTCAGAGGCTCAGGTTAGCAACACGACATC 703  
Qy 159 ThrspthrgluileargilleuglyalaphhehglylsasnProleuLysasPhe 178  
Dh 704 AATAGGCTGGCGTCCGTGCTGCTGCCAGGCTGAGAGCTCCCTGCGAG---CTG 760  
Qy 179 GlnleuhsneulaleuAglasnarValserSeraspolytrpleuAlaphemercly 198  
Dh 761 GAGCGCTCAAGCTGGAGAGCTGGGTGTGACATCAGACAACCTCCGGAGCTGTGGGC 820  
Qy 199 Val 199  
Dh 821 ATT 823

## RESULT 9

US-09-724-676-19370  
; Sequence 19370, Application US/09724676  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724.676  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 19370  
; LENGTH: 945  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-676-19370

Alignment Scores:  
Pred. No.: 0.00879 Length: 945  
Score: 118.00 Matches: 41  
Percent Similarity: 45.96% Conservative: 33  
Best Local Similarity: 25.47% Mismatches: 81  
Query Match: 11.28% Indels: 6  
Gaps: 4

US-09-697-089-2\_COPY\_762\_965 (1-204) x US-09-724-676-19370 (1-945)

Qy 41 Seraspilleglylu---glymetaspyrlllevalysserleuserSerGIuProCys 59  
Dh 382 AACGAGCTGGCGGCGATGCGGCTGATTCGCTGCCAGGCGCTGCAGACCCCTCCCTGC 441  
Qy 60 AspleugluuileglnleuValserCysleuserAlasnaVallylsleu 79  
Dh 442 AAGATCCAGAACTGCAGACTGCCAAGACTGCTGAGCGGGCGGCTGGGGCTCTG 501  
Qy 80 AlaglnasnleuhsasnleuVallylsleuserlleuhspleuserSerGIuasnTTParg 99  
Dh 502 TCCAGCAGCTACGACCCCTGCCACCCCTGCAGAGCTGCACCTCAGAGCAACTCTTG 561  
Qy 100 GlulysaspyllyasnGlualaleuHsGlu---leuileasparGmetasnaValleuGlu 118  
Dh 562 GGGATCGGGGCTGCAGCTGCTGCGAAGAGACTCTCTGAGCCCCCGGCGGCTGGA 621  
Qy 119 Glnleuthralaleumelleuprotprglycysaspyalglnglyserleuserleu 138  
Dh 622 AAG-----CTGCAGCTGGAGTATTGGACGCTCTCGGTGGCAGCTGGAGCCCTG 672  
Qy 139 LeulyshtleugluvalProglneulvallylsleuglyleuLysasnTTPargleu 158  
Dh 673 GCGTCCTGCTCAGGCGCAAGCCGACTTCAGAGGCTCAGGTTAGCAACACGACATC 732

Qy 159 ThrspthrgluileargilleuglyalaphhehglylsasnProleuLysasPhe 178  
Dh 733 AATAGGCTGGCGTCCGTGCTGCTGCCAGGCTGAGAGCTCCCTGCGAG---CTG 789  
Qy 179 GlnleuhsneulaleuAglasnarValserSeraspolytrpleuAlaphemercly 198  
Dh 790 GAGCGCTCAAGCTGGAGAGCTGGGTGTGACATCAGACAACCTCCGGAGCTGTGGGC 849  
Qy 199 Val 199  
Dh 850 ATT 852

## RESULT 10

US-09-724-676A-19370  
; Sequence 19370, Application US/09724676A  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724.676A  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 19370  
; LENGTH: 945  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-676A-19370

Alignment Scores:  
Pred. No.: 0.00879 Length: 945  
Score: 118.00 Matches: 41  
Percent Similarity: 45.96% Conservative: 33  
Best Local Similarity: 25.47% Mismatches: 81  
Query Match: 11.28% Indels: 6  
Gaps: 4

US-09-697-089-2\_COPY\_762\_965 (1-204) x US-09-724-676A-19370 (1-945)

Qy 41 Seraspilleglylu---glymetaspyrlllevalysserleuserSerGIuProCys 59  
Dh 382 AACGAGCTGGCGGCGATGCGGCTGATTCGCTGCCAGGCGCTGCAGACCCCTCCCTGC 441  
Qy 60 AspleugluuileglnleuValserCysleuserAlasnaVallylsleu 79  
Dh 442 AAGATCCAGAACTGCAGACTGCCAAGACTGCTGAGCGGGCGGCTGGGGCTCTG 501  
Qy 80 AlaglnasnleuhsasnleuVallylsleuserlleuhspleuserSerGIuasnTTParg 99  
Dh 502 TCCAGCAGCTACGACCCCTGCCACCCCTGCAGAGCTGCACCTCAGAGCAACTCTTG 561  
Qy 100 GlulysaspyllyasnGlualaleuHsGlu---leuileasparGmetasnaValleuGlu 118  
Dh 562 GGGATCGGGGCTGCAGCTGCTGCGAAGAGACTCTCTGAGCCCCCGGCGGCTGGA 621  
Qy 119 Glnleuthralaleumelleuprotprglycysaspyalglnglyserleuserleu 138  
Dh 622 AAG-----CTGCAGCTGGAGTATTGGACGCTCTCGGTGGCAGCTGGAGCCCTG 672  
Qy 139 LeulyshtleugluvalProglneulvallylsleuglyleuLysasnTTPargleu 158  
Dh 673 GCGTCCTGCTCAGGCGCAAGCCGACTTCAGAGGCTCAGGTTAGCAACACGACATC 732  
Qy 159 ThrspthrgluileargilleuglyalaphhehglylsasnProleuLysasPhe 178  
Dh 733 AATAGGCTGGCGTCCGTGCTGCTGCCAGGCTGAGAGCTCCCTGCGAG---CTG 789  
Qy 179 GlnleuhsneulaleuAglasnarValserSeraspolytrpleuAlaphemercly 198  
Dh 790 GAGCGCTCAAGCTGGAGAGCTGGGTGTGACATCAGACAACCTCCGGAGCTGTGGGC 849  
Qy 199 Val 199  
Dh 199 Val 199







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OY 100 GluLysAspGlyAsnGluAlaLeuHISGlu---LeuIleAspArgMetAsnValLeuGlu 118
Db 749 GGGGATCGGGGCTGCAAGCTGCTGCGAAGACTCTGACCCCGCCAGTCCGCGCTGGAA 808
OY 119 GlnLeuThrAlaLeuMetLeuProTrrpGlyCysAspValGlnGlySerLeuSerSerLeu 138
Db 809 AAG-----CTGCAGCTGAGTATTCACAGCTCTCGGCTGCCAGCTGCCAGGCCCTG 859
OY 139 LeuLysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTrrpArgLeu 158
Db 860 GCCTCCGCTCAGGCGCCAGCCGACTTCAGAGAGCTCAGCGTTAGCAACAACGACATC 919
OY 159 ThrAspThrGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnPhe 178
Db 920 AATGAGCTGGCGCTGCTGTGCTGTGCCAGGCGCTGAGAGACTCCCGCTGCCAG---CTG 976
OY 179 GlnGlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrrpLeuAlaPheMetGly 198
Db 977 GAGGCGCTCAAGCTGAGAGCTGCGGTGTGACATCAGACACTGCCGGGAGCTGTGCGGC 1036
OY 199 Val 199
Db 1037 ATT 1039
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Job time : 195.895 secs

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